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43804

SEARCH REQUEST FORM

Access DB#

CRFE

Scientific and Technical Information Center

Requester's Full Name: Natalie Davis Examiner #: 78462 Date: 6-4-01
 Art Unit: 1642 Phone Number 308-6410 Serial Number: 09/587574
 Mail Box and Bldg/Room Location: 9E12 CM 9B09 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: 92-97

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10

Also search conductive for diagnosis + treatment of tumors. see claims 1, 6, + 21

Search claim 15.

Point of Contact:
 Beverly Shears
 Technical Info. Specialist
 CM1 12C14 Tel: 308-4994

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	Type of Search	Vendors and cost where applicable
Searcher: <u>Beverly 24994</u>	NA Sequence (#) _____	STN <u>✓</u> _____
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Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>06-11-01</u>	Litigation <u>1</u>	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) <u>CGN</u>

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09/587574

FILE 'REGISTRY' ENTERED AT 11:09:26 ON 11 JUN 2001
E CONDUCTINE/CN

FILE 'CAPLUS' ENTERED AT 11:09:46 ON 11 JUN 2001

L1 0 S CONDUCTINE

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:10:14 ON 11 JUN 2001

L2 6 S L1

L3 6 DUP REM L2 (0 DUPLICATES REMOVED)

L3 ANSWER 1 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1996-024402 JAPIO
TITLE: GAME BALL PASSING SENSOR
INVENTOR: YOSHIKAWA TOSHISUKE
PATENT ASSIGNEE(S): KYOWA GIKEN KK, JP (CO)
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 08024402	A	19960130	Heisei	(6) A63F007-02

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1994-169178 19940721

ORIGINAL: JP06169178 Heisei

SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 96, No. 1

AN 1996-024402 JAPIO

AB PURPOSE: To prevent an erroneous operation by electromagnetic wave
or external light, and precisely detect the passing of game ball by
making an operating piece pushed into a switch housing part when the
ball passes the through-hole of a switch case, thereby a switch is
brought into non-conductive state and the passing of the
ball is detected.

CONSTITUTION: When no game ball passes a through-hole 30, one end of
an operating piece 70 supported in the inner part of a switch
housing part 40 is in the state capable of protruding into the
through-hole 30, and the energizing force of a torsion spring 60
acts on the free end part on the other end to energize the operating
piece 70 in the protruding direction. Both ends of the torsion
spring 60 come into contact with a fixed pin 54 and a contact pin 53
in this state to hold the conductive state between the connecting
terminals 51, 52 of a base 50. When a game ball passes the
through-hole 30, the operating piece 70 is pushed against the
energizing force of the torsion spring 60. Thus, one end of the
torsion spring 60 is pushed in and separated from the contact pin 53
to bring the connecting terminals 51, 52 into the non-conductive

Searcher : Shears 308-4994

state, thereby the passing of the game ball can be detected.

L3 ANSWER 2 OF 6 MEDLINE
 ACCESSION NUMBER: 90181913 MEDLINE
 DOCUMENT NUMBER: 90181913 PubMed ID: 2560672
 TITLE: [Sodium conductin of the human brain: purification and functional characterization].
 La conductine au sodium du cerveau humain: purification et caracterisation fonctionnelle.
 AUTHOR: Materne-De Rycker C
 SOURCE: BULLETIN ET MEMOIRES DE L ACADEMIE ROYALE DE MEDECINE DE BELGIQUE, (1989) 144 (8-9) 426-33.
 Journal code: BOX; 7608462. ISSN: 0377-8231.
 PUB. COUNTRY: Belgium
 LANGUAGE: Journal; Article; (JOURNAL ARTICLE)
 FILE SEGMENT: French
 ENTRY MONTH: Priority Journals
 ENTRY DATE: 199004
 Entered STN: 19900601
 Last Updated on STN: 19900601
 Entered Medline: 19900426

AB A sodium channel enriched preparation was obtained from human brain. Human sodium channel appeared as a heterocomplex peptide alpha beta 1 beta 2. Functional properties of the protein were maintained since, after reconstitution into liposomes, ion fluxes were sensitive to sodium channel specific toxins and to membrane potential. Moreover, the reconstituted protein showed a well defined ionic selectivity.

L3 ANSWER 3 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 1988-347509 [49] WPIDS
 DOC. NO. NON-CPI: N1988-263366
 TITLE: Semiconductor shift register in memory output state
 - has two conductive type transistor connected in series between power supply terminal and node.
 DERWENT CLASS: U14
 INVENTOR(S): NAKAGAWA, K; TAKEUCHI, Y
 PATENT ASSIGNEE(S): (TOKE) TOSHIBA KK
 COUNTRY COUNT: 5
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 293808	A	19881207	(198849)*	EN	15
R: DE FR GB					
JP 63304494	A	19881212	(198904)		
US 4856034	A	19890808	(198939)		14
EP 293808	B1	19930929	(199339)	EN	16

Searcher : Shears 308-4994

R: DE FR GB
DE 3884460 G 19931104 (199345)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 293808	A	EP 1988-108632	19880530
JP 63304494	A	JP 1987-139405	19870603
US 4856034	A	US 1988-199914	19880527
EP 293808	B1	EP 1988-108632	19880530
DE 3884460	G	DE 1988-3884460	19880530
		EP 1988-108632	19880530

FILING DETAILS:

PATENT NO	KIND	PATENT NO
DE 3884460	G Based on	EP 293808

PRIORITY APPLN. INFO: JP 1987-139405 19870603

AN 1988-347509 [49] WPIDS

AB EP 293808 A UPAB: 19930923

The circuit has a logic circuit (12) with two inputs connected to receive a control clock signal (Phi G) and an input signal (Vin) a two ~~conductine~~ type transistors (P11 P12) are connected in series between a power supply terminal and a node. The first transistor (P11) has a gate connected to receive an output signal of the logic circuit. The other transistor (P12) has a gate connected to receive the control clock signal.

A third transistor (N11) of a different conductive type connects the first node and the second power supply terminal together.

The transistor gate is connected to receive the output signal of the logic circuit.

USE/ADVANTAGE - Latch circuit or swift register in the output stage of the memory.

3

ABEQ US 4856034 A UPAB: 19930923

The semiconductor integrated circuit consists of a three-valued logic circuit connected to receive an output signal of a logic circuit to receive at one input a control clock signal and at the other input an input signal. A flip-flop circuit is composed of a clocked inverter to receive the output signal of the three-valued logic circuit, and another inverter.

ABEQ EP 293808 B UPAB: 19931123

A semiconductor integrated circuit, comprising: a logic circuit (12) consisting of a NOR gate (72) or a NAND gate (82) and having a first

and a second input connected to receive a control clock signal (G) and an input signal (Vin), respectively; first and second transistors (P11, P12) of a first conductivity type connected in series between a first power supply terminal (Vcc) and a first node (1), said first transistor (P11) having a gate connected to receive an output signal of said logic circuit, and said second transistor (P12) having a gate connected to receive the control clock signal; a third transistor (N11) of a second conductivity type connected between said first node and a second power supply terminal (Vss) and having a gate connected to receive the output signal of said logic circuit; fourth and fifth transistors (P13, P14) of the first conductivity type connected in series between said first power supply terminal and a second node (2) connected to said first node, said fourth transistor (P14) having a gate connected to receive the output signal of said logic circuit, and said fifth transistor (P13) having a gate connected to a third node (3); sixth and seventh transistors (N14, N13) of the second conductivity type connected in series between said second power supply terminal and said second node, said sixth transistor (N14) having a gate connected to receive the clock signal, and said seventh transistor (N13) having a gate connected to said third node; an eighth transistor (P15) of the first conductivity type connected between said third node and said first power supply terminal and having a gate connected to said second node; and a ninth transistor (N15) of the second conductivity type connected between said third node and said second power supply terminal, and having a gate connected to said second node; an output signal (Vout) of said semiconductor integrated circuit being taken from at least one of said second node and said third node.

Dwg.1/10

L3 ANSWER 4 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 1978-A8315A [04] WPIDS
 TITLE: Insulated splice and terminal - is made from crimped composite strip of non-conductive and electrically conducting materials.
 DERWENT CLASS: V04
 INVENTOR(S): FISCHER, E M; MEISINGER, W R; ZAHN, I
 PATENT ASSIGNEE(S): (GEST-N) GEN STAPLE CO
 COUNTRY COUNT: 1
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 4067105	A	19780110	(197804)*		

PRIORITY APPLN. INFO: US 1973-335417 19730223; US 1974-537532

Searcher : Shears 308-4994

19741230; US 1976-711604 19760804

AN 1978-A8315A [04] WPIDS

AB US 4067105 A UPAB: 19930901

An elongated layer of non-conductive materials is adhered to an elongated layer of electrically conductive material so as to form a composite supply strip. A predetermined length is severed and crimped about the elements to be joined until the electrically conductive material is in electrical contact with the elements and so that the non-conductive material forms an outer insulated layer enclosing the splice or at least a portion of the terminal.

In a pref. method there is further step of causing the non-conductive material of the splice to "flow" whereby a resultant sealed splice is produced which is impervious to moisture and other contaminants. PRef. the non-conductive material is a thermoplastic resin and the conductive material is brass.

L3 ANSWER 5 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1977-115854 JAPIO

TITLE: ELECTRICALLY CONDUCTIVE RESIN AND
INTERMEDIATES AND ELECTRICALLY CONDUCTIVE COATED
PAPERS

INVENTOR: JIYOSEFU RII GAANAA

PATENT ASSIGNEE(S): DOW CHEM CO:THE, US (CO 000723)

PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 52115854	A	19770928	Showa	(2) C08L025-06

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1977-29130 19770316

ORIGINAL: JP52029130 Showa

PRIORITY APPLN. INFO.: US1976 668335 19760319

AN 1977-115854 JAPIO

L3 ANSWER 6 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1977-019984 JAPIO

TITLE: MANUFACTURE PROCESS FOR A ISOLATION LAYER USED
TO MAKE A SEMICONDUCTOR ELEMENT

INVENTOR: KOMATSU RYOSAKU; HARUHARA YOSHIO

PATENT ASSIGNEE(S): NIPPON TELEGR & TELEPH CORP <NTT>, JP (CO
000422)

PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC

09/587574

JP 52019984 A 19770215 Showa (2) H01L021-76

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1975-96053 19750807

ORIGINAL: JP50096053 Showa

SOURCE: PATENT ABSTRACTS OF JAPAN, Unexamined
Applications, Section: E, Sect. No. 34, Vol. 1,
No. 851, P. 1733 (19770809)

AN 1977-019984 JAPIO

AB PURPOSE: To pour p type ion to the N type semiconductor substrate an
order to make a p type **conductine** area as a isolation
layer. In this way, we make plural isolation layers at the same time
with a desired size and high precision, saving the manufacture work.

FILE 'REGISTRY' ENTERED AT 11:14:12 ON 11 JUN 2001
E CONDUCTIN/CN

L4 2 SEA ABB=ON PLU=ON ("CONDUCTIN (HUMAN FETAL BRAIN
REDUCED)"/CN OR "CONDUCTIN (HUMAN)"/CN)

FILE 'CAPLUS' ENTERED AT 11:14:41 ON 11 JUN 2001

L5 25 SEA ABB=ON PLU=ON L4 OR CONDUCTIN

L6 15 SEA ABB=ON PLU=ON L5 AND (TUMOUR OR TUMOR OR NEOPLAS?
OR CANCER? OR CARCIN?)

L6 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2001:208094 CAPLUS

DOCUMENT NUMBER: 134:247261

TITLE: Agents for treating human diseases, especially
for treating **tumors** such as colon
cancers and melanomas or for
regenerating tissue and promoting hair growth
INVENTOR(S): Birchmeier, Walter; Von Kries, Jens-peter
PATENT ASSIGNEE(S): Max-Delbruck-Centrum fur Molekulare Medizin,
Germany

SOURCE: PCT Int. Appl., 28 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001019353	A2	20010322	WO 2000-DE3104	20000907
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,				

Searcher : Shears 308-4994

09/587574

LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

DE 19944404 A1 20010322 DE 1999-19944404 19990916

PRIORITY APPLN. INFO.: DE 1999-19944404 A 19990916

AB The invention relates to agents for treating human diseases which are based on substances that specifically influence the binding of .beta.-catenin with LEF-1/TCF transcription factors, APC or conductin/axin. The invention particularly relates to the identification and use of hydrophobic pockets on the mol. surface in the proximity of the essential binding points for the binding partners of .beta.-catenin with the aim of optimizing these substances. The invention also relates to the use of the substances, preferably for treating tumors, e.g. colon cancers and melanomas, or for regenerating tissue and promoting hair growth.

L6 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:735507 CAPLUS

DOCUMENT NUMBER: 134:28066

TITLE: Mutations in AXIN2 cause colorectal cancer with defective mismatch repair by activating .beta.-catenin/TCF signaling

AUTHOR(S): Liu, Wanguo; Dong, Xiangyang; Mai, Ming; Seelan, Ratnam S.; Taniguchi, Ken; Krishnadath, Kausilia K.; Halling, Kevin C.; Cunningham, Julie M.; Qian, Chiping; Christensen, Eric; Roche, Patrick C.; Smith, David I.; Thibodeau, Stephen N.

CORPORATE SOURCE: Div. of Experimental Pathol., Dep. of Lab. Med. and Pathol., Mayo Clinic and Mayo Med. Sch., Rochester, MN, USA

SOURCE: Nat. Genet. (2000), 26(2), 146-147
CODEN: NGENEC; ISSN: 1061-4036

PUBLISHER: Nature America Inc.

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB Colorectal cancer (CRC) with defective DNA mismatch repair (MMR) is assocd. with alterations in one of several DNA MMR genes. Here we show that AXIN2 encoding a Wnt signaling component, is mutated in 11 of 45 CRC with defective MMR. We tested the functional importance of AXIN2 mutations in the development of CRC with defective MMR in a TCF reporter assay. Our findings now provide a link between defective MMR and the activation of TCF-dependent transcription, as mutations in AXIN2 alter the APC

Searcher : Shears 308-4994

pathway.

REFERENCE COUNT: 14
 REFERENCE(S): (1) Behrens, J; Science 1998, V280, P596 CAPLUS
 (2) Boland, C; Cancer Res 1998, V58, P5248
 CAPLUS
 (3) Chan, E; Nature Genet 1999, V21, P410 CAPLUS
 (4) Ganguly, A; Proc Natl Acad Sci USA 1993,
 V90, P10325 CAPLUS
 (5) Ishitani, T; Nature 1999, V399, P798 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:651706 CAPLUS
 DOCUMENT NUMBER: 134:1816
 TITLE: Hot spots in .beta.-catenin for interactions
 with LEF-1, **conductin** and APC
 AUTHOR(S): Von Kries, Jens Peter; Winbeck, Georgia;
 Asbrand, Christian; Schwarz-Romond, Thomas;
 Sochnikova, Natalia; Dell'Oro, Andrea; Behrens,
 Jurgen; Birchmeier, Walter
 CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine,
 Berlin, 13093, Germany
 SOURCE: Nat. Struct. Biol. (2000), 7(9), 800-807
 CODEN: NSBIEW; ISSN: 1072-8368
 PUBLISHER: Nature America Inc.
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Interactions between .beta.-catenin and LEF-1/TCF, APC and
conductin/axin are essential for wnt-controlled
 stabilization of .beta.-catenin and transcriptional activation. The
 wnt signal transduction pathway is important in both embryonic
 development and tumor progression. We identify here amino
 acid residues in .beta.-catenin that distinctly affect its binding
 to LEF-1/TCF, APC and **conductin**. These residues form sep.
 surface clusters, termed hot spots, along the armadillo superhelix
 of .beta.-catenin. We also show that complementary charged and
 hydrophobic amino acids are required for formation of the bipartite
 .beta.-catenin-LEF-1 transcription factor. Moreover, we demonstrate
 that **conductin**/axin binding to .beta.-catenin is essential
 for .beta.-catenin degrdn., and that APC acts as a cofactor of
conductin/axin in this process. Binding of APC to
conductin/axin activates the latter and occurs between their
 SAMP and RGS domains, resp.

REFERENCE COUNT: 50
 REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
 (2) Aberle, H; J Cell Sci 1994, V107, P3655
 CAPLUS
 (3) Behrens, J; Nature 1996, V382, P638 CAPLUS

Searcher : Shears 308-4994

(4) Behrens, J; Science 1998, V280, P596 CAPLUS
 (5) Brunner, E; Nature 1997, V385, P829 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:547045 CAPLUS

DOCUMENT NUMBER: 134:27977

TITLE: Control of .beta.-catenin signaling in
 tumor development

AUTHOR(S): Behrens, Jurgén

CORPORATE SOURCE: Max-Delbrück-Center for Molecular Medicine,
 Berlin, 13122, Germany

SOURCE: Ann. N. Y. Acad. Sci. (2000), 910 (Colorectal
 Cancer), 21-35

CODEN: ANYAA9; ISSN: 0077-8923

PUBLISHER: New York Academy of Sciences

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review, with 72 refs. The wnt signal transduction pathway is involved in various differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component .beta.-catenin: in the absence of wnts, .beta.-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts .beta.-catenin is stabilized and can assoc. with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/.beta.-catenin complexes activate specific wnt target genes. In tumors, .beta.-catenin degrading is blocked by mutations of .beta.-catenin or of the tumor suppressor gene product APC. As a consequence, .beta.-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. Thus, control of .beta.-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degrading of cytoplasmic .beta.-catenin. The complex includes APC, the serine/threonine kinase GSK3.beta., and .beta.-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin down-regulates .beta.-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize .beta.-catenin. Fragments of APC that contain a conductin-binding domain also block .beta.-catenin degrading. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization anal. shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin

controls wnt signaling by assembling the essential components of the .beta.-catenin degrdn. pathway. Alterations of conductin function may lead to tumor formation.

REFERENCE COUNT: 72

REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
(2) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
(3) Aoki, M; Proc Natl Acad Sci 1999, V96, P139 CAPLUS
(4) Bauer, A; Proc Natl Acad Sci 1998, V95, P14787 CAPLUS
(5) Behrens, J; Cancer Metastasis Rev 1999, V18, P15 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:275313 CAPLUS

DOCUMENT NUMBER: 132:313670

TITLE: Coated substrates for blood, plasma, or tissue washing and columns equipped with these substrates

INVENTOR(S): Dunzendorfer, Udo; Will, Gottfried

PATENT ASSIGNEE(S): Germany

SOURCE: Ger. Offen., 30 pp.

CODEN: GWXXBX

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 19845286	A1	20000427	DE 1998-19845286	19981001
EP 1004598	A2	20000531	EP 1999-118541	19990918
EP 1004598	A3	20000607		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: DE 1998-19845286 19981001

AB Columns, filters, cannulas, etc. contg. substrates coated with specific antibodies can be used during plasmapheresis to remove pathogenic cytokines such as tumor necrosis factor (TNF), anti-TNF, fragments of TNF or anti-TNF, or TNF transport proteins from blood, plasma, or tissues. The substrates may addnl. be coated with antibodies to microbial or viral pathogens or mixts. of pathogens as well as to polysaccharide antigens, viral capsids, microbial antigens, reverse transcriptase, endothelin, protein A, etc. Selective removal of these pathogens, antigens, proteins, etc. leaves all normal plasma components unchanged and obviates the need for supplementation of the plasma with these components. Suitable

substrates include polymers, polymer-coated metals, cellulose derivs., starch, and Sepharose; these may be derivatized for covalent binding of the pathogens or pathogenic mols. Thus, Escherichia coli pyelonephritis was successfully treated by plasmapheresis coupled with columns loaded with anti-TNF-.alpha. for 14 days, 4 h/day, as detd. by decreases in plasma TNF-.alpha. levels and colony counts in urine cultures.

L6 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:94336 CAPLUS
DOCUMENT NUMBER: 133:56735
TITLE: The regulation of .beta.-catenin degradation and cancer
AUTHOR(S): Kishida, Shosei; Kikuchi, Akira
CORPORATE SOURCE: Sch. Med., Hiroshima Univ., Hiroshima, 734-8551, Japan
SOURCE: Mol. Med. (Tokyo) (2000), 37(2), 166-175
CODEN: MOLMEL; ISSN: 0918-6557
PUBLISHER: Nakayama Shoten
DOCUMENT TYPE: Journal; General Review
LANGUAGE: Japanese

AB A review with 37 refs. The structure of .beta.-catenin is described. .beta.-Catenin accumulates in colon cancer and malignant melanoma. .beta.-Catenin is degraded by the ubiquitin/proteasome system. Axin (conductin) possesses regulators of G protein signaling (RGS) for binding APC at N-terminus, GSK-3.beta. and .beta.-catenin binding domains at central region, and DIX region at C-terminus. Wnt protein releases .beta.-catenin from the Axin complex.

L6 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:53973 CAPLUS
DOCUMENT NUMBER: 132:303902
TITLE: The yin-yang of TCF/.beta.-catenin signaling
AUTHOR(S): Barker, Nick; Morin, Patrice J.; Clevers, Hans
CORPORATE SOURCE: Department of Immunology, University Hospital, Utrecht, 85500, Neth.
SOURCE: Adv. Cancer Res. (2000), 77, 1-24
CODEN: ACRSAJ; ISSN: 0065-230X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 90 refs. Wingless/Wnt signaling directs cell-fate choices during embryonic development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a no. of key developmental decisions such as dorsal-ventral

patterning in *Xenopus*. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic β -catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of β -catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the N terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including *Siamois* and *Nodal* related gene-3 in *Xenopus*, *engrailed* and *Ultrabithorax* in *Drosophila* via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by β -catenin/Armadillo. In the absence of Wingless/Wnt signals, a key neg. regulator of the pathway, GSK3 β , is activated, which mediates the downregulation of cytoplasmic β -catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear β -catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An addnl. corepressor protein, CREB-binding protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3 β , and Axin/**Conductin**, are instrumental in the regulation of β -catenin/Armadillo. In APC-deficient colon carcinoma cell lines, β -catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/ β -catenin complexes as a result of dominant mutations in the N terminus of β -catenin that render it insensitive to downregulation by APC, GSK3 β , and Axin/**Conductin**. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/ β -catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer. (c) 2000 Academic Press.

REFERENCE COUNT:

90

REFERENCE(S):

- (2) Barker, N; Am J Pathol 1999, V154, P29
CAPLUS
- (3) Behrens, J; Nature (London) 1996, V382, P638
CAPLUS
- (4) Behrens, J; Science 1998, V280, P596 CAPLUS
- (5) Bhanot, P; Nature (London) 1996, V382, P225

CAPLUS

(6) Bienz, M; Trends Genet 1994, V10, P22 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:737696 CAPLUS
DOCUMENT NUMBER: 132:90977
TITLE: Identification and characterization of E-APC, a novel Drosophila homolog of the tumor suppressor APC
AUTHOR(S): Hamada, Fumihiko; Murata, Yoji; Nishida, Ayumu; Fujita, Fumitaka; Tomoyasu, Yoshinori; Nakamura, Makoto; Toyoshima, Kumao; Tabata, Tetsuya; Ueno, Naoto; Akiyama, Tetsu
CORPORATE SOURCE: Department of Oncogene Research, Research Institute for Microbial Diseases, Osaka University, Suita, 565-0871, Japan
SOURCE: Genes Cells (1999), 4(8), 465-474
CODEN: GECEFL; ISSN: 1356-9597
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We have identified a novel Drosophila homolog of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with 7 armadillo repeats, 2 copies of the 15-amino acid repeat, 5 copies of the 20-amino acid repeat, and 1 Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the Drosophila homolog of .beta.-catenin) in vitro, destabilizes intracellular .beta.-catenin, and suppresses .beta.-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in Drosophila. Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signaling pathway by down-regulating the level of Arm in Drosophila.

REFERENCE COUNT: 35

REFERENCE(S): (1) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
(2) Baeg, G; EMBO J 1995, V14, P5618 CAPLUS
(3) Behrens, J; Science 1998, V280, P596 CAPLUS
(4) Cadigan, K; Genes Dev 1997, V11, P3286 CAPLUS
(5) Hamada, F; Science 1999, V283, P1739 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:733931 CAPLUS
DOCUMENT NUMBER: 131:333485
TITLE: Signaling through .beta.-catenin and Lef/Tcf

AUTHOR(S): Novak, A.; Dedhar, S.
 CORPORATE SOURCE: Sunnybrook Health Science Center, Toronto, ON,
 M4N 3M5, Can.
 SOURCE: Cell. Mol. Life Sci. (1999), 56(5/6), 523-537
 CODEN: CMLSFI; ISSN: 1420-682X
 PUBLISHER: Birkhaeuser Verlag
 DOCUMENT TYPE: Journal; General Review
 LANGUAGE: English

AB A review with 167 refs. is given. .beta.-Catenin plays a structural role in cell adhesion by binding to cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of .beta.-catenin acting as a coactivator with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through .beta.-catenin is regulated by modulating its degrdn. and nuclear translocation. In the absence of an activating signal, phosphorylation of .beta.-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/ conductin causes .beta.-catenin to interact with the .beta.-transducin repeat-contg. protein which results in its ubiquitination and degrdn. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of .beta.-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates .beta.-catenin-Lef/Tcf signaling. ILK phosphorylates CISK3 to inhibit its activity and translocates .beta.-catenin into the nucleus. In addn., ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the .beta.-catenin-Lef/Tcf signaling pathway, nuclear .beta.-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or CREB-binding protein corepressors from Lef/ Tcf resulting in stimulation of transcription. During development, .beta.-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the .beta.-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

REFERENCE COUNT: 167

REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
 (2) Aberle, H; J Cell Biochem 1996, V61, P514 CAPLUS
 (4) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
 (5) Aoki, M; Proc Natl Acad Sci USA 1999, V96, P139 CAPLUS
 (7) Axelrod, J; Science 1996, V271, P1826 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:549289 CAPLUS

DOCUMENT NUMBER: 131:194280

TITLE: Agents for treating cancer and other human illnesses based on .beta.-catenin

INVENTOR(S): Birchmeier, Walter; Von Kries, Jens-Peter

PATENT ASSIGNEE(S): Max-Delbrueck-Centrum fuer Molekulare Medizin, Germany

SOURCE: PCT Int. Appl., 26 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9942481	A2	19990826	WO 1999-DE554	19990222
WO 9942481	A3	20000210		
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
DE 19909251	A1	19990826	DE 1999-19909251	19990222
EP 1054899	A2	20001129	EP 1999-913097	19990222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI				

PRIORITY APPLN. INFO.: DE 1998-19807390 A 19980221
 WO 1999-DE554 W 19990222

AB C.beta.-catenin is a central mol. of the Wnt signal path. Increasing .beta.-catenin in the cell leads to its translocation into the cell nucleus and to its interaction with transcription factors of the LEF-1/TCF family. This can lead to colonic **cancers** and melanomas (oncogenic signal path). However, .beta.-catenin also interacts with the **tumor-suppressor** genes APC, **conductin**, and E-cadherin, which have a contrary effect on the cell (antioncogenic effect). Peptides derived from LEF-1-/TCF-4 transcription factors and analogous mols. can be used in the treatment of **tumors**, esp. colonic **cancers** and melanomas. These peptides and analogous mols. influence the interaction between .beta.-catenin and LEF-1/TCF. The peptides comprise parts of the LEF-1/TCF-4 transcription factors and variants and mutations thereof, preferably the 10-40 N-terminal amino acids of LEF-1 or TCF-4, as well as peptides derived from the armadillo region of .beta.-catenin which were identified as interaction domains with LEF-1/TCF, APC, **conductin**, and E-cadherin. The peptides constituting interaction domains with APC or **conductin** can increase the concn. of .beta.-catenin in

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the cell. These last mols. can be used to influence the formation of tissues and organs, e.g. to promote hair growth.

IT 221220-50-4, **Conductin** (human)

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(interaction with .beta.-catenin, modulators of; agents for treating **cancer** and other human illnesses based on .beta.-catenin)

L6 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:189197 CAPLUS

DOCUMENT NUMBER: 130:232471

TITLE: The protein **conductin** and its application for diagnosis and gene therapy of colon **cancer**

INVENTOR(S): Behrens, Jurgen; Birchmeier, Walter

PATENT ASSIGNEE(S): Max-Delbrück-Centrum für Molekulare Medizin, Germany

SOURCE: PCT Int. Appl., 22 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9911780	A2	19990311	WO 1998-DE2621	19980901
WO 9911780	A3	19990527		
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
DE 19840875	A1	19990512	DE 1998-19840875	19980901
EP 1029047	A2	20000823	EP 1998-954120	19980901
R: AT, BE, CH, DE, DK, FR, GB, IT, LI, NL, SE, FI				

PRIORITY APPLN. INFO.:

DE 1997-19738205 A 19970902

WO 1998-DE2621 W 19980901

AB The invention concerns the novel protein **conductin** that is able to regulate the .beta.-catenin function and interacts with the **tumor** suppressor adenomatous polyposis coli (APC); and its application in the gene therapy of colon **cancer**. The 840 amino acid contg. protein contains domains with various activities: 78-200 is the RGS (Regulator of G-Protein Signalling) binding sequence; 343-396 is the GSK 3.beta. (glycogen synthase kinase 3.beta.) binding sequence; 397-465 is the .beta.-catenin binding sequence; 783-833 is the Dishevelled homol. region. Mutations, variants and fragments of **conductin** with the corresponding coding genes and mRNA sequences are also included. Antibodies and

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nucleic acid probes for the detection of c nductin are part of the diagnosis tools. For therapeutic purposes a vector contg. the conductin gene is constructed; substances that activate and reactivate conductin in the body are co-administered, e.g. a substance that activates the c nductin promoter or stabilizes mRNA. The effect of conductin was proved using SW480 cells with APC mutation and thus increased .beta.-catenin level. Introduction of conductin resulted in the decrease of .beta.-catenin to the same concn. as in non APC mutated SW480 cells. In an expt. with Xenopus embryos it was shown that conductin inhibits the Wnt/Wingless signaling pathway via its interaction with .beta.-catenin.

IT 221220-50-4, Conductin (human)

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)

(amino acid sequence; protein conductin and application for diagnosis and gene therapy of colon cancer)

L6 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:179719 CAPLUS

DOCUMENT NUMBER: 131:16667

TITLE: APC protein: protein interactions and cellular functions

AUTHOR(S): Jais, Philippe; Laurent-Puig, Pierre; Olschwang, Sylviane

CORPORATE SOURCE: Unite des Marqueurs Genetiques des Cancers (UMGC), Institut Gustave-Roussy, Villejuif, 94805, Fr.

SOURCE: Gastroenterol. Clin. Biol. (1998), 22(12), 1071-1080

CODEN: GCBIDC; ISSN: 0399-8320

PUBLISHER: Masson Editeur

DOCUMENT TYPE: Journal; General Review

LANGUAGE: French

AB A review with 112 refs., discussing structures of APC gene and protein; functions of APC protein in epithelial cell homeostasis and cell adhesion; assocn. of APC protein with .beta.-catenin, conductin, and GSK3.beta. in normal and transformed cells and other proteins-assocns.

REFERENCE COUNT: 112

REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
(3) Behrens, J; Nature 1996, V382, P638 CAPLUS
(4) Behrens, J; Science 1998, V280, P596 CAPLUS
(5) Beinhauer, J; J Cell Biol 1997, V139, P717 CAPLUS
(6) Beroud, C; Nucleic Acids Res 1996, V24, P121 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2001 ACS
 ACCESSION NUMBER: 1999:134134 CAPLUS
 DOCUMENT NUMBER: 131:14675
 TITLE: Cloning of the Human Homolog of Conduction
 (AXIN2), a Gene Mapping to Chromosome 17q23-q24
 AUTHOR(S): Mai, Ming; Qian, Chipping; Yokomizo, Akira;
 Smith, David I.; Liu, Wanguo
 CORPORATE SOURCE: Division of Experimental Pathology, Mayo
 Clinic/Foundation, Rochester, MN, 55905, USA
 SOURCE: Genomics (1999), 55(3), 341-344
 CODEN: GNMCEP; ISSN: 0888-7543
 PUBLISHER: Academic Press
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Conduction or Axil, an Axin homolog, plays an important role in the regulation of .beta.-catenin stability in the Wnt signaling pathway. To facilitate the mol. anal. of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3.beta. (96.3%), Dsh (98%), and .beta.-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast cancer, neuroblastoma, and other tumors. Human AXIN2 is thus a very strong candidate involved in multiple tumor types.
 (c) 1999 Academic Press.

IT 226387-63-9, Conduction (human fetal brain reduced)
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; cloning of the human homolog of conductin (AXIN2), a gene mapping to chromosome 17q23-q24)

REFERENCE COUNT: 22
 REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
 (2) Aberle, H; J Cell Sci 1994, V107, P3655 CAPLUS
 (3) Barlund, M; Genes Chromosomes Cancer 1997, V20, P372 CAPLUS
 (4) Behrens, J; Nature 1996, V382, P638 CAPLUS
 (5) Behrens, J; Science 1998, V280, P596 CAPLUS
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2001 ACS
 ACCESSION NUMBER: 1999:106086 CAPLUS

Searcher : Shears 308-4994

09/587574

DOCUMENT NUMBER: 130:323365
TITLE: Identification of APC2, a homolog of the
adenomatous polyposis coli tum r
suppressor
AUTHOR(S): Van Es, J. H.; Kirkpatrick, C.; Van de Wetering,
M.; Molenaar, M.; Miles, A.; Kuipers, J.;
Destree, O.; Peifer, M.; Clevers, H.
CORPORATE SOURCE: Department of Immunology, University Hospital,
Utrecht, 3508 GA, Neth.
SOURCE: Curr. Biol. (1999), 9(2), 105-108
CODEN: CUBLE2; ISSN: 0960-9822
PUBLISHER: Current Biology Publications
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We report the identification and genomic structure of APC homologs.
Mammalian APC2, which closely resembles APC in overall domain
structure, was functionally analyzed and shown to contain 2 SAMP
domains, both of which are required for binding to **conductin**
. Like APC, APC2 regulates the formation of active
.beta.-catenin-Tcf complexes, as demonstrated using transient
transcriptional activation assays in APC-/- colon **carcinoma**
cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may
therefore have comparable functions in development and
cancer.

REFERENCE COUNT: 23
REFERENCE(S): (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
(2) Behrens, J; Nature 1996, V382, P638 CAPLUS
(3) Behrens, J; Science 1998, V280, P596 CAPLUS
(4) Brunner, E; Nature 1997, V385, P829 CAPLUS
(5) Cadigan, K; Genes Dev 1997, V11, P3286
CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1998:302214 CAPLUS
TITLE: Functional interaction of an axin homolog,
conductin, with .beta.-catenin, APC and
GSK3.beta.
AUTHOR(S): Behrens, Jurgens; Jerchow, Boris-Alexander;
Wurtele, Martin; Grimm, Jan; Asbrand, Christian;
Wirtz, Ralph; Kuhl, Michael; Wedlich, Doris;
Birchmeier, Walter
CORPORATE SOURCE: Max Delbrück Cent. Molecular Med., Berlin,
13122, Germany
SOURCE: Science (Washington, D. C.) (1998), 280(5363),
596-599
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of

Searcher : Shears 308-4994

09/587574

DOCUMENT TYPE: Science
Journal
LANGUAGE: English

AB Control of stability of .beta.-catenin is central in the wnt signaling pathway. Here, the protein **conductin** was found to form a complex with both .beta.-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). **Conductin** induced .beta.-catenin degrdn., whereas mutants of **conductin** that were deficient in complex formation stabilized .beta.-catenin. Fragments of APC that contained a **conductin**-binding domain also blocked .beta.-catenin degrdn. Thus, **conductin** is a component of the multiprotein complex that directs .beta.-catenin to degrdn. and is located downstream of APC. In *Xenopus* embryos, **conductin** interfered with wnt-induced axis formation.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:17:14 ON 11 JUN 2001)

L7 57 S L6

L8 22 DUP REM L7 (35 DUPLICATES REMOVED)

L8 ANSWER 1 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 2001-246094 [26] WPIDS

DOC. NO. CPI: C2001-074206

TITLE: Agent for tumor therapy, tissue regeneration or stimulation of hair growth, comprising inhibitor of binding of beta-catenin to LEF-1/TCF-transcription factors, APC or **conductin**, obtained by specific screening method.

DERWENT CLASS: B04 D16

INVENTOR(S): BIRCHMEIER, W; VON KRIES, J

PATENT ASSIGNEE(S): (DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT: 94

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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DE 19944404	A1	20010322	(200126)*		14
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WO 2001019353	A2	20010322	(200126)	GE	
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE
DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ
PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN
YU ZA ZW

Searcher : Shears 308-4994

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 19944404	A1	DE 1999-19944404	19990916
WO 2001019353	A2	WO 2000-DE3104	20000907

PRIORITY APPLN. INFO: DE 1999-19944404 19990916

AN 2001-246094 [26] WPIDS

AB DE 19944404 A UPAB: 20010515

NOVELTY - An agent (I) for therapy of human disorders, comprising an inhibitor of the binding of beta -catenin to LEF-1/TCF-transcription factors, APC (undefined) or **conductin**, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for identifying agents (I), comprising identifying hydrophobic pockets in the vicinity of essential binding sites in the beta -catenin molecule, and synthesizing compounds which fit in these pockets.

ACTIVITY - Cytostatic.

No biological data is given.

MECHANISM OF ACTION - Inhibition of binding of beta -catenin to LEF-1/TCF-transcription factors, APC or **conductin**.

USE - For therapy of tumors (e.g. colon **carcinoma** or melanoma), for tissue regeneration or for stimulation of hair growth (claimed).

Dwg.0/3

L8 ANSWER 2 OF 22 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 2001083138 EMBASE

TITLE: Oncogenic targets of .beta.-catenin-mediated transcription in molecular pathogenesis of intestinal polyposis.

AUTHOR: Watson S.A.

CORPORATE SOURCE: S.A. Watson, Academic Unit of Cancer Studies, University of Nottingham, Nottingham NG7 2UH, United Kingdom. sue.watson@nottingham.ac.uk

SOURCE: Lancet, (24 Feb 2001) 357/9256 (572-573).

Refs: 14

ISSN: 0140-6736 CODEN: LANCAO

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; Note

FILE SEGMENT: 016 Cancer
022 Human Genetics
029 Clinical Biochemistry
048 Gastroenterology

LANGUAGE: English

L8 ANSWER 3 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

09/587574

ACCESSION NUMBER: 2000-293152 [25] WPIDS
DOC. NO. NON-CPI: N2000-219772
DOC. NO. CPI: C2000-088675
TITLE: Novel human tumor suppressor gene,
adenomatous polyposis coli (APC)-2, used in the
diagnosis, prevention, and treatment of
cancer.
DERWENT CLASS: B04 C06 D16 P14 S03
INVENTOR(S): CLEVERS, J C; PELFER, M A; VAN ES, J H
PATENT ASSIGNEE(S): (UYUT-N) RIJKSUNIV UTRECHT
COUNTRY COUNT: 89
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000018913	A1	20000406	(200025)*	EN	42
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM					
EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ					
LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD					
SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 9960106	A	20000417	(200035)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000018913	A1	WO 1999-NL595	19990924
AU 9960106	A	AU 1999-60106	19990924

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9960106	A Based on	WO 200018913

PRIORITY APPLN. INFO: EP 1998-203237 19980925

AN 2000-293152 [25] WPIDS

AB WO 200018913 A UPAB: 20000524

NOVELTY - Isolated and/or recombinant nucleic acid (NA) or a specific fragment, homolog or derivative thereof (I), corresponding to a gene located at position 19p13.3 in humans and comprising the 2397 base pair (bp) sequence given in the specification (adenomatous polyposis coli (APC)-2), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an expression vector comprising (I);

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- (2) a cell comprising (1) or the expression vector of (1);
- (3) an animal comprising the cell of (2);
- (4) a protein, derivative, or fragment encoded by (1) or produced by the cell of (2);
- (5) an antibody directed against the protein of (4);
- (6) identifying a candidate drug (especially a drug for use in a cancer patient), by using of the cell of (2), animal of (3), protein of (4), or antibody of (5); and
- (7) diagnosing cancer by using (1), the cell of (2), animal of (3), protein of (4), or antibody of (5).

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - The adenomatous polyposis coli (APC)-2 tumor suppressor gene controls the Wnt pathway by the formation of a complex with GSK-3b, axin/conductin and beta -catenin, inducing the rapid degradation of the latter.

USE - The adenomatous polyposis coli (APC)-2 polynucleotides are used for the diagnosis (claimed), prevention and treatment of cancer. They are also used for the recombinant production of APC-2 proteins. The methods are used to identify candidate drugs (claimed), especially for use in the treatment of cancers, preferably a fetal cancer, cancers with a stem cell phenotype, brain, lung, kidney or intestinal cancer (all claimed).

ADVANTAGE - None given.

DESCRIPTION OF DRAWING(S) - The figure shows the comparison of adenomatous polyposis coli (APC) and APC-2. Domain structures conserved between these APC relatives are indicated in various boxes.

Dwg.1A/4

L8 ANSWER 4 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)
 ACCESSION NUMBER: 2000:808103 SCISEARCH
 THE GENUINE ARTICLE: 366KD
 TITLE: Differential regulation of glycogen synthase kinase 3 beta by insulin and Wnt signaling
 AUTHOR: Ding V W; Chen R H; McCormick F (Reprint)
 CORPORATE SOURCE: UNIV CALIF SAN FRANCISCO, CANC RES INST, 2340 SUTTER ST, BOX 0128, SAN FRANCISCO, CA 94115 (Reprint);
 UNIV CALIF SAN FRANCISCO, CANC RES INST, SAN FRANCISCO, CA 94143
 COUNTRY OF AUTHOR: USA
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (20 OCT 2000) Vol. 275, No. 42, pp. 32475-32481.
 Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.
 ISSN: 0021-9258.
 DOCUMENT TYPE: Article; Journal
 FILE SEGMENT: LIFE

09/587574

LANGUAGE: English
REFERENCE COUNT: 53

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Glycogen synthase kinase 3 beta (GSK3 beta) is a key component in many biological processes including insulin and Wnt signaling. Since the activation of each signaling pathway results in a decrease in GSK3 beta activity, we examined the specificity of their downstream effects in the same cell type. Insulin induces an increased activity of glycogen synthase but has no influence on the protein level of beta-catenin. In contrast, Wnt increases the cytosolic pool of beta-catenin but not glycogen synthase activity. We found that, unlike insulin, neither the phosphorylation status of the serine9 residue of GSK3 beta nor the activity of protein kinase B is regulated by Wnt. Although the decrease in GSK3 beta activity is required, GSK3 beta may not be the limiting component for Wnt signaling in the cells that we examined. Our results suggest that the axin-conductin complexed GSK3 beta may be dedicated to Wnt rather than insulin signaling. Insulin and Wnt pathways regulate GSK3 beta through different mechanisms, and therefore lead to distinct downstream events.

L8 ANSWER 5 OF 22 MEDLINE
ACCESSION NUMBER: 2000455676 MEDLINE
DOCUMENT NUMBER: 20423090 PubMed ID: 10966653
TITLE: Hot spots in beta-catenin for interactions with LEF-1, conductin and APC.
AUTHOR: von Kries J P; Winbeck G; Asbrand C; Schwarz-Romond T; Sochnikova N; Dell'Oro A; Behrens J; Birchmeier W
CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Robert-Rossle-Strasse 10, 13093 Berlin, Germany.
SOURCE: NATURE STRUCTURAL BIOLOGY, (2000 Sep) 7 (9) 800-7. Journal code: B98; 9421566. ISSN: 1072-8368.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000928

AB Interactions between beta-catenin and LEF-1/TCF, APC and conductin/axin are essential for wnt-controlled stabilization of beta-catenin and transcriptional activation. The wnt signal transduction pathway is important in both embryonic development and tumor progression. We identify here amino acid residues in beta-catenin that distinctly affect its binding to LEF-1/TCF, APC and conductin. These residues form separate surface clusters, termed hot spots, along the armadillo superhelix

Searcher : Shears 308-4994

of beta-catenin. We also show that complementary charged and hydrophobic amino acids are required for formation of the bipartite beta-catenin-LEF-1 transcription factor. Moreover, we demonstrate that conductin/axin binding to beta-catenin is essential for beta-catenin degradation, and that APC acts as a cofactor of conductin/axin in this process. Binding of APC to conductin/axin activates the latter and occurs between their SAMP and RGS domains, respectively.

L8 ANSWER 6 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS
 ACCESSION NUMBER: 2000:275471 BIOSIS
 DOCUMENT NUMBER: PREV2000000275471
 TITLE: Human conductin (Axin2), like its mouse counterpart, binds to APC, GSK3beta and beta-catenin.
 AUTHOR(S): Dong, Xiangyang (1); Mai, Ming (1); Seelan, Ratnam (1); Qian, Chiping (1); Smith, David I. (1); Liu, Wanguo (1)
 CORPORATE SOURCE: (1) Mayo Clin, Rochester, MN USA
 SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2000) No. 41, pp. 745. print..
 Meeting Info.: 91st Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA April 01-05, 2000
 ISSN: 0197-016X.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 7 OF 22 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2000123741 MEDLINE
 DOCUMENT NUMBER: 20123741 PubMed ID: 10656974
 TITLE: Biochemical interactions in the wnt pathway.
 AUTHOR: Seidensticker M J; Behrens J
 CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Robert-Rossle-Strasse 10, 13122, Berlin, Germany.
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Feb 2) 1495 (2) 168-82. Ref: 143
 Journal code: AOW; 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200005
 ENTRY DATE: Entered STN: 20000512
 Last Updated on STN: 20000512

09/587574

Entered Medline: 20000502

AB The wnt signal transduction pathway is involved in many differentiation events during embryonic development and can lead to tumor formation after aberrant activation of its components. The cytoplasmic component beta-catenin is central to the transmission of wnt signals to the nucleus: in the absence of wnts beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and associates with HMG box transcription factors of the LEF/TCF family. In tumors, beta-catenin degradation is blocked by mutations of the tumor suppressor gene APC (adenomatous polyposis coli), or of beta-catenin itself. As a consequence, constitutive TCF/beta-catenin complexes are formed and activate oncogenic target genes. This review discusses the mechanisms that silence the pathway in cells that do not receive a wnt signal and goes on to describe the regulatory steps involved in the activation of the pathway.

L8 ANSWER 8 OF 22 MEDLINE

DUPLICATE 3

ACCESSION NUMBER: 2001019501 MEDLINE
DOCUMENT NUMBER: 20472311 PubMed ID: 11017067
TITLE: Mutations in AXIN2 cause colorectal cancer with defective mismatch repair by activating beta-catenin/TCF signalling.
AUTHOR: Liu W; Dong X; Mai M; Seelan R S; Taniguchi K; Krishnadath K K; Halling K C; Cunningham J M; Qian C; Christensen E; Roche P C; Smith D I; Thibodeau S N
CORPORATE SOURCE: Division of Experimental Pathology, Department of Laboratory Medicine and Pathology, Mayo Clinic and Mayo Medical School, Rochester, Minnesota, USA..
liu.wanguo@mayo.edu
CONTRACT NUMBER: CA 48031 (NCI)
CA 60117 (NCI)
SOURCE: NATURE GENETICS, (2000 Oct) 26 (2) 146-7.
Journal code: BRO. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001108

L8 ANSWER 9 OF 22 MEDLINE

DUPLICATE 4

ACCESSION NUMBER: 2000400028 MEDLINE
DOCUMENT NUMBER: 20369556 PubMed ID: 10911903
TITLE: Control of beta-catenin signaling in tumor development.

Searcher : Shears 308-4994

AUTHOR: Behrens J
 CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Berlin, Germany.. jbehren@mdc-berlin.de
 SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (2000 Jun) 910 21-33; discussion 33-5. Ref: 72
 Journal code: 5NM; 7506858. ISSN: 0077-8923.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200008
 ENTRY DATE: Entered STN: 20000824
 Last Updated on STN: 20000824
 Entered Medline: 20000817

AB The wnt signal transduction pathway is involved in various differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component beta-catenin: in the absence of wnts, beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and can associate with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/beta-catenin complexes activate specific wnt target genes. In tumors, beta-catenin degradation is blocked by mutations of beta-catenin or of the tumor suppressor gene product APC. As a consequence, beta-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. Thus, control of beta-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degradation of cytoplasmic beta-catenin. The complex includes APC, the serine/threonine kinase GSK3 beta, and beta-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin downregulates beta-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize beta-catenin. Fragments of APC that contain a conductin-binding domain also block beta-catenin degradation. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization analysis shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin controls wnt signaling by assembling the essential components of the beta-catenin degradation pathway. Alterations of

conductin function may lead to tumor formation.

L8 ANSWER 10 OF 22 MEDLINE

DUPLICATE 5

ACCESSION NUMBER: 2000017120 MEDLINE
 DOCUMENT NUMBER: 20017120 PubMed ID: 10549354
 TITLE: The Yin-Yang of TCF/beta-catenin signaling.
 AUTHOR: Barker N; Morin P J; Clevers H
 CORPORATE SOURCE: Department of Immunology, University Hospital,
 Utrecht, The Netherlands.
 SOURCE: ADVANCES IN CANCER RESEARCH, (2000) 77 1-24. Ref:
 100
 Journal code: 2J6; 0370416. ISSN: 0065-230X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000111
 Last Updated on STN: 20000111
 Entered Medline: 19991123

AB Wingless/Wnt signaling directs cell-fate choices during embryonic development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a number of key developmental decisions such as dorsal-ventral patterning in Xenopus. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic beta-catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of beta-catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the N terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including Siamois and Nodal related gene-3 in Xenopus, engrailed and Ultrabithorax in Drosophila via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by beta-catenin/Armadillo. In the absence of Wingless/Wnt signals, a key negative regulator of the pathway, GSK3 beta, is activated, which mediates the downregulation of cytoplasmic beta-catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear beta-catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An additional corepressor protein, CREB-binding

protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3 beta, and Axin/Conductin, are instrumental in the regulation of beta-catenin/Armadillo. In APC-deficient colon carcinoma cell lines, beta-catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/beta-catenin complexes as a result of dominant mutations in the N terminus of beta-catenin that render it insensitive to downregulation by APC, GSK3 beta, and Axin/Conductin. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/beta-catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer

L8 ANSWER 11 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 1999-214706 [18] WPIDS
 DOC. NO. NON-CPI: N1999-158020
 DOC. NO. CPI: C1999-063258
 TITLE: Tumor-suppressing protein
 conductin - used for treatment and
 diagnosis of tumors.
 DERWENT CLASS: B04 D16 S03
 INVENTOR(S): BEHRENS, J; BIRCHMEIER, W
 PATENT ASSIGNEE(S): (DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
 COUNTRY COUNT: 22
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9911780	A2	19990311	(199918)*	GE	21
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
DE 19840875	A1	19990512	(199925)		
EP 1029047	A2	20000823	(200041)	GE	
R: AT BE CH DE DK FI FR GB IT LI NL SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9911780	A2	WO 1998-DE2621	19980901

Searcher : Shears 308-4994

09/587574

DE 19840875 A1
EP 1029047 A2

DE 1998-19840875 19980901
EP 1998-954120 19980901
WO 1998-DE2621 19980901

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1029047	A2 Based on	WO 9911780

PRIORITY APPLN. INFO: DE 1997-19738205 19970902

AN 1999-214706 [18] WPIDS

AB WO 9911780 A UPAB: 19990511

NOVELTY - The protein conductin (I) and its variants, mutants and fragments are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) composition for diagnosing tumors comprising an agent that detects (I), the (I)-encoding gene (II) or derived mRNA; (2) composition for treating tumors containing an agent that activates or reactivates (I) in vivo; (3) cDNA (III) that encodes (I), its variants, mutants or fragments; (4) use of (II) for gene therapy of tumors; and (5) partial sequences of the adenomatosis polyposis coli (APC) protein comprising amino acids (aa) 1464-1604, 1516-1595, 1690-1778 or 1995-2083 as RGS-domain interaction sites (RGS = regulator of G-protein signaling).

USE - Detecting presence or amount of (I), at protein or nucleic acid levels, is used to diagnose tumors, while agents that (re)activate (I) are used for tumor therapy. Antitumor. (I) binds to beta -catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signaling pathway in vertebrates. (I) also binds to APC fragments and, in conjunction with APC, acts as a tumor suppressor. In SW840 cells APC is mutated, leading to increased levels of beta -catenin in cytoplasm and the nucleus. When (I) was introduced into these cells, beta -catenin was depleted in both cell compartments, with the effect being as strong as that for wild-type APC.
Dwg.0/4

L8 ANSWER 12 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-470389 [40] WPIDS

DOC. NO. CPI: C1999-138212

TITLE: Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor suppressor gene products.

DERWENT CLASS: B04 D16

INVENTOR(S): BIRCHMEIER, W; VON KRIES, J

Searcher : Shears 308-4994

09/587574

PATENT ASSIGNEE(S): (DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
COUNTRY COUNT: 22
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 19909251	A1	19990826	(199940)*		15
WO 9942481	A2	19990826	(199942)	GE	
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
EP 1054899	A2	20001129	(200063)	GE	
R: AT BE CH DE DK ES FI FR GB GR IE IT LI NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 19909251	A1	DE 1999-19909251	19990222
WO 9942481	A2	WO 1999-DE554	19990222
EP 1054899	A2	EP 1999-913097	19990222
		WO 1999-DE554	19990222

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1054899	A2 Based on	WO 9942481

PRIORITY APPLN. INFO: DE 1998-19807390 19980221

AN 1999-470389 [40] WPIDS

AB DE 19909251 A UPAB: 19991004

NOVELTY - Agent (A) for treating human disease is based on substances (I) that modulate (inhibit or promote) the interaction of beta -catenin (bC) with transcription factors or products of tumor suppressor genes.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (a) peptide (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptide and related molecules (III) from the armadillo domain (arm units 3-8) of bC, and mutants of the complete bC molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, **conductin** or E-cadherin; and (c) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of bC with LEF-1/TCF, APC, **conductin** or E-cadherin.

ACTIVITY - Antitumor.

MECHANISM OF ACTION - bC is a key compound in the Wnt signaling pathway and is involved in development of tumors.

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Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, **conductin** or E-cadherin is anti-oncogenic.

USE - (A) which inhibit interaction are particularly used to treat **tumors**, especially **carcinoma** of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth.
Dwg.0/6

L8 ANSWER 13 OF 22 MEDLINE

DUPLICATE 6

ACCESSION NUMBER: 2000047719 MEDLINE

DOCUMENT NUMBER: 20047719 PubMed ID: 10580987

TITLE: beta-catenin signaling and **cancer**.

AUTHOR: Morin P J

CORPORATE SOURCE: Laboratory of Biological Chemistry, Gerontology
Research Center, National Institute on Aging, 5600
Nathan Shock Drive, Baltimore, MD 21224, USA..
MorinP@grc.nia.nih.gov

SOURCE: BIOESSAYS, (1999 Dec) 21 (12) 1021-30. Ref: 88
Journal code: 9YY; 8510851. ISSN: 0265-9247.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200002

ENTRY DATE: Entered STN: 20000209
Last Updated on STN: 20000209
Entered Medline: 20000203

AB Since its discovery as a protein associated with the cytoplasmic region of E-cadherin, beta-catenin has been shown to perform two apparently unrelated functions: it has a crucial role in cell-cell adhesion in addition to a signaling role as a component of the Wnt/wg pathway. Wnt/wg signaling results in beta-catenin accumulation and transcriptional activation of specific target genes during development. It is now apparent that deregulation of beta-catenin signaling is an important event in the genesis of a number of malignancies, such as colon **cancer**, melanoma, hepatocellular **carcinoma**, ovarian **cancer**, endometrial **cancer**, medulloblastoma pilomatricomas, and prostate **cancer**. beta-catenin mutations appear to be a crucial step in the progression of a subset of these **cancers**, suggesting an important role in the control of cellular proliferation or cell death. The APC/beta-catenin pathway is highly regulated and includes players such as GSK3-beta, CBP, Groucho, Axin, **Conductin**, and TCF. c-MYC and cyclin D1 were recently identified as a key transcriptional targets of this pathway.

Searcher : Shears 308-4994

and additional targets are likely to emerge. Published 1999 John Wiley & Sons, Inc.

L8 ANSWER 14 OF 22 MEDLINE DUPLICATE 7
 ACCESSION NUMBER: 2001120045 MEDLINE
 DOCUMENT NUMBER: 21079826 PubMed ID: 11212302
 TITLE: Signaling through beta-catenin and Lef/Tcf.
 AUTHOR: Novak A; Dedhar S
 CORPORATE SOURCE: Cancer Research, S-218, Sunnybrook Health Science Centre, Toronto, Ontario, Canada.
 SOURCE: CELLULAR AND MOLECULAR LIFE SCIENCES, (1999 Oct 30) 56 (5-6) 523-37. Ref: 167

 Journal code: CLE. ISSN: 1420-682X.
 PUB. COUNTRY: Switzerland
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered PubMed: 20010209
 Entered Medline: 20010215

AB Beta-catenin plays a structural role in cell adhesion by binding to cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of beta-catenin acting as a coactivator with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through beta-catenin is regulated by modulating its degradation and nuclear translocation. In the absence of an activating signal, phosphorylation of beta-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/conductin causes beta-catenin to interact with the beta-transducin repeat-containing protein which results in its ubiquitination and degradation. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of beta-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates beta-catenin-Lef/Tcf signaling. ILK phosphorylates GSK3 to inhibit its activity and translocates beta-catenin into the nucleus. In addition, ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the beta-catenin-Lef/Tcf signaling pathway, nuclear beta-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or

CREB-binding protein corepressors from Lef/Tcf resulting in stimulation of transcription. During development, beta-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the beta-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

L8 ANSWER 15 OF 22 MEDLINE

DUPLICATE 8

ACCESSION NUMBER: 1999457298

MEDLINE

DOCUMENT NUMBER: 99457298 PubMed ID: 10526234

TITLE: Identification and characterization of E-APC, a novel *Drosophila* homologue of the tumour suppressor APC.

AUTHOR: Hamada F; Murata Y; Nishida A; Fujita F; Tomoyasu Y; Nakamura M; Toyoshima K; Tabata T; Ueno N; Akiyama T

CORPORATE SOURCE: Department of Oncogene Research, Research Institute for Microbial Diseases, Osaka University, 3-1 Yamadaoka, Suita 565-0871, Japan. and.

SOURCE: GENES TO CELLS, (1999 Aug) 4 (8) 465-74.
Journal code: CUF; 9607379. ISSN: 1356-9597.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199912

ENTRY DATE: Entered STN: 20000113

Last Updated on STN: 20000915

Entered Medline: 19991223

AB BACKGROUND: Mutations in the adenomatous polyposis coli (APC) tumour suppressor gene are implicated in the genesis of colorectal cancers. The product of the APC gene forms a complex with beta-catenin, glycogen synthase kinase 3beta (GSK-3beta) and Axin/conductin, and induces the degradation of beta-catenin. RESULTS: We have identified a novel *Drosophila* homologue of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with seven armadillo repeats, two copies of the 15-amino acid repeat, five copies of the 20-amino acid repeat, and one Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the *Drosophila* homologue of beta-catenin) in vitro, destabilizes intracellular beta-catenin, and suppresses beta-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in *Drosophila*. CONCLUSION: Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signalling pathway by down-regulating the level of Arm in *Drosophila*.

09/587574

L8 ANSWER 16 OF 22 MEDLINE

DUPLICATE 9

ACCESSION NUMBER: 1999168905 MEDLINE
DOCUMENT NUMBER: 99168905 PubMed ID: 10049590
TITLE: Cloning of the human homolog of **conductin**
(AXIN2), a gene mapping to chromosome 17q23-q24.
AUTHOR: Mai M; Qian C; Yokomizo A; Smith D I; Liu W
CORPORATE SOURCE: Department of Laboratory Medicine and Pathology, Mayo
Clinic/Foundation, Rochester, Minnesota 55905, USA.
CONTRACT NUMBER: CA48031 (NCI)
SOURCE: GENOMICS, (1999 Feb 1) 55 (3) 341-4.
Journal code: GEN; 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF078165
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990524

AB **Conductin** or Axil, an Axin homolog, plays an important role in the regulation of beta-catenin stability in the Wnt signaling pathway. To facilitate the molecular analysis of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3beta (96.3%), Dsh (98%), and beta-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast **cancer**, neuroblastoma, and other **tumors**. Human AXIN2 is thus a very strong candidate involved in multiple tumor types.

L8 ANSWER 17 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)

ACCESSION NUMBER: 2000:63768 SCISEARCH
THE GENUINE ARTICLE: 274MZ
TITLE: Modulation of Wnt signaling by Axin and Axil
AUTHOR: Kikuchi A (Reprint)
CORPORATE SOURCE: HIROSHIMA UNIV, SCH MED, DEPT BIOCHEM, MINAMI KU,
1-2-3 KASUMI, HIROSHIMA 7348551, JAPAN (Reprint)
COUNTRY OF AUTHOR: JAPAN
SOURCE: CYTOKINE & GROWTH FACTOR REVIEWS, (SEP-DEC 1999)
Vol. 10, No. 3-4, pp. 255-265.
Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD
LANE, KIDLINGTON, OXFORD OX5 1GB, OXON, ENGLAND.
ISSN: 1359-6101.

Searcher : Shears 308-4994

09/587574

DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 97

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The Wnt signaling pathway is conserved in various species from worms to mammals, and, plays important roles in development, cellular proliferation, and differentiation. The molecular mechanisms by which the Wnt signal regulates cellular functions are becoming increasingly well understood. Wnt stabilizes cytoplasmic beta-catenin, which stimulates the expression of genes including c-myc, c-jun, fra-1, and cyclin D1. Axin and its homolog Axil, newly recognized as components of the Wnt signaling pathway, negatively regulate this pathway. Other components of the Wnt signaling pathway, including Dvl, glycogen synthase kinase-3 beta (GSK-3 beta), beta-catenin, and adenomatous polyposis coli (APC), interact with Axin, and the phosphorylation and stability of beta-catenin are regulated in the Axin complex. Axil has similar functions to Axin. Thus, Axin and Axil act as scaffold proteins in the Wnt signaling pathway, thereby modulating the Wnt-dependent cellular functions.
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L8 ANSWER 18 OF 22 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 1999147086 MEDLINE
DOCUMENT NUMBER: 99147086 PubMed ID: 10021369
TITLE: Identification of APC2, a homologue of the adenomatous polyposis coli tumour suppressor.
AUTHOR: van Es J H; Kirkpatrick C; van de Wetering M; Molenaar M; Miles A; Kuipers J; Destree O; Peifer M; Clevers H
CORPORATE SOURCE: Department of Immunology, University Hospital, P.O. Box 85500, 3508 GA, Utrecht, The Netherlands.
SOURCE: CURRENT BIOLOGY, (1999 Jan 28) 9 (2) 105-8.
JOURNAL CODE: B44; 9107782. ISSN: 0960-9822.
PUB. COUNTRY: ENGLAND: United Kingdom
JOURNAL: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF091430; GENBANK-AJ012652; GENBANK-AJ130783; GENBANK-AJ130784; GENBANK-AJ130785; GENBANK-AJ130786; GENBANK-AJ130787; GENBANK-AJ130788; GENBANK-AJ130789; GENBANK-AJ130790; GENBANK-AJ130791; GENBANK-AJ130792; GENBANK-AJ130793; GENBANK-AJ130794; GENBANK-AJ130795; GENBANK-AJ130796; GENBANK-AJ131187
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990402
Last Updated on STN: 20000303
Entered Medline: 19990323

Searcher : Shears 308-4994

AB The adenomatous polyposis coli (APC) tumour-suppressor protein controls the Wnt signalling pathway by forming a complex with glycogen synthase kinase 3beta (GSK-3beta), axin/ conductin and betacatenin. Complex formation induces the rapid degradation of betacatenin. In colon carcinoma cells, loss of APC leads to the accumulation of betacatenin in the nucleus, where it binds to and activates the Tcf-4 transcription factor (reviewed in [1] [2]). Here, we report the identification and genomic structure of APC homologues. Mammalian APC2, which closely resembles APC in overall domain structure, was functionally analyzed and shown to contain two SAMP domains, both of which are required for binding to conductin. Like APC, APC2 regulates the formation of active betacatenin-Tcf complexes, as demonstrated using transient transcriptional activation assays in APC -/- colon carcinoma cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may therefore have comparable functions in development and cancer.

L8 ANSWER 19 OF 22 JICST-EPlus COPYRIGHT 2001 JST

ACCESSION NUMBER: 990756513 JICST-EPlus

TITLE: Arthroscopic treatment for dorsal wrist ganglion.

AUTHOR: NISHIKAWA SHINJI; ARAI KOICHI; TAKEUCHI KAZUNARI; FUKUDA AKIRA; WADA KAN'ICHIRO

CORPORATE SOURCE: Mutsu Gen. Hosp.

SOURCE: Kansetsukyo (Arthroscopy), (1999) vol. 24, no. 1, pp. 85-90. Journal Code: L0107A (Fig. 7, Ref. 9)
ISSN: 0910-223X

PUB. COUNTRY: Japan

DOCUMENT TYPE: Conference; Article

LANGUAGE: Japanese

STATUS: New

AB In excising a ganglion located at the dorsum of the wrist joint, one may lose sight of the base of the ganglion, which may result in a recurrence of the condition; or the surgical procedure may leave a large, unsightly surgical cicatrix on the dorsum of the hand due to the size of the lesion. To eliminate these problems, we have been conductin surgery on ganglions of the dorsal wrist joint under arthroscopy. The details are reported below. A total of 16 joints(10 right and 6 left) in 16 patients(7 males and 9 females, ages ranging from 12 to 83 years, with a mean of 42 years) have undergone the arthroscopic procedure. A nodule was palpated at the center of the dorsum of the wrist in each patients and all reported pain that was associated with movement. Six had experienced repeated recurrences for six months or more; the condition had developed for the first time in eight(among whom, two had been subjected to repeated aspiration therapy); and the condition had returned in one following surgical therapy. MRI was conducted prior to surgery to confirm that there was communication between the ganglion and the

scapholunate joint (SL joint). Arthroscopy was conducted at portals I-II and a probe and a shaver were inserted through portals IV-V. The position of the base of the ganglion that was palpated at the dorsum of the scapholunate ligament (SL ligament) was confirmed under arthroscopy and excised with the shaver. No recurrence was noted and the postoperative course was satisfactory for a follow-up period that lasted from 2 to 15 months (mean, 6.4). The method introduced above applies to all ganglions that originate at the SL joint: but it is particularly suitable for large growths that are likely to leave prominent surgical scars or for radical treatment of those that return repeatedly after aspiration and cause pain associated with wrist movement. (author abst.)

L8 ANSWER 20 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS
 ACCESSION NUMBER: 1999:174930 BIOSIS
 DOCUMENT NUMBER: PREV199900174930
 TITLE: Cloning of the human homolog of conduction (AXIN2), a gene mapping to chromosome 17q23-24.
 AUTHOR(S): Mai, M. (1); Qian, C.; Yokomizo, A.; Smith, D. I.; Liu, W.
 CORPORATE SOURCE: (1) Div. Exp. Pathol., Dep. Lab. Med. Pathol., Rochester, MN 55905 USA
 SOURCE: Proceedings of the American Association for Cancer Research Annual Meeting, (March, 1999) Vol. 40, pp. 34.
 Meeting Info.: 90th Annual Meeting of the American Association for Cancer Research Philadelphia, Pennsylvania, USA April 10-14, 1999 American Association for Cancer Research
 . ISSN: 0197-016X.
 DOCUMENT TYPE: Conference
 LANGUAGE: English

L8 ANSWER 21 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 11
 ACCESSION NUMBER: 1999:165640 BIOSIS
 DOCUMENT NUMBER: PREV199900165640
 TITLE: APC protein: Protein interactions and cellular functions.
 AUTHOR(S): Jais, Philippe (1); Laurent-Puig, Pierre; Olschwang, Sylviane
 CORPORATE SOURCE: (1) Unite Marqueurs Genet. Cancers, Inst. Gustave-Roussy, 39 rue Camille-Desmoulins, 94805 Villejuif Cedex France
 SOURCE: Gastroenterologie Clinique et Biologique, (Dec., 1998) Vol. 22, No. 12, pp. 1071-1080.
 ISSN: 0399-8320.
 DOCUMENT TYPE: General Review
 LANGUAGE: French

L8 ANSWER 22 OF 22 MEDLINE

DUPLICATE 12

ACCESSION NUMBER: 1998221239 MEDLINE

DOCUMENT NUMBER: 98221239 PubMed ID: 9554852

TITLE: Functional interaction of an axin homolog,
conductin, with beta-catenin, APC, and
GSK3beta.AUTHOR: Behrens J; Jerchow B A; Wurtele M; Grimm J; Asbrand
C; Wirtz R; Kuhl M; Wedlich D; Birchmeier WCORPORATE SOURCE: Max Delbruck Center for Molecular Medicine,
Robert-Rossle-Strasse 10, 13122 Berlin, Germany.

SOURCE: SCIENCE, (1998 Apr 24) 280 (5363) 596-9.

Journal code: UJ7; 0404511. ISSN: 0036-8075.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF073788

ENTRY MONTH: 199805

ENTRY DATE: Entered STN: 19980514

Last Updated on STN: 20000303

Entered Medline: 19980507

AB Control of stability of beta-catenin is central in the wnt signaling pathway. Here, the protein **conductin** was found to form a complex with both beta-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). **Conductin** induced beta-catenin degradation, whereas mutants of **conductin** that were deficient in complex formation stabilized beta-catenin. Fragments of APC that contained a **conductin**-binding domain also blocked beta-catenin degradation. Thus, **conductin** is a component of the multiprotein complex that directs beta-catenin to degradation and is located downstream of APC. In *Xenopus* embryos, **conductin** interfered with wnt-induced axis formation.

(FILE 'CAPLUS' ENTERED AT 11:20:11 ON 11 JUN 2001)

L9 150 SEA FILE=CAPLUS ABB=ON PLU=ON CONDUCTING(3A) (PROTEIN
OR PEPTIDE)L10 3 SEA FILE=CAPLUS ABB=ON PLU=ON L9 AND (TUMOUR OR TUMOR
OR NEOPLAS? OR CANCER? OR CARCIN?)

L11 3 S L10 NOT L6

L11 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1996:427508 CAPLUS

DOCUMENT NUMBER: 125:135608

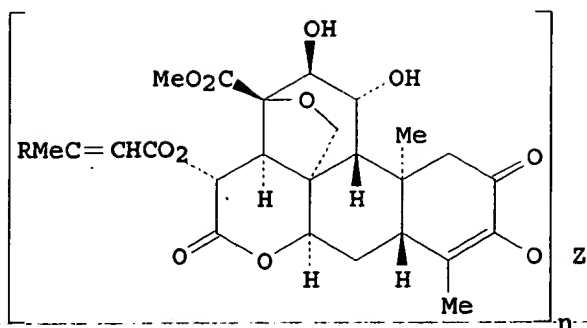
TITLE: Co-translational effects of temperature on

membrane insertion and orientation of
P-glycoprotein sequences
AUTHOR(S): Zhang, Jian-Ting; Chong, Crispina H.
CORPORATE SOURCE: Dep. Physiol. Biophys., Univ. Texas Med. Branch,
Galveston, TX, 77555-0641, USA
SOURCE: Mol. Cell. Biochem. (1996), 159(1), 25-31
CODEN: MCBIB8; ISSN: 0300-8177
DOCUMENT TYPE: Journal
LANGUAGE: English

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. In may also function as a peptide transporter, a vol.-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp1 Pgp is expressed in more than one topos. form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by sol. cytoplasmic factors. Different topos. structures of Pgp may be related to its different functions. This study examd. the effects of translation temp. on the membrane insertion process and the topologies of Pgp. The rabbit reticulocyte lysate expression system was used to show that translation at different temps. affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgp1 Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp mols. may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temp. sensitive manner. Manipulating temp. may provide a way to understand the structure-function relationship of Pgp and help overcome Pgp-related multidrug resistance of cancer cells.

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1982:400304 CAPLUS
DOCUMENT NUMBER: 97:304
TITLE: Antitumor agents. XLVIII: structure-activity relationships of quassinoids as in vitro protein synthesis inhibitors of P-388 lymphocytic leukemia tumor cell metabolism
AUTHOR(S): Liou, Y. F.; Hall, I. H.; Okano, M.; Lee, K. H.; Chaney, S. G.
CORPORATE SOURCE: Sch. Med., Univ. North Carolina, Chapel Hill, NC, 27514, USA
SOURCE: J. Pharm. Sci. (1982), 71(4), 430-5
CODEN: JPMSAE; ISSN: 0022-3549
DOCUMENT TYPE: Journal
LANGUAGE: English
GI



- I, R=CHMe₂, Z=H, n=1
 II, R=Me, Z=H, n=1
 III, R=Me, Z=COCH₂CO, n=2

AB A series of brusatol, bisbrusatol, and bruceantin esters were examd. for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compds. which produced high antileukemic activities resulted in ID₅₀ of 5.4-15.5 .mu.M for inhibition of whole cell protein synthesis, ID₅₀ of 1.3-13 .mu.M for inhibition of endogenous protein synthesis in cell homogenates, and ID₅₀ of 1.9-6 .mu.M for inhibition of polyuridine directed polyphenylalanine synthesis using runoff ribosomes and a pH 5 enzyme prepn. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. bruceantin (I) [41451-75-6], brusatol (II) [14907-98-3], and bisbrusatolyl malonate (III) [80096-78-2] allowed a runoff of the polyribosomes to 80-S free ribosomes. However, formation of the ternary complex and 80-S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80-S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H]methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. Apparently, the free 80-S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. Thus, quassinoids are elongation inhibitors of tumor cells. A strong correlation was obsd. between potent antileukemic activity and the ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells.

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L11 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1960:24381 CAPLUS

DOCUMENT NUMBER: 54:24381

ORIGINAL REFERENCE NO.: 54:4860c-d

TITLE: The nature of the interaction of biologically active agents with tissue constituents

AUTHOR(S): Mason, R.

CORPORATE SOURCE: Univ. Coll., London

SOURCE: Acta Unio Intern. contra Cancrum (1959), 15, 650-1

DOCUMENT TYPE: Journal

LANGUAGE: Unavailable

AB The electronic structure of carcinogen-protein mol. complexes was examd. theoretically and the possibility of charge transfer in the complex discussed. A banded-electronic model of a protein suggests that electron transfer within such a mol. complex will take place only when the energy levels of the mols. of the complex are closely matched. Aromatic carcinogens satisfy a precise criterion for such matching of levels, and carcinogenesis is to be assocd. with the induction of conducting properties in the protein.

(FILE 'MEDLINE', BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:22:50 ON 11 JUN 2001)

L12 18 S L10

L13 18 S L12 NOT (L2 OR L7)

L14 9 DUP REM L13 (9 DUPLICATES REMOVED)

L14 ANSWER 1 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 2001-266373 [27] WPIDS

DOC. NO. NON-CPI: N2001-190479

DOC. NO. CPI: C2001-080736

TITLE: Detection of proteins by using a protein fingerprinting system which comprises linearizing the protein, labeling a first amino acid residue type and detecting first and second residue types, useful in the diagnosis of cancer.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): BRENT, R; BURBULIS, I E; CARLSON, R H

PATENT ASSIGNEE(S): (MOLE-N) MOLECULAR SCI INST INC

COUNTRY COUNT: 93

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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WO 2001025794	A2	20010412	(200127)*	EN	55
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
MW MZ NL OA PT SD SE SL SZ TZ UG ZW

Searcher : Shears 308-4994

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE
 DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
 KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ
 PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU
 ZA ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001025794	A2	WO 2000-US26958	20000929

PRIORITY APPLN. INFO: US 1999-412732 19991005

AN 2001-266373 [27] WPIDS

AB WO 200125794 A UPAB: 20010518

NOVELTY - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

DETAILED DESCRIPTION - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

In detail, M1 comprises:

- (a) linearizing the protein molecule with a denaturation means;
- (b) labeling each of the first type of amino acid residue with a tag;
- (c) detecting the fingerprint of the protein with a detection means, by detecting a first fingerprint constituent imparted by the tag and a second fingerprint constituent imparted by the second type of amino acid residue.

INDEPENDENT CLAIMS are also included for the following:

(1) identifying a protein molecule having at least two different amino acid residue types in a sample containing several proteins, by linearizing each protein as in M1 step (a), isolating the protein, conducting steps (b) and (c) of M1, and comparing the fingerprint obtained (optionally using a computer receiving signals from the detection means) to a library of fingerprints of known protein molecules;

(2) a library of fingerprint values of known proteins, listing the identity of the proteins and first and second (and optionally third) fingerprint constituents of each protein, being representative of the number and sequence of the first and second

(and optionally third) types of amino acid residues respectively;

(3) characterizing protein molecules, by isolating the protein and using M1 which is modified such that first and second types of amino acid types are both labeled with different tags;

(4) protein molecules having an identifiable fingerprint, comprising two amino acid residue types each separately tagged, or three amino acid types (optionally including tryptophan), imparting up to six fingerprint constituents by using combinations of excitation and emitted radiations; and

(5) identifying a protein in a sample containing several proteins, following the method of (1) which is modified such that first and second residue types are both labeled with different tags.

USE - The method is useful to enable rapid identification of protein molecules, especially in biological samples e.g. plant, microorganism or animal (especially human) tissues or cells e.g. in clinical or research applications to identify aberrant or mutant forms of proteins involved in diseases such as cancers or inherited disorders such as cystic fibrosis and hemophilia. It also enables the production of a library of known proteins and their corresponding fingerprints, useful to identify unknown proteins in a sample.

Dwg.0/33

L14 ANSWER 2 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD
 ACCESSION NUMBER: 2001-050022 [06] WPIDS
 DOC. NO. NON-CPI: N2001-038339
 DOC. NO. CPI: C2001-013790
 TITLE: Assessing translocation of proteins such as glucose transporter GLUT4, cystic fibrosis transmembrane conductance regulator by using modified protein of interest comprising the protein and detectable tags.
 DERWENT CLASS: B04 D16 S03
 INVENTOR(S): BOGAN, J S; LODISH, H
 PATENT ASSIGNEE(S): (GEHO) GEN HOSPITAL CORP; (WHED) WHITEHEAD INST BIOMEDICAL RES
 COUNTRY COUNT: 93
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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WO 2000075188	A1	20001214	(200106)*	EN	75
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
 MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK
 DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP
 KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL
 PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU

09/587574

ZA ZW

AU 2000054775 A 20001228 (200119)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000075188	A1	WO 2000-US15904	20000609
AU 2000054775	A	AU 2000-54775	20000609

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000054775	A Based on	WO 200075188

PRIORITY APPLN. INFO: US 1999-154078 19990915; US 1999-138237
19990609

AN 2001-050022 [06] WPIDS

AB WO 200075188 A UPAB: 20010126

NOVELTY - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

DETAILED DESCRIPTION - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

The method (I) comprises:

(a) culturing mammalian cells (test cells) expressing MP, under a condition or a stimulus to be assessed for its effects on translocation of the protein of interest;

(b) determining a value corresponding to proportion of MP at the cell membrane to total MP in the test cells that produces a test value; and

(c) comparing the test value with a control value, where the control value corresponds to the proportion of MP at the cell membrane to MP in control cells, where the control cells are the same cells as are cultured in (a), except that the control cells are not cultured under the condition or stimulus to be assessed, where the test value greater than the control value indicates that translocation of MP has occurred.

INDEPENDENT CLAIMS are also included for the following:

(1) determining (II) whether a protein of interest undergoes

Searcher : Shears 308-4994

translocation from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or stimulator, comprising:

- (a) culturing cells that express MP in the absence of the stimulator producing cultured cells;
- (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, by producing a control value;
- (c) culturing cells that express MP under the same conditions as in (a) and in the presence of the stimulator, by producing test cells;
- (d) determining the relative proportion of MP at the plasma membrane of test cells to total MP in the test cells, by producing a test value; and
- (e) comparing the control value and the test value, where a test value that is greater than the control value indicates that protein of interest undergoes translocation following stimulation of the cells by the stimulator;

(2) identifying (III) a drug which enhances translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells by:

- (a) culturing cells which express RT in the presence of a candidate drug;
- (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, producing a test value; and
- (c) comparing the test value with the control value, which is the relative proportion of the protein of interest at the plasma membrane to MP in cells cultured under same conditions in the absence of drug, where the test value greater than the control value indicates that the candidate drug enhances translocation of the protein of interest; and

(3) eukaryotic cells (IV) expressing MP comprising a protein of interest and a detectable tag in an extracellular domain and at least 1 detectable tag in an intracellular domain, where the tags are different from each other and the protein of interest undergoes translocation in the eukaryotic cells upon contact with or exposure to a condition.

USE - The method is useful for determining translocation of a protein of interest such as aquaporin-2, cystic fibrosis transmembrane conductance regulator, gastric H⁺/K⁺ATPase, in particular GLUT4 from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or a stimulator. (III) is useful for assessing the effect of a drug on translocation of a protein such as GLUT4. Such drugs are useful in treating insulin resistance such as in adult-onset diabetes, obesity and polycystic ovary syndrome.

ADVANTAGE - Translocation of the protein of interest can be

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easily assessed using the tags. The tags can be detected individually, quantified and the addition of tags does not alter trafficking of the protein of interest.

Dwg.0/7

L14 ANSWER 3 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-571821 [48] WPIDS

DOC. NO. CPI: C1999-166854

TITLE: New isolated RGS-GEF polypeptides, used to develop products for modulating, e.g. cell proliferation and integrin-mediated interactions.

DERWENT CLASS: B04 D16

INVENTOR(S): BOLLAG, G; HART, M J; JIANG, X; KOZASA, T; POLAKIS, P; ROSCOE, W; STERNWEIS, P

PATENT ASSIGNEE(S): (ONYX-N) ONYX PHARM INC; (TEXA) UNIV TEXAS SYSTEM

COUNTRY COUNT: 82

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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WO 9947557	A2	19990923	(199948)*	EN	75
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RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
MW NL OA PT SD SE SL SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI
GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT
LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT UA UG UZ VN YU ZW

AU 9931038	A	19991011	(200008)		
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EP 1064373	A2	20010103	(200102)	EN	
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R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9947557	A2	WO 1999-US6051	19990318
AU 9931038	A	AU 1999-31038	19990318
EP 1064373	A2	EP 1999-912727	19990318
		WO 1999-US6051	19990318

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9931038	A Based on	WO 9947557
EP 1064373	A2 Based on	WO 9947557

PRIORITY APPLN. INFO: US 1998-78634 19980318

Searcher : Shears 308-4994

AN 1999-571821 [48] WPIDS

AB WO 9947557 A UPAB: 19991122

NOVELTY - Isolated RGS-guanine nucleotide exchange factor (GEF) polypeptides are new.

DETAILED DESCRIPTION - A novel isolated RGS-GEF polypeptide or a biologically active fragment consists of an RGS domain of a GEF protein.

INDEPENDENT CLAIMS are also included for the following:

(1) an isolated RGS-GEF polypeptide or a biologically active fragment comprising an RGS domain of a GEF protein, with the proviso that the polypeptide does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain;

(2) an isolated RGS-GEF polypeptide, or a biologically active fragment, where the polypeptide is selected from p115 Rho-GEF, Lsc, KIAA380, and where the polypeptide is mutated in the RGS domain, and where the polypeptide has a specific binding affinity for a G protein alpha subunit (GAS), or a GTPase activating activity for a GAS;

(3) an isolated RGS-GEF nucleic acid consisting of a nucleotide sequence (NS) encoding a polypeptide comprising an RGS domain of a GEF protein;

(4) a nucleic acid as in (3) but, where the polypeptide does not include a DH domain or a PH domain;

(5) a transformed cell containing a nucleic acid as in (4);

(6) a vector comprising a nucleic acid as in (4), and

(7) identifying or assaying a molecule that:

(a) inhibits or enhances binding of a monomeric G protein guanine nucleotide exchange factor to a GAS comprising:

(i) incubating the GAS, or fragments with the monomeric G protein nucleotide exchange factor, or fragments, in the presence and absence of a test molecule, and

(ii) determining whether the presence of the test molecule inhibits or enhances binding between the monomeric G-protein guanine nucleotide exchange factor and the GAS;

(b) inhibits or enhances a stimulatory effect of a GEF on a GAS GTPase activity comprising:

(i) as in (ai), and

(ii) determining whether the presence of the test molecule inhibits or enhances the stimulatory effect of the GEF protein on GAS GTPase activity;

(c) specifically inhibits the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising conducting a first assay by:

(i) incubating an activated GAS, or its fragments, with a GEF protein, or fragments, and a monomeric G protein, or its fragments, in the presence and absence of a test inhibitor;

(ii) conducting a second assay by incubating a GEF protein, or fragments, and a monomeric G protein. or fragments in the presence

and absence of the test inhibitor, and

(iii) determining whether any inhibitory effect of the test inhibitor in the first assay is greater than any inhibitory effect of the test inhibitor in the second assay;

(d) specifically enhances the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising:

(i) conducting a first assay by incubating an activated GAS, or fragments with a GEF protein, and fragments, and a monomeric G protein, or fragments in the presence and absence of a test enhancer;

(ii) as in (cii), but in the presence/absence of the test enhancer, and

(iii) determining whether any enhancing effect of the test enhancer in the first assay is greater than any enhancing effect of the test enhancer in the second assay;

(e) mimics the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein comprising:

(i) identifying a test compound that exhibits a binding affinity for the RGS domain of GEF proteins, or fragments, incubating a GEF protein or fragments, and monomeric G protein, or fragments in the presence or absence of the test compound, and

(ii) determining whether the test compound exhibits a stimulatory effect on GEF mediated nucleotide exchange of a monomeric G protein, and

(f) mimics the stimulatory effect of an RGS domain of a GEF protein on GTPase activity of a GAS comprising:

(i) identifying a test compound that exhibits a binding affinity for a GAS, and

(ii) incubating a GTP loaded GAS in the presence or absence of the test compound to determine whether the test compound has a stimulatory effect on GAS GTPase activity.

USE - The RGS-GEF polypeptides can be used for modulating an activity of a GAS (claimed). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), growth control, morphogenesis, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of transgenic animals.

ADVANTAGE - None given.

Dwg.0/18

L14 ANSWER 4 OF 9 MEDLINE

DUPLICATE 1

ACCESSION NUMBER: 1999439712 MEDLINE

Searcher : Shears 308-4994

09/587574

DOCUMENT NUMBER: 99439712 PubMed ID: 10508919
TITLE: A novel ADP-ribosylation like factor (ARL-6),
interacts with the **protein-**
conducting channel SEC61beta subunit.
AUTHOR: Ingley E; Williams J H; Walker C E; Tsai S; Colley S;
Sayer M S; Tilbrook P A; Sarna M; Beaumont J G;
Klinken S P
CORPORATE SOURCE: Laboratory for Cancer Medicine, Department of
Biochemistry, The University of Western Australia and
Royal Perth Hospital, Perth, W.A., Australia.
SOURCE: FEBS LETTERS, (1999 Oct 1) 459 (1) 69-74.
Journal code: EUH; 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF031903; GENBANK-AF133669; GENBANK-AF133670;
GENBANK-AF133910; GENBANK-AF133911; GENBANK-AF133912;
GENBANK-AF133913
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991101

AB We report here the isolation of a new member of the ADP-ribosylation factor (ARF)-like family (ARL-6) present in the J2E erythroleukemic cell line, but not its myeloid variants. Consistent with this lineage-restricted expression, ARL-6 mRNA increased with erythropoietin-induced maturation of J2E cells, and decreased with interleukin 6-induced differentiation of M1 monoblastoid cells. In tissues, ARL-6 mRNA was most abundant in brain and kidney. While ARL-6 protein was predominantly cytosolic, its membrane association increased following exposure to GTP-gammaS, like many members of the ARF/ARL family. Using the yeast two-hybrid system, six molecules which interact with ARL-6 were identified including SEC61beta, a subunit of the heterotrimeric **protein conducting** channel SEC61p. Co-immunoprecipitation of ARL-6 confirmed a stable association between ARL-6 and SEC61beta in COS cells. These results demonstrate that ARL-6, a novel member of the ADP-ribosylation factor-like family, interacts with the SEC61beta subunit.

L14 ANSWER 5 OF 9 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1997-183797 JAPIO
TITLE: PHYSIOLOGICALLY ACTIVE PROTEIN RHOTEKIN
INVENTOR: NARUMIYA SHU
PATENT ASSIGNEE(S): KIRIN BREWERY CO LTD, JP (CO 330755)
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
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Searcher : Shears 308-4994

 JP 09183797 A 19970715 Heisei (6) C07K014-47

JP

APPLICATION INFORMATION

ST19N FORMAT: JP1995-354328 19951228
 ORIGINAL: JP07354328 Heisei
 SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
 Applications, Vol. 97, No. 7

AN 1997-183797 JAPIO

AB PURPOSE: TO BE SOLVED: To obtain a new protein having activated
 Rho-protein binding ability, inhibiting Rho-protein GTPase activity,
 thus capable of inhibiting tumor development and
 metastasis through neutralizing Rho-protein involving tumor
 development and metastasis.

CONSTITUTION: protein is a new physiologically active protein
 Rhotekin (or its modified product), which has activated Rho-protein
 binding ability and inhibits Rho-protein GTPase activity, containing
 part or the whole of an amino acid sequence of the formula, or an
 equivalent sequence thereto. This protein is capable of neutralizing
 the Rho protein closely involving tumor development and
 metastasis, thus of inhibiting tumor development and
 metastasis. This new protein is obtained by
 conducting a library screening by yeast-two-hybrid system
 using mouse fetal cDNA library to isolate the gene of mouse's
 activated Rho- protein-binding protein followed by integrating a
 vector with the gene which is then manifested in host cells.

L14 ANSWER 6 OF 9 MEDLINE

DUPLICATE 2

ACCESSION NUMBER: 96408699 MEDLINE

DOCUMENT NUMBER: 96408699 PubMed ID: 8813706

TITLE: Co-translational effects of temperature on membrane
 insertion and orientation of P-glycoprotein
 sequences.

AUTHOR: Zhang J T; Chong C H

CORPORATE SOURCE: Department of Physiology and Biophysics, University
 of Texas Medical Branch, Galveston 77555-0641, USA.

CONTRACT NUMBER: CA-64539 (NCI)

SOURCE: MOLECULAR AND CELLULAR BIOCHEMISTRY, (1996 Jun 7) 159
 (1) 25-31.

Journal code: NGU; 0364456. ISSN: 0300-8177.

PUB. COUNTRY:

Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199612

ENTRY DATE:

Entered STN: 19970128

Last Updated on STN: 19970128

Entered Medline: 19961210

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. It may also function as a peptide transporter, a volume-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp 1 Pgp is expressed in more than one topological form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by soluble cytoplasmic factors. Different topological structures of Pgp may be related to its different functions. In this study, we examined the effects of translation temperature on the membrane insertion process and the topologies of Pgp. Using the rabbit reticulocyte lysate expression system, we showed that translation at different temperatures affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgp 1 Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp molecules may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temperature sensitive manner. We speculate that manipulating temperature may provide a way to understand the structure-function relationship of Pgp and help overcome Pgp-related multidrug resistance of cancer cells.

L14 ANSWER 7 OF 9 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 96381595 MEDLINE
 DOCUMENT NUMBER: 96381595 PubMed ID: 8789608
 TITLE: Expression of mRNAs of multiple growth factors and receptors by neuronal cell lines: detection with RT-PCR.
 AUTHOR: Zaheer A; Zhong W; Lim R.
 CORPORATE SOURCE: Department of Neurology, University of Iowa College of Medicine and Veterans Affairs Medical Center, Iowa City 52242, USA.
 SOURCE: NEUROCHEMICAL RESEARCH, (1995 Dec) 20 (12) 1457-63. Journal code: NX9; 7613461. ISSN: 0364-3190.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199610
 ENTRY DATE: Entered STN: 19961106
 Last Updated on STN: 20000303
 Entered Medline: 19961018

AB Neurons and glia are capable of both secreting and responding to a large variety of growth factors. However, information on multiple expression of growth factors and their receptors was usually obtained from uncorrelated observations, using cells from various

animals of origin, developmental stages, growth phases, culture ages and culture conditions. Because of its specificity and extreme sensitivity, reverse transcription-polymerase chain reaction (RT-PCR) is uniquely suitable to study a large panel of growth factors and their receptors from a limited cell sample, free of these intervening variables. In this paper we evaluate the expression of mRNA of a total of 35 growth factor-related proteins by conducting RT-PCR on three neuronal cell lines: the PC12 rat pheochromocytoma line, the MAH rat sympathoadrenal progenitor line, and the N18 mouse neuroblastoma line. Three types of results are presented. The first confirms the existing knowledge such as the presence of Trk-A (NFG receptor) in PC12. The second consists of new information that expands and extends earlier observations, such as the presence of CNTF receptor complex in PC12, which explains our previous report that CNTF enhances the biological effects of NGF on these cells. The third consists of novel information that leads the way to further experimentation by the more conventional methods. These include the strong expression of Trk-B by MAH, predicting the biological responsiveness of MAH to BDNF and NT-4, and the expression of CNTF receptor in N18. Our results also suggest that CNTF is an autocrine factor for PC12 and MAH, since both lines express the growth factor as well as the receptor. Thus, RT-PCR is a valuable tool in growth factor research that can be used in complement to, and interactively with, other approaches such as bioassay, receptor binding, and immunochemical determination. It will be particularly useful for screening a large number of growth factors in minute areas of the brain in patients suffering from neurodegenerative diseases such as Parkinson's and Alzheimer's.

L14 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2001 BIOSIS
 ACCESSION NUMBER: 1991:333595 BIOSIS
 DOCUMENT NUMBER: BR41:30145
 TITLE: REGULATION OF SQUAMOUS CELL MARKER SMALL PROLINE-RICH
 PROTEIN IN CONDUCTING AIRWAY
 EPITHELIUM.
 AUTHOR(S): AN G; ROBINSON C B; TESFAIZZI J; CARLSON D M; WU R
 CORPORATE SOURCE: CALIF. PRIMATE RES. CENT., UNIV. CALIF., DAVIS,
 CALIF. 95616.
 SOURCE: INTERNATIONAL CONFERENCE OF THE AMERICAN LUNG
 ASSOCIATION AND THE AMERICAN THORACIC SOCIETY,
 ANAHEIM, CALIFORNIA, USA, MAY 12-15, 1991. AM REV
 RESPIR DIS, (1991) 143 (4 PART 2), A515.
 CODEN: ARDSBL. ISSN: 0003-0805.
 DOCUMENT TYPE: Conference
 FILE SEGMENT: BR; OLD
 LANGUAGE: English

L14 ANSWER 9 OF 9 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 82216354 MEDLINE
 DOCUMENT NUMBER: 82216354 PubMed ID: 7086652
 TITLE: Antitumor agents XLVIII: Structure-activity relationships of quassinoids as in vitro protein synthesis inhibitors of P-388 lymphocytic leukemia tumor cell metabolism.
 AUTHOR: Liou Y F; Hall I H; Okano M; Lee K H; Chaney S G
 CONTRACT NUMBER: CA 17625 (NCI)
 CA 22929 (NCI)
 CA 26466 (NCI)
 SOURCE: JOURNAL OF PHARMACEUTICAL SCIENCES, (1982 Apr) 71 (4) 430-5.
 Journal code: JO7; 2985195R. ISSN: 0022-3549.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 198208
 ENTRY DATE: Entered STN: 19900317
 Last Updated on STN: 19980206
 Entered Medline: 19820826

AB A series of brusatol, bisbrusatol, and bruceantin esters were examined for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compounds which produced high T/C % values (170-272) resulted in ID50 of 5.4-15.5 microM for inhibition of whole cell protein synthesis, ID50 of 1.3-13 microM for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 microM for inhibition of polyuridine directed polyphenylalanine synthesis using "runoff" ribosomes and a "pH 5" enzyme preparation. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. Bruceantin, brusatol, and bisbrusatolyl malonate allowed a runoff of the polyribosomes to 80S free ribosomes. However, formation of the ternary complex and 80S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H]methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. These studies also suggest that the free 80S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. This proves quassinoids are elongation inhibitors of tumor cells. A strong correlation was observed between

09/587574

potent antileukemic activity and the ability to inhibit protein
synthesis in P-388 lymphocytic leukemia cells.

FILE 'HOME' ENTERED AT 11:25:17 ON 11 JUN 2001

Searcher : Shears 308-4994

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: June 7, 2001, 00:26:58 ; Search time 80.96 Seconds
(without alignments)
86.846 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639

Sequence: 1 WTKSLHSLGQDQAYLFRT.....VMEENAVQFLTSDILEYV 123

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	639	100.0	840	20	W93570 Human conductin pr
2	639	100.0	840	20	W93569 Human conductin pr
3	407	63.7	992	20	W96265 Murine axlin. Mus
4	401	62.8	900	20	W96264 Human axlin. Homo
5	186.5	29.2	235	21	Y97153 Human regulator of
6	177.5	27.8	235	21	Y97154 Murine regulator o
7	167.5	26.2	116	20	Y41020 RGS2 protein RGS r
8	167.5	26.2	220	21	B56929 Human prostate can
9	165	25.8	217	21	B43847 Human cancer assoc
10	164.5	25.7	116	20	Y41021 RGS3 protein RGS r
11	161	25.2	115	20	Y41019 RGS1 protein RGS r

12	160	25.0	181	19	W44834 Human p26 protein.
13	160	25.0	207	21	B54360 Human pancreatic c
14	160	25.0	243	19	W30561 Human regulator of
15	156.5	24.5	118	20	Y41001 Mouse RGS2 protein
16	156	24.4	181	19	W44833 Rat p26 protein se
17	155	24.3	181	19	W44835 Mouse p26 protein.
18	154.5	24.2	181	19	W62075 Human regulator of
19	154.5	24.2	181	21	Y53931 A human regulator
20	153	23.9	115	20	Y41024 RGS10 protein RGS
21	152.5	23.9	118	20	Y41000 Rat RGS4 protein R
22	146.5	22.9	116	20	Y41022 RGS4 protein RGS r
23	140.5	22.0	201	19	W59293 Mouse RAR1.1 prot
24	139.5	21.8	116	20	Y41028 Human GAIP protein
25	136.5	21.4	116	20	Y41026 RGS14 protein RGS
26	136.5	21.4	202	17	R88995 p53 response prote
27	136.5	21.4	202	18	W08133 Human cytokine res
28	136.5	21.4	202	19	W59294 Human RAR1.1 prot
29	136.5	21.4	202	21	Y87952 Human CRI protein.
30	135.5	21.2	159	19	W30560 Human regulator of
31	128	20.0	119	20	Y41004 Rat RGS14 protein
32	127.5	20.0	210	21	B41985 Human OREX ORF179
33	127	19.9	117	20	Y41027 rap1/2B.P. protein
34	125.5	19.6	118	20	Y41002 Human GAIP protein
35	123.5	19.3	217	21	B44826 Gene 48 human secr
36	123.5	19.3	217	21	B44827 Human secreted pro
37	123.5	19.3	555	18	W10167 Nematode regulator
38	116.5	18.2	116	20	Y41018 RET-RGS1 protein R
39	115	18.0	445	21	Y99655 Human GTPase assoc
40	114	17.8	123	18	W10178 Regulator of G-pro
41	113	17.7	119	20	Y41003 Rat RGS12 protein
42	110	17.2	117	20	Y41025 RGS12 protein RGS
43	101	15.8	420	18	W10168 Human regulator of
44	98	15.3	115	20	Y41023 RGS7* protein RGS
45	78	12.2	772	18	W34567 Thermotoga maritima

ALIGNMENTS

RESULT 1	
ID W93570	W93570 standard; Protein; 840 AA.
XX W93570;	
XX AC	
XX DT	17-JUN-1999 (first entry)
XX DE	Human conductin protein.
XX KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;
KW	tumour suppressor.
XX OS	
OS	Homo sapiens.
XX PN	
PN	W09911780-A2.
XX PD	
PD	11-MAR-1999.
XX PF	
PF	01-SEP-1998; 98WO-DE02621.
XX PR	
PR	02-SEP-1997; 97DE-1038205.
XX PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI	
PI	Behrens J, Birchmeier W;
XX DR	
DR	WPI; 1999-214706/18.
XX DR	N-PSDB; X23370.
XX PT	
PT	Tumor-suppressing protein conductin - used for treatment and
PT	diagnosis of tumors

XX Claim 11; Fig 3; 22pp; German.
 PS
 CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy. While
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 CC
 XX Sequence 840 AA:

Query Match 100.0%; Score 639; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2,7e-66;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFROMLKDKTLRVAKAIYKR 60
 Db 78 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFROMLKDKTLRVAKAIYKR 137
 QY 61 YIENNSVSKOLKPAKTYIRDPGIRKQOIGSVMPDOATEIOAVMEENAYQVFLTSDIYL 120
 Db 138 YIENNSVSKQIKPATKYIRDPGIRKQIGSVMDQATEIGAVMEENAYQVFLTSDIYL 197
 QY 121 EYV 123
 Db 198 EYV 200

RESULT 2
 ID W93569 standard; Protein; 840 AA.
 AC W93569;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE Human conductin protein.

XX Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
 KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
 KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
 KW tumour suppressor.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 78..200
 FT Domain /note="Regulator of G protein signalling domain as
 FT Binding-site 343..396 described in claim 12"
 FT /note="GSK-3-beta binding region as described in
 FT Binding-site 397..465 claim 13"
 FT /note="Beta-catenin binding domain as described in
 FT Region 783..833 claim 14"
 FT /note="Dishevelled homology region as described in
 FT claim 15"

XX WO9911780-A2.
 XX 11-MAR-1999.
 XX PD
 XX 01-SEP-1998; 98WO-DE02621.
 XX PF
 XX 02-SEP-1997; 97DE-1038205.
 XX PR
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PA
 XX

PI Behrens J, Birchmeier W;
 XX
 DR WPI; 1999-214706/18.
 DR N-PSDB; X23369.
 XX
 PT Tumor-suppressing protein conductin - used for treatment and
 PT diagnosis of tumors
 XX
 PS Claim 11; Fig 1; 22pp; German.
 XX

CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 CC
 XX Sequence 840 AA:

Query Match 100.0%; Score 639; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2,7e-66;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFROMLKDKTLRVAKAIYKR 60
 Db 78 WTKSLHSLLGDDGAYLFRFLERKCVDTLDFWACNGFROMLKDKTLRVAKAIYKR 137
 QY 61 YIENNSVSKOLKPAKTYIRDPGIRKQOIGSVMPDOATEIOAVMEENAYQVFLTSDIYL 120
 Db 138 YIENNSVSKQIKPATKYIRDPGIRKQIGSVMDQATEIGAVMEENAYQVFLTSDIYL 197
 QY 121 EYV 123
 Db 198 EYV 200

RESULT 3
 ID W96265 standard; Protein; 992 AA.
 AC W96265;
 XX
 DT 14-JUN-1999 (first entry)
 XX
 DE Murine axin.

XX Axin; cancer; breast cancer; colorectal cancer;
 KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin.
 XX
 OS Mus musculus.

XX WO9902179-A1.
 XX 21-JAN-1999.
 XX PD
 XX 09-JUL-1998; 98WO-US14414.
 XX PF
 XX 10-JUL-1997; 97US-0890865.
 XX PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX PA
 XX Constantini F, Zeng L;
 XX
 XX WPI; 1999-120510/10.
 XX DR N-PSDB; X09013.
 XX
 XX Newly isolated nucleic acid encoding "axis inhibition" protein
 PT (Axin) - useful for detecting, diagnosing and treating cancer

XX XX

FT	Misc-difference 111	/note-	"Makes direct contact with G-ship
F-1			

FT MISC-difference 112 /note= "Makes direct contact with G-alpha-1"
 FT MISC-difference 115 /note= "forms part of hydrophobic core"
 FT MISC-difference 116 /note= "forms part of hydrophobic core"
 FT MISC-difference 138 /note= "forms part of hydrophobic core"
 FT MISC-difference 139 /note= "forms part of hydrophobic core"
 FT MISC-difference 142 /note= "forms part of hydrophobic core"
 FT MISC-difference 143 /note= "forms part of hydrophobic core"
 FT MISC-difference 151 /note= "forms part of hydrophobic core"
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 FT MISC-difference 198 /note= "forms part of hydrophobic core"
 PN MO200046236-A2.
 XX 10-ADG-2000.
 PF 04-FEB-2000; 2000MO-US02977.
 XX 04-FEB-1999; 99US-0244314.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Hodge MR, Yowe D;
 XX WPI: 2000-532893/48.
 DR N-PSDB; A52089.
 PT Novel regulator of G-protein signaling nucleic acids and polypeptides,
 PT useful as diagnostic and investigative tools and to treat G-protein
 PT signaling disorders
 PS Claim 8; Page 102; 105pp; English.
 CC The RGS (regulators of G-protein signaling) protein genes, clones h16395
 CC and m1975, were identified in human and murine spleen cDNA libraries. The
 CC C-terminal location of the RGS domain is consistent with RGSs known to
 CC act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-1
 CC linked receptors support rapid adhesion and directed migration of
 CC leukocytes and other cell types. The novel RGS proteins may be used to
 CC modulate cell adhesion and chemotaxis, e.g. for aiding wound repair.
 CC The RGS proteins, related cDNAs and anti-RGS antibodies are useful for
 CC modulation, diagnosis and treatment of immune and respiratory disorders.
 SO Sequence 235 AA;

Query Match 29.2%; Score 186.5; DB 21; Length 235;
 Best Local Similarity 34.6%; Pred. No. 5,9e-14;
 Matches 44; Conservative 25; Mismatches 43; Indels 15; Gaps 3;
 QY 1 WPKSLSLIGDDGALFETPIFERKCVTLDFWACNGFR-----QMNLKDTKTLRYA 54
 Db 83 wgesfklshldglaeftrfkfseentlefwiacedfkkskpgqqlhik-----a 135
 QY 55 KAIYKRIENNSVSKOLKPKATKTYIRDGIRKQOIGSVWFDOAQREIQAVMEENAYVEL 114
 Db 136 kaiyekfiqtdapkenuldfhkevtinsitqptlth--fdaagsryqimeqdsytrfl 193
 QY 115 TSDIYLE 121
 Db 194 ksdilyd 200
 RESULT 6
 Y97154
 ID Y97154 standard; Protein; 235 AA.
 AC Y97154;
 DE 04-DEC-2000 (first entry)
 XX Murine regulator of G-protein signaling protein.
 KW RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
 KW G-alpha protein; cell adhesion; chemotaxis; vlnetrary; immunosuppressor;
 KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
 KW cyostatic; hepatotropic; anti-anaemic; modulator; gene therapy.
 OS Mus sp.
 XX
 FH Key
 FT Domain
 FT Location/Qualifiers
 FT 82..201
 FT /label= RGS_domain
 FT MISC-difference 83
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 90
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 100
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 103
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 104
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 107
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 109
 FT /note= "Makes direct contact with G-alpha-1"
 FT MISC-difference 111
 FT /note= "Makes direct contact with G-alpha-1"
 FT MISC-difference 112
 FT /note= "Makes direct contact with G-alpha-1"
 FT MISC-difference 115
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 116
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 138
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 139
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 142
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 143
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 151
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 152
 FT /note= "forms part of hydrophobic core"
 FT MISC-difference 154
 FT /note= "Makes direct contact with G-alpha-1"

FT MISC-difference 183 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 184 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 187 /note= "forms part of hydrophobic core"
FT MISC-difference 188 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 189 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 191 /note= "forms part of hydrophobic core"
FT MISC-difference 192 /note= "Makes direct contact with G-alpha-1"
FT MISC-difference 193 /note= "forms part of hydrophobic core"
FT MISC-difference 193 /note= "forms part of hydrophobic core"
FT MISC-difference 198 /note= "forms part of hydrophobic core"
FT MISC-difference 198 /note= "forms part of hydrophobic core"
PN WO200046236-A2.
PD 10-AUG-2000.
PF 04-FEB-2000: 2000MO-US02977.
PR 04-FEB-1999: 99US-0244314.
PA (MILL-) MILLENNIUM PHARM INC.
PI Hodge MR, Yowe D;
XX WPI: 2000-532893/48.
DR N-PSDB: A52090.
XX Novel regulator of G-protein signaling nucleic acids and polypeptides,
PT useful as diagnostic and investigative tools and to treat G-protein
PT signaling disorders
XX
XX Claim 8: Page 104; 105pp; English.
XX
XX The RGS (regulators of G-protein signaling) protein genes, clones h16395
CC and m1975, were identified in human and murine spleen cDNA libraries. The
CC respectively. Both proteins have unique N- and C-terminal sequences. The
CC C-terminal location of the RGS domain is consistent with RGSs known to
CC act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-1
CC linked receptors support rapid adhesion and directed migration of
CC leukocytes and other cell types. The novel RGS proteins may be used to
CC modulate cell adhesion and chemotaxis, e.g. for aiding wound repair.
CC The RGS proteins, related cDNAs and anti-RGS antibodies are useful for
CC modulation, diagnosis and treatment of immune and respiratory disorders.
CC
XX
SQ Sequence 235 AA:

Query Match 27.8%; Score 177.5; DB 21; Length 235;
Best Local Similarity 31.7%; Pred. No. 6.7e-13;
Matches 39; Conservative 28; Mismatches 53; Indels 3; Gaps 2;

OY 1 WTRSLSLGDDGAVLFRFLERKCVDTLDFWFCNGFRONMLKDTKTLRVAKAIYKR 60
DB 83 wseafdkllshrgvdaftfkfktefseentefwacedfkck-epqqlkxakayek 141
OY 61 YIENNSVSKQLKPARTYIRDGIRKQOIGSVMPDQOTETQAVMEENAVOVLTSIDYL 120
DB 142 ftdndpkeknidftkrevlakslagptlins--fdtqgsrvyqjmehsykrflksetyl 199
OY 121 EYV 123
DB 200 h11 202

RESULT 7

Y41020
ID Y41020 standard; protein; 116 AA.
XX
XX Y41020;
AC
XX
XX 06-DEC-1999 (first entry)
DT
XX
XX RGS2 protein RGS region.
DE
XX
XX RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer;
XX G protein alpha subunit; cell proliferation; growth control; hemostasis;
XX morphogenesis; stress fiber formation; integrin-mediated interaction;
XX embryonic development; tumor cell growth; cell death; leukocyte homing;
XX bone resorption; clot retraction; db1 homology domain; mechanical stress;
XX pleckstrin homology domain.
OS
XX
XX Unidentified.
XX
XX WO9947557-A2.
PN
XX
XX 23-SEP-1999.
PD
XX
XX 18-MAR-1999: 99MO-US06051.
PF
XX
XX 18-MAR-1998: 98US-0078634.
PR
XX
XX (ONYX-) ONYX PHARM INC.
PA
XX
XX Bollag G, Hart MJ, Roscoe W, Polakis P, Sternweis P, Kozasa T;
PI Jiang X;
XX
XX WPI: 1999-571821/48.
DR
XX
XX New isolated RGS-GEF polypeptides, used to develop products for
PT modulating, e.g. cell proliferation and Integrin-mediated interactions
PT
XX
XX Disclosure; Fig 18; 75pp; English.
PS
XX
XX The invention relates to isolated RGS-guanine nucleotide exchange factor
CC (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an
CC RGS domain of a GEF protein and does not comprise a db1 homology (DH)
CC domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can
CC be used for modulating an activity of a G protein alpha subunit (GAS).
CC The products can be used for the regulation of biological pathways in
CC which a RGS-GEF polypeptide is involved, particularly pathological
CC conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth
CC control, stress fiber formation, and integrin-mediated interactions, such
CC as embryonic development, tumor cell growth and metastasis, programmed
CC cell death, hemostasis, leukocyte homing and activation, bone resorption,
CC clot retraction, and the response of cells to mechanical stress. The
CC products can also be used for detection, diagnosis and production of
CC transgenic animals. Sequences Y41014-028 represent RGS regions of several
CC proteins.
CC
XX
SQ Sequence 116 AA:

Query Match 26.2%; Score 167.5; DB 20; Length 116;
Best Local Similarity 32.8%; Pred. No. 4e-12;
Matches 39; Conservative 20; Mismatches 57; Indels 3; Gaps 2;

OY 1 WTRSLSLGDDGAVLFRFLERKCVDTLDFWFCNGFRONMLKDTKTLRVAKAIYKR 60
DB 1 wseafdkllshrgvdaftfkfktefseentefwacedfkck-spqklssarkxytd 59
OY 61 YIENNSVSKQLKPARTYIRDGIRKQOIGSVMPDQOTETQAVMEENAVOVLTSIDYL 119
DB 60 flekapkeknidftkrliaqnl--deatsgcttaqkrvysimnnsyprllesefy 116

RESULT 8
B56929

[illegible][illegible]

OY 59 KRIENSVSVKOLKPAATKYIRDGIRKQIGSMFDOAQTEIQAVMEENAVQVLTSDI 118
 Db 57 kafyhsda--akqindfirtrestakkikaprcctcdaekwlyltmekdsyrfllksdi 114
 OY 119 Y 119
 Db 115 Y 115

RESULT 12
 W44834
 ID W44834 standard; peptide: 181 AA.
 AC W44834;
 NC W44834;
 DT 21-JUL-1998 (first entry)
 DE Human p26 protein.
 DE Human p26 protein.
 DE Human p26; brain; hybridisation; dephosphorylase inhibitory activity;
 KM probe; rat; haematogenesis.
 KM Homo sapiens.
 OS JP09299092-A.
 PN 25-NOV-1997.
 PD 26-DEC-1996; 96JP-0347877.
 PF 12-MAR-1996; 96JP-0055196.
 PR (TAKE) TAKEDA CHEM IND LTD.
 PA WPI: 1998-056555/06.
 DR N-PSDB; V19304.
 XX Mammalian p26 proteins and their related DNA - useful for screening
 PT for de-phosphorylase inhibitory compounds
 PS Claim 1; Fig 2: 40pp; Japanese.
 XX
 PS This amino acid sequence represents the human p26 protein. The encoding
 CC gene sequence was isolated from a human thymus cDNA library by phage
 CC plaque hybridisation using the rat p26 cDNA sequence (V19303) as a probe.
 CC The screening isolated the corresponding 889 bp sequence. p26 protein is
 CC useful as a reagent for screening for compounds having dephosphorylase
 CC inhibitory activity. It is also useful as a treating and preventive
 CC agent for diseases related to the haematogenic system.
 CC
 SO Sequence 181 AA;

Query Match 25.0%; Score 160; DB 19; Length 181;
 Best Local Similarity 32.0%; Pred. No. 5.4e-11;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSLHSLLGDGDGAVLEFTELEKRCVDTLDFWACNGFRQNLKDKTKLRVAKAIYKR 60
 Db 38 waaslenlledepegvkrifreikfeeseenvlflwaccedfkmgdk-tgmqekakeiynt 96
 OY 61 YIENNSVSVKOLKPAATKYIRDGIRKQIGSMFDOAQTEIQAVMEENAVQVLTSDIYL 120
 Db 97 fl--ssksssgvnnveggrlnekllieep-hplmtgkldqgflnltmkydsysrflksdflf 153
 OY 121 EX 122
 Db 154 Kh 155

RESULT 13
 B54360

ID B54360 standard; Protein: 207 AA.
 AC B54360;
 NC 09-MAR-2001 (first entry)
 DT Human pancreatic cancer antigen protein sequence SEQ ID NO:812.
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:812.
 DE Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KM detection; diagnosis; identification; cytostatic; neuroprotective;
 KM neotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KM antinflammatory; cardiant; gene therapy; chromosome mapping;
 KM linkage analysis; tissue identification; tissue typing; forensic;
 KM neutral; immune system; muscular; reproductive; gastrointestinal;
 KM pulmonary; cardiovascular; renal; proliferative.
 OS Homo sapiens.
 OS WO200055320-A1.
 PN 21-SEP-2000.
 PD 08-MAR-2000; 2000WO-US05989.
 PF 12-MAR-1999; 99US-0124270.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI WPI: 2000-579444/54.
 DR N-PSDB; C99125.
 XX New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 XX Claim 11; Page 1267-1268; 1379pp; English.
 PS C98773 to C99231 encode the human pancreatic cancer associated proteins,
 CC called pancreatic cancer antigens, given in B54008 to B54466. The human
 CC pancreatic cancer antigens have cytostatic, neuroprotective, neotropic,
 CC immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and
 CC antinflammatory activities, and can be used in gene therapy. The
 CC polynucleotide and proteins can be used for preventing, treating, or
 CC ameliorating a medical condition or in assays for diagnosing a
 CC pathological condition or a susceptibility to one in a subject. Binding
 CC partners to the proteins and the activity of the proteins can be
 CC identified. The pancreatic cancer antigens can be used to detect, treat
 CC or prevent pancreatic disorders, especially cancer. Agonists and
 CC antagonists to the antigens can be screened for. The pancreatic cancer
 CC antigen polynucleotides can be used to design nucleic acid hybridisation
 CC probes that can be used in chromosome mapping, linkage analysis, tissue
 CC identification and/or typing and a variety of forensic and diagnostic
 CC methods. The proteins can be used to generate antibodies which are used
 CC to purify, detect and target the polypeptides, including both in vivo
 CC and in vitro diagnostic and therapeutic methods. The proteins can be
 CC used to treat or prevent neural, immune system, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal or proliferative
 CC disorders. C99232 to C99240 and B54467 represent sequences used in the
 CC exemplification of the present invention.
 CC
 SO Sequence 207 AA;

Query Match 25.0%; Score 160; DB 21; Length 207;
 Best Local Similarity 32.0%; Pred. No. 6.4e-11;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSLHSLLGDGDGAVLEFTELEKRCVDTLDFWACNGFRQNLKDKTKLRVAKAIYKR 60
 Db 64 waaslenlledepegvkrifreikfeeseenvlflwaccedfkmgdk-tgmqekakeiynt 122

QY 61 YIENNSVSKOLKPAKTYIRDCIKKQIGSVMEFDOQTEIQAVMEENAYVELTSDIYL 120
 Db 123 FL--SSKASSQVNVGSGRIKNEKILEEP-hpImfGkIqdgIflmkydsYsrIksdIfI 179
 QY 121 EY 122
 Db 180 Kh 181

RESULT 14
 W30561
 ID W30561 standard; Protein: 243 AA.
 AC W30561;
 DT 18-JAN-1999 (first entry)
 DE Human regulator of G-protein signalling 2 (RGPS-2).
 XX Regulator of G-protein signalling 2; RGPS-2; human;
 KM G-protein coupled receptor; signal transduction; inflammation;
 KM cell proliferation; cancer; diagnosis; therapy.
 XX Homo sapiens.
 OS
 FH Key
 FT Location/Qualifiers
 FT 126..142
 FT /note="potential G-protein coupled receptor
 FT signature"
 FT 58..177
 FT /note="RGF motif"
 FT 8..11
 FT /note="Asn may be N-glycosylated"
 FT 235..238
 FT /note="potential cAMP- and cGMP-dependent protein
 FT kinase phosphorylation site"
 FT 11..14
 FT /note="potential casein kinase II phosphorylation
 FT site"
 FT 66..69
 FT /note="potential casein kinase II phosphorylation
 FT site"
 FT 220..223
 FT /note="potential casein kinase II phosphorylation
 FT site"
 FT 93..95
 FT /note="potential protein kinase C phosphorylation
 FT site"
 FT 97..99
 FT /note="potential protein kinase C phosphorylation
 FT site"
 FT 161..164
 FT /note="potential protein kinase C phosphorylation
 FT site"
 FT Modified-site
 PN W09844115-A2.
 PD 08-OCT-1998.
 PF 31-MAR-1998; 98MO-US06336.
 PR 31-MAR-1997; 97US-0829110.
 PA (INCY-) INCYTE PHARM INC.
 PI Goli SK, Hillman JL;
 DR WPI: 1998-557112/47.
 DR N-PSDB; V45442.
 PT New regulators of G-protein signalling - useful for, e.g. diagnosis,
 PT prevention and treatment of cancer and inflammation
 XX

PS Claim 19; Page 45; 65pp; English.
 XX This is the amino acid sequence of a novel human regulator of
 CC G-protein signalling, termed RGPS-2. It was deduced from a
 CC consensus nucleic acid sequence (see V45442) derived from thymus
 CC and other cDNA clones. RGPS-2 shares 46% and 37% identity with
 CC human BL34 and RGS4, respectively. It shows significant
 CC expression in inflamed, immortalised or cancerous cells and
 CC tissues. The invention provides 2 regulators of G-protein
 CC signalling, i.e. RGPS-2 and RGS-1 (see W30560). The invention
 CC also features nucleic acids encoding RGS polypeptides,
 CC oligonucleotides, peptide nucleic acids, fragments, portions or
 CC antisense molecules, and expression vectors and host cells. It
 CC also features antibodies specific for RGPS, and pharmaceutical
 CC compositions comprising purified RGPS. It also provides methods
 CC for stimulating cell proliferation using an RGPS or an agonist of
 CC RGPS and for treating or preventing disorders (e.g. cancer)
 CC associated with cell proliferation and inflammation using an
 CC antagonist of RGPS.
 XX

Sequence 243 AA:
 SQ
 Query Match 25.0%; Score 160; DB 19; Length 243;
 Best Local Similarity 32.0%; Pred. No. 7.8e-11;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

QY 1 WYSLSHSLGDDGAGVLEFRFLERKCVDTLDFWACNGFRONKDKTFLRAKAIYKR 60
 Db 100 waaslenllledegvkrffeflkfeseenvlfwlacedfkmgdk-tgmqekakeymt 158
 QY 61 YIENNSVSKOLKPAKTYIRDCIKKQIGSVMEFDOQTEIQAVMEENAYVELTSDIYL 120
 Db 159 FL--SSKASSQVNVGSGRIKNEKILEEP-hpImfGkIqdgIflmkydsYsrIksdIfI 215
 QY 121 EY 122
 Db 216 Kh 217

RESULT 15
 ID Y41001
 Y41001 standard; protein: 118 AA.
 AC Y41001;
 DT 06-DEC-1999 (first entry)
 DE Mouse RGS2 protein RGS domain fragment.
 XX RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer;
 KM G-protein alpha subunit; cell proliferation; growth control; hemostasis;
 KM morphogenesis; stress fiber formation; integrin-mediated interaction;
 KM embryonic development; tumor cell growth; cell death; leukocyte homing;
 KM bone resorption; clot retraction; db1 homology domain; mechanical stress;
 KM pieckstrin homology domain.
 XX Mus sp.
 OS
 PN W09947557-A2.
 PD 23-SEP-1999.
 PF 18-MAR-1999; 99MO-US06051.
 PR 18-MAR-1998; 98US-0078634.
 PA (ONYX-) ONYX PHARM INC.
 PI Bollag G, Hart MJ, Roscoe W, Polakis P, Sternweis P, Kozasa T;
 DR Jang X;
 DR WPI: 1999-571821/48.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 00:32:07 ; Search time 40.76 Seconds
(without alignments)
57.972 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WIKSLHSLGDDGAYLFR.....YMEENAYQVLTSDIYLEYV 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Issued Patents, AA: *
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	167.5	26.2	211 2	US-08-748-483-4 Sequence 4, Appl1
2	165	25.8	119 2	US-08-588-258B-31 Sequence 31, Appl1
3	165	25.8	119 3	US-08-460-505-31 Sequence 31, Appl1
4	165	25.8	119 5	PCT-US96-08295-31 Sequence 31, Appl1
5	165	25.8	196 2	US-08-829-110-5 Sequence 5, Appl1
6	165	25.8	196 2	US-08-748-483-3 Sequence 3, Appl1
7	160	25.0	243 2	US-08-829-110-3 Sequence 3, Appl1
8	158	24.7	121 2	US-08-588-258B-32 Sequence 32, Appl1
9	158	24.7	121 3	US-08-460-505-37 Sequence 32, Appl1
10	158	24.7	121 5	PCT-US96-08295-32 Sequence 32, Appl1
11	155.5	24.3	205 2	US-08-829-110-6 Sequence 6, Appl1
12	155.5	24.3	205 2	US-08-748-483-5 Sequence 6, Appl1
13	154.5	24.2	181 2	US-08-748-483-1 Sequence 1, Appl1
14	140.5	22.0	201 2	US-08-726-228-2 Sequence 2, Appl1
15	140.5	22.0	201 3	US-08-870-815-2 Sequence 2, Appl1
16	140.5	22.0	201 4	US-08-949-004-2 Sequence 2, Appl1
17	136.5	21.4	202 1	US-08-274-318-2 Sequence 2, Appl1
18	136.5	21.4	202 2	US-08-463-081B-2 Sequence 2, Appl1
19	136.5	21.4	202 2	US-08-461-379A-2 Sequence 2, Appl1
20	136.5	21.4	202 2	US-08-462-390B-2 Sequence 2, Appl1
21	136.5	21.4	202 2	US-08-754-108-2 Sequence 2, Appl1
22	136.5	21.4	202 3	US-08-870-815-4 Sequence 2, Appl1
23	136.5	21.4	202 3	US-08-463-074B-2 Sequence 2, Appl1
24	136.5	21.4	202 3	US-08-465-585C-2 Sequence 2, Appl1
25	136.5	21.4	202 3	US-08-652-446-2 Sequence 2, Appl1
26	136.5	21.4	202 4	US-08-949-004-4 Sequence 4, Appl1
27	135.5	21.2	159 2	US-08-829-110-1 Sequence 1, Appl1

28	133	20.8	123 2	US-08-588-258B-39 Sequence 39, Appl1
29	133	20.8	123 5	PCT-US96-08295-39 Sequence 39, Appl1
30	124.5	19.5	555 2	US-08-588-258B-24 Sequence 24, Appl1
31	124.5	19.5	555 3	US-08-460-505-24 Sequence 24, Appl1
32	124.5	19.5	555 5	PCT-US96-08295-24 Sequence 24, Appl1
33	116	18.2	118 2	US-08-588-258B-38 Sequence 38, Appl1
34	116	18.2	118 5	PCT-US96-08295-38 Sequence 38, Appl1
35	114	17.8	123 2	US-08-588-258B-1 Sequence 1, Appl1
36	114	17.8	123 3	US-08-460-505-1 Sequence 1, Appl1
37	114	17.8	123 5	PCT-US96-08295-1 Sequence 1, Appl1
38	113	17.7	119 2	US-08-588-258B-30 Sequence 30, Appl1
39	113	17.7	119 3	US-08-460-505-30 Sequence 30, Appl1
40	113	17.7	119 5	PCT-US96-08295-30 Sequence 30, Appl1
41	101	15.8	420 2	US-08-588-258B-40 Sequence 40, Appl1
42	101	15.8	420 5	PCT-US96-08295-40 Sequence 40, Appl1
43	64	10.0	764 1	US-08-375-300-4 Sequence 4, Appl1
44	64	10.0	764 3	US-09-177-431-4 Sequence 4, Appl1
45	64	10.0	764 5	PCT-US95-16930-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-748-483-4
Sequence 4, Application US/08748483
Patent No. 595314
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,483
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET INFORMATION: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 292037
US-08-748-483-4
Query Match 26.2%; Score 167.5; DB 2; Length 211;
Best Local Similarity 32.8%; Pred. No. 2.3e-13;

[illegible]

```

1      RESULT 2
2      US-08-588-258B-31
3      : Sequence 31, Application US/08588258B
4      : Patent No. 5929207
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: H. Robert Horvitz et al.
9      : TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
10     :
11     : NUMBER OF SEQUENCES: 41
12     :
13     : CORRESPONDENCE ADDRESS:
14     :
15     : ADDRESSEE: Clark & Elbing LLP
16     : STREET: 176 Federal Street
17     : CITY: Boston
18     :
19     : STATE: MA
20     :
21     : COUNTRY: USA
22     :
23     : ZIP: 02110
24     :
25     : COMPUTER READABLE FORM:
26     :
27     : MEDIUM TYPE: Floppy disk
28     : COMPUTER: IBM PC compatible
29     : OPERATING SYSTEM: Windows 95
30     : SOFTWARE: FastSeq Version 2.0
31     :
32     : CURRENT APPLICATION DATA:
33     :
34     : APPLICATION NUMBER: US/08/588,258B
35     : FILING DATE: January 12, 1996
36     :
37     : CLASSIFICATION: 435
38     :
39     : ATTORNEY/AGENT INFORMATION:
40     :
41     : NAME: Bleker-Brady, Kristina
42     : REGISTRATION NUMBER: 39,109
43     : REFERENCE/DOCKET NUMBER: 01997/216001
44     :
45     : TELECOMMUNICATION INFORMATION:
46     :
47     : TELEPHONE: 617-428-0200
48     :
49     : TELEFAX: 617-428-7045
50     :
51     :
52     : INFORMATION FOR SEQ ID NO: 31:
53     :
54     : SEQUENCE CHARACTERISTICS:
55     :
56     : LENGTH: 119 amino acids
57     : TYPE: amino acid
58     : STRANDEDNESS: not relevant
59     :
60     : TOPOLOGY: linear
61     :
62     : MOLECULE TYPE: protein
63     :
64     : US-08-588-258B-31

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	Query Match	25.8%;	Score 165;	DB 2;	Length 119;	
	Best Local Similarity	32.8%;	Pred. No. 2,2e-13;			
	Matches	40;	Conservative	28;	Mismatches	46;
					Indels	8;
					Gaps	3
OY	1 WTKSHSLIGDDGAYLERTFLERECVOTLDWTFACNGFR--QNMKTPTKLRAKAIY	58				
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Dd	2 MSQSLEKLLANTGGONVGESFLKSEPSSENIETWLACEYDKTESDLPCK---AEIYY	57				
OY	59 KRYIENNSVSVSKOLKPATRTYIRDCIKRKOQLGSVMFDQAOTEIAQVMEENAVOFTTSDI	118				
	: : : : : : : : : : : :					
Dd	58 KAFVHSDA-AKQINIDFRETSTAKRIKAPPTTCEDENQAKVIYTLMDKDSIPRLKS DI	115				
OY	119 YL 120					
Dd	116 YL 117					
 RESULT 3 US-08-460-505-31 ; Sequence 31, Application US/08460505						

/ Patent No.6069296
 / GENERAL INFORMATION:
 / APPLICANT: Horvitz, Robert H.
 / APPLICANT: Koelle, Michael
 / TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
 / NUMBER OF SEQUENCES: 37
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fish & Richardson P.C.
 / STREET: 225 Franklin Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02110-2804
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/460,505
 / FILING DATE: 02-JUN-1995
 / CLASSIFICATION: 800
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Bleker-Brady, Kristina
 / REGISTRATION NUMBER: 39,109
 / REFERENCE/DOCKET NUMBER: 01997/214001
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 617/542-5070
 / TELEFAX: 617/542-8906
 / TELEX: 200154
 / INFORMATION FOR SEQ ID NO: 31:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 119 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: not relevant
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / OS-08-460-505-31

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Query Match Similarity      25.8%; Score 165; DB 3; Length 119;
Best Local Similarity      32.8%; Pred. No. 2, 2e-13;
Matches      40; Conservative      28; Mismatches      46; Indels      8; Gaps      3

OY      1 WTKSLHLLGDGDGAYLFFETFLEREKCVDTLDWFACNGFR--QMNLIKDTLTVAKAIY 58
      1:::1 11:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1
Db      2 WSOSLEKLANOTGQNVFSGFLKSESEENIEFWLACEDYKKTESDLPCK---AEELI 57

OY      59 KYIENSNVSVSKOLKPAKFTYIRDIGKKQIQISWEPDQATELQAVMENNAQVFLTSDI 118
      1:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1 1:::1
Db      58 KAFVSDA-AKQINIDFRTRESTAKKIKAPPTCGDEAKQVIYTMLEKSDYPRFLKSDI 115

OY      119 YL 120
      11
Db      116 YL 117

RESULT      4
PCT-US96-08295-31
: Sequence 31, Application PC/RUS9608295
: GENERAL INFORMATION:
: APPLICANT: Massachusetts Institute of Technology
: TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 728966
; US-08-748-483-3

Query Match
Best Local Similarity 32.8%; Score 165; DB 2; Length 196;
Matches 40; Conservative 28; Mismatches 46; Indels 8; Gaps 3;

OY 1 WTKSLHSLGDDGAVLFRFLERKCYDITLDFWFCNGFR--OMNLKDTYTLRVAKAIYR 58
Db 69 WQSLEKLANOTGONVGFSLKSEFSENEIEFWLACEDYKTESDILPCK---AEIY 124
OY 59 KYIENNSVSKQLKPAKTYIRDGIRKQOIGSVFDOAQTEIOAVENAYGVFLTSDI 118
Db 125 KAFVHSDA--AKQINIDRRTRESTAKKIKAPTPTCPDEAKVITTEKDSYPRFLKSDI 182
OY 119 YL 120
Db 183 YL 184

RESULT 7
US-08-829-110-3
; Sequence 3; Application US/08829110
; Patent No. 5882890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,110
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0259 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-0555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

LIBRARY: THYMOT02
; CLONE: 343504
; US-08-829-110-3

Query Match
Best Local Similarity 25.0%; Score 160; DB 2; Length 243;
Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSLHSLGDDGAVLFRFLERKCYDITLDFWFCNGFRQMKDKITLRVAKAIYR 60
Db 100 WASLENLEDEGVKRFREFLKFSESENEVFWLACEDFKMDDK--TQMEKAEIYMT 158
OY 61 YIENNSVSKQLKPAKTYIRDGIRKQOIGSVFDOAQTEIOAVENAYGVFLTSDI 120
Db 159 FL--SSKASQVNVGQSLNKEKILEEP-HPLMFQKLDQIFNLKDYDSRFLKSDFL 215
OY 121 EY 122
Db 216 KH 217

RESULT 8
US-08-588-258B-32
; Sequence 32; Application US/08588258B
; Patent No. 5929207
; GENERAL INFORMATION:
; APPLICANT: H. Robert Horvitz et al.
; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,258B
; FILING DATE: January 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/216001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-588-258B-32

Query Match
Best Local Similarity 24.7%; Score 158; DB 2; Length 121;
Matches 38; Conservative 20; Mismatches 59; Indels 2; Gaps 2;

OY 1 WTKSLHSLGDDGAVLFRFLERKCYDITLDFWFCNGFRQMKDKITLRVAKAIYR 60
Db 2 WSEAFDELLASKYGLAFAFRFLKSECENEIEFWLACEDFKFKTK--SPKLSKARKIYTD 60
OY 61 YIENNSVSKQLKPAKTYIRDGIRKQOIGSVFDOAQTEIOAVENAYGVFLTSDI 119

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

RESULT 9

US-08-460-505-32

Sequence 32, Application US/08460505

Patent No. 6069296

GENERAL INFORMATION:

APPLICANT: Horvitz, Robert H.

APPLICANT: Koelle, Michael

TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,505

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Bieker-Brady, Kristina

REGISTRATION NUMBER: 39,109

REFERENCE/DOCKET NUMBER: 01997/214001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-460-505-32

Query Match 24.7%; Score 158; DB 3; Length 121;

Best Local Similarity 31.9%; Pred. No. 1.7e-12;

Matches 38; Conservative 20; Mismatches 39; Indels 2; Gaps 2;

Qy 1 WTKSLSLGDDGAVLFRFLERKCVDTLDFWFCNGFRONMLKDTKTLRVAKAIYKR 60

Db 2 WSEAFDELLASKYGLAFAFLKSECEENIEFWLACEDFKTKR-SFOKLSSARKIYTD 60

Qy 61 YIENNSVSKQLPKATKTYIRDCIKKQOIGSVFDDAQETIOAVMEENAYOVLTSDIY 119

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/08295

FILING DATE: 31-MAY-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/588,258

FILING DATE: 12-JAN-96

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Bieker-Brady, Kristina

REGISTRATION NUMBER: 39,109

REFERENCE/DOCKET NUMBER: 01997/216001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-08295-32

Query Match 24.7%; Score 158; DB 5; Length 121;

Best Local Similarity 31.9%; Pred. No. 1.7e-12;

Matches 38; Conservative 20; Mismatches 59; Indels 2; Gaps 2;

Qy 1 WTKSLSLGDDGAVLFRFLERKCVDTLDFWFCNGFRONMLKDTKTLRVAKAIYKR 60

Db 2 WSEAFDELLASKYGLAFAFLKSECEENIEFWLACEDFKTKR-SFOKLSSARKIYTD 60

Qy 61 YIENNSVSKQLPKATKTYIRDCIKKQOIGSVFDDAQETIOAVMEENAYOVLTSDIY 119

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

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Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

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Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

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Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Qy 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

Db 61 FIKKAPKEINIDFQRTKTLA-AQNTQEAATSGCFTTAQKRVYSILMENNYPRLSESEFY 118

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? INFORMATION FOR SEQ ID NO: 1:
?
? SEQUENCE CHARACTERISTICS:
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? LENGTH: 181 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? IMMEDIATE SOURCE:
?
? LIBRARY: Consensus

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2001, 00:39:27 ; Search time 56.43 Seconds
(without alignments)
149.795 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639

Sequence: 1 WTKSLSLSLGDDGAYLFTFT.....VMEENAYOVFLTSDIYL 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	639	100.0	838	2	T08423	Axin homolog Ax11
2	407	63.7	832	2	T08422	negative regulator
3	172.5	27.0	519	2	S78089	G-protein signalin
4	167.5	26.2	211	2	IS3020	G-0/G-1 switch reg
5	160	25.0	173	2	S71812	RG510 protein - hu
6	158.5	24.8	533	2	T31002	hypothetical prote
7	158	24.7	196	2	S43436	B cell activation
8	155.5	24.3	205	2	S78221	G-protein signalin
9	143.5	22.5	181	2	JC7228	G-protein signalin
10	133	20.8	284	2	T15700	hypothetical prote
11	130	20.3	544	2	JC5503	G-protein signalin
12	124.5	19.5	558	2	T21468	hypothetical prote
13	121.5	19.0	169	2	T21034	hypothetical prote
14	121.5	19.0	181	2	T21035	hypothetical prote
15	115	18.0	1387	2	JC5502	G-protein signalin
16	112.5	17.6	244	2	T13580	hypothetical prote
17	107.5	16.8	251	2	S43576	C0585.7 protein (C
18	106	16.6	270	2	T22213	hypothetical prote
19	97.5	15.3	234	2	T26672	hypothetical prote
20	97	15.2	274	2	T22214	hypothetical prote
21	93.5	14.6	303	2	T29513	hypothetical prote
22	87.5	13.7	473	2	T19337	hypothetical prote
23	85	13.3	317	1	A42431	3-oxoacyl-lacyl-ca
24	85	13.3	1010	2	T41077	hypothetical struc
25	78.5	12.3	698	2	S55974	SSR2 protein - yea
26	78	12.2	843	2	H72204	pullulanase - Ther
27	76.5	12.0	719	2	S60771	developmental regu
28	75.5	11.8	216	2	T15317	hypothetical prote
29	73	11.4	469	2	T00429	probable peclnest

30	73	11.4	1276	2	T09204	probable tail-host
31	73	11.4	1291	2	T09273	probable tail-host
32	72.5	11.3	382	2	E64686	myosin-like prote
33	72.5	11.3	431	2	C71954	hypothetical prote
34	71.5	11.2	190	2	E71475	probable translat
35	71.5	11.2	1131	2	T41943	major DNA binding
36	71.5	11.2	1305	2	D82923	DNA-directed RNA p
37	71	11.1	157	2	I50817	MHC class I protei
38	70.5	11.0	268	2	S63621	cyma protein - Kie
39	70.5	11.0	413	2	S73643	MG349 homolog G12
40	70.5	11.0	421	2	T43406	cullin-3 - fission
41	70.5	11.0	785	2	T38359	cullin 3 homolog
42	70.5	11.0	798	2	S62405	hypothetical prote
43	70.5	11.0	949	2	D82293	isolectinyl-rRNA syn
44	70.5	11.0	1607	2	T21982	hypothetical prote
45	70	11.0	190	2	B72021	translation elonga

ALIGNMENTS

```

RESULT 1
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi,
Mol. Cell. Biol. 18, 2867-2875, 1998
A:Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: Z16414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAMB>
A:Cross-references: EMBL:AF017757; NID:93080758; PIDN:AMC40089.1; PID:93080759
A:Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match          100.0%; Score 639; DB 2; Length 838;
Best local Similarity 100.0%; Pred. No. 7.6e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLSLGDDGAYLFTFTLERKCVDTLDFWACNGFRQNNLDTKTLRVAKAIYKR 60
    |||||||
DB 78 WTKSLSLGDDGAYLFTFTLERKCVDTLDFWACNGFRQNNLDTKTLRVAKAIYKR 137
    |||||||

QY 61 YIENNSVSKQLRPARTYIRDIKQOIGSVFDDAQRTIQAVMEENAYOVFLTSDIYL 120
    |||||||
DB 138 YIENNSVSKQLRPARTYIRDIKQOIGSVFDDAQRTIQAVMEENAYOVFLTSDIYL 197
    |||||||

QY 121 EYV 123
    |||
DB 198 EYV 200
    |||

RESULT 2
T08422
negative regulator axin [Imported] - rat
N:Alternate names: fAxin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Murali, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A:Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: Z16413; MUID:98151361
A:Accession: T08422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IKB>

```

A:Cross references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A:Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Query Match	63.7%	Score 407	DB 2	Length 832
Best Local Similarity	61.9%	Pred. No. 7.8e-31		
Matches 78	Conservative 21	Mismatches 23	Indels 4	Gaps 2
QY	1	WTKSLHSLDGDODGAYLFTPTFLEREKCVDTLDFWFCAGCFROMLKDPT---	KTLPRAKAI	57
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	90	WAESSLHLLDDOGISLFTFLKQEGCADDLDFWACAGCFKFLPCCSNNEKKRIKARAI		149
QY	58	YRKRTI-ENNSVSVSKOLCPATKTYINDGJIKKQIGSWMFDAQTEIQAWENNAVYQVFLTS		116
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	150	YRKRYILDSNGIVSRQTKPATKSFIKDCVWKKQIDPAMEDQAQTEIGSTWENNTYPRSLNS		209
QY	117	DITLEY		122
		: : : : :		
Db	210	DITLEY		215

RESULT 3
S78089
G-protein signaling regulator RGS3 - human
C/Species: Homo sapiens (man)
C/Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 24-Nov-1999
C/Accession: S78089; S68436
R/Druey, K.
submitted to the EMBL Data Library, May 1995
A/Reference number: S78089
A/Accession: S78089
A/Molecule type: mRNA
A/Residues: 1-519 <DRU>
A/Cross-references: EMBL:U27655; NID:q12i6368; PID:q12i6369
R/Druey, K.M.; Blumer, K.J.; Kang, V.H.; Kehrl, J.H.
Nature 379, 742-746, 1996
A/File: Inhibition of G-protein-mediated MAP kinase activation by a new mammalian gene
A/Reference number: A58012; MUID:96L78495
A/Accession: S68436
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-355, 'K', 357-519 <DRW>
A/Cross-references: EMBL:U27655
A/Note: The sequence from Fig. 1b is inconsistent with that from Fig. 1a in having 356-

RESULT 4
 153020
 S-0/G-1 switch regulatory protein 8 - human
 M:Alternate names: helix-loop-helix phosphoprotein; regulator of G-protein signaling 2
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
 C:Accession: 153020; I65984
 R:Siderovski, D.P.; Heximer, S.P.; Fotsdyke, D.R.

DNA Cell Biol 13, 125-147, 1994
A:Title: A human gene encoding a putative basic helix-loop-helix phosphoprotein whose
A:Reference number: I53020; MUID:94235158
A:Accession: 153020
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-211 <RES>
A:Cross-references: GB:L13391; NID:g292036; PIDN:AAA20680.1; PID:g292037
A:Accession: 165984
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-211 <RES>
A:Cross-references: GB:L1463; NID:g292054; PIDN:AMC37587.1; PID:g292055
C:Genetics:
A:Gene: GDB:RG82; G058
A:Cross-references: GDB:355647; OMIM:600861
A:Map position: 1q31-1q31
A:Introns: 37/2, 71/2, 92/1, 147/3
C:Superfamily: B-cell activation protein BL34
C:Keywords: phosphoprotein

Query Match	32.2%	Score 167.5	DB 2	Length 211
Best Local Similarity	26.8%	Pred. No. 9e-09		
Matches	39	Conservative	20	Mismatches 57; Indels 3; Gaps 2

QY	1	WTSLSILSDGDGALFPTLPFLREKCYDITLDIFWACNGCFQNMUKDTKTLRAKAIYKR	60
DB	80	WSAPFDELLASKTGCLAAFPALKSEFCENIEFWACDDEKTKY-SPOKSSSKRRKIYTD	138
QY	61	YIINNSVSKOLKPAKTYIYRDKIGIKQOIGSVMEQDAOTELQAVMEENAYOVFLTSDIY	119
DB	139	FIKEKPKENINIDFQKTLIAONT--QATSGGCTTYAKRKRYSLSENNSSVPRLEEEFY	195

```

RESULT      5
S71812
RGS10 protein - human
C:/Species: Homo sapiens (man)
C:/Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999
C:/Accession: S71812
R:/Hunt, T.W.; Fields, T.A.; Casey, P.J.; Peralta, E.G.
Nature 363, 175-177, 1996
A:/Title: RGS10 is a selective activator of Galpha(i) GTPase activity.
A:/Reference number: S71812; MUID:96371048
A:/Accession: S71812
A:/status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:/molecule type: mRNA
A:/Residues: 1-173 <HDN>
A:/superfamily: B-cell activation protein BL34

```

RESULT 6
T31002
hypotheoretical protein F56B6.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

A:Accession: T21034
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-169 <M12>
A:Cross-references: EMBL:Z50005; PIDN:CAA90295.1; GSPDB:GN00028; CESP:F16H9.1a
A:Experimental source: clone F16H9
R:Gardner, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19398
A:Accession: T21270
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-169 <M12>
A:Cross-references: EMBL:Z67882; PIDN:CAA91803.1; GSPDB:GN00028; CESP:F16H9.1a
A:Experimental source: clone F22E10
C:Genetics:
A:Gene: CESP:F16H9.1a
A:Map position: X
A:Introns: 16/2; 31/2; 52/1; 91/3
C:Superfamily: B-cell activation protein BL34

Query Match 19.0%; Score 121.5; DB 2; Length 169;
Best Local Similarity 27.5%; Pred. No. 0.00016;
Matches 33; Conservative 25; Mismatches 57; Indels 5; Gaps 3;

OY 1 WTKSLHSLGDGDGAYLFFFLEREKCVDTLDFWFCNGF-ROMNLKDTKTLRAKAIYK 59
DB 40 WSOSEFNLKMRAGOKYFAFLKGEYSDENILFWQACEELKREKNAE--KIEEKARIYE 97
OY 60 RYIENNSVSKOLKPAKTKYIRDGIRKQOIGSVMPDOAQTEIOAVMEENAYOVFLTSIDY 119
DB 98 DTSLSPREVSLSRVRIVNTNMGPSAST--PDEAONQITTLQKRDSTYPRFLASNTY 155

RESULT 14
T21035
hypothetical protein F16H9.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T21035; T21272
R:Gardner, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19363
A:Accession: T21035
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <M12>
A:Cross-references: EMBL:Z50005; PIDN:CA854219.1; GSPDB:GN00028; CESP:F16H9.1b
A:Experimental source: clone F16H9
R:Gardner, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19398
A:Accession: T21272
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <M12>
A:Cross-references: EMBL:Z67882; PIDN:CA854230.1; GSPDB:GN00028; CESP:F16H9.1b
A:Experimental source: clone F22E10
C:Genetics:
A:Gene: CESP:F16H9.1b
A:Map position: X
A:Introns: 28/2; 43/2; 64/1; 103/3
C:Superfamily: B-cell activation protein BL34

Query Match 19.0%; Score 121.5; DB 2; Length 181;
Best Local Similarity 27.5%; Pred. No. 0.00018;
Matches 33; Conservative 25; Mismatches 57; Indels 5; Gaps 3;

OY 1 WTKSLHSLGDGDGAYLFFFLEREKCVDTLDFWFCNGF-ROMNLKDTKTLRAKAIYK 59
DB 52 WSOSEFNLKMRAGOKYFAFLKGEYSDENILFWQACEELKREKNAE--KIEEKARIYE 109

OY 60 RYIENNSVSKOLKPAKTKYIRDGIRKQOIGSVMPDOAQTEIOAVMEENAYOVFLTSIDY 119
DB 110 DTSLSPREVSLSRVRIVNTNMGPSAST--PDEAONQITTLQKRDSTYPRFLASNTY 167

RESULT 15
JC5502
G-protein signaling regulator 12 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5502
R:Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
Biochem. Biophys. Res. Commun. 233: 770-777, 1997
A:Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
A:Accession: JC5502; MUID:97312490
A:Molecule type: mRNA
A:Residues: 1-1387 <SNO>
A:Cross-references: GB:U92280; NID:92088557; PIDN:AMC53176.1; PID:92088558
C:Comment: This protein functions as GTPase activating protein. It interacts with ras
F:18-80/Domain: RhoGAP-like #status predicted <RH1>
F:712-761/Domain: GH1 #status predicted <GH1>
F:765-800/Domain: GH2 #status predicted <GH2>
F:804-828/Domain: GH3 #status predicted <GH3>
F:1204-1220/Region: conserved #status predicted
F:1266-1295/Region: coiled heptad repeat (S-P-X-S-A)

Query Match 18.0%; Score 115; DB 2; Length 1387;
Best Local Similarity 29.1%; Pred. No. 0.007;
Matches 37; Conservative 19; Mismatches 61; Indels 10; Gaps 4;

OY 1 WTKSLHSLGDGDGAYLFFFLEREKCVDTLDFWFCNGF-ROMNLKDTKTLRAKAIYK 59
DB 712 WAYSFRLQDPYGVYFSDFLKRFSEENILFWQACEFCSHPADKKELSYRAHEIFS 771
OY 60 RYIENNSVSKOLKPA---TKTYIRDGIRKQOIGSVMPDOAQTEIOAVMEENAYOVFLTS 116
DB 772 KFL-----CSKATTPVNDISOALADILNAPHPD-MFKEQOLQIFLMLKFDSTYTRFLKS 825
OY 117 DYLEYV 123
DB 826 QLYQECV 832

Search completed: June 7, 2001, 02:03:20
Job time: 5033 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:03:32 ; Search time 39.03 seconds
(without alignments)
107.953 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WTKSLHSLGDDQCAVLFRT.....VMEENAVQVFLTSIDYLEYV 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	639	100.0	838	1 AXN2_RAT	070240 ratu
2	639	100.0	840	1 AXN2_MOUSE	088566 mus musculu
3	624	97.7	843	1 AXN2_HUMAN	097251 homo sapien
4	560	87.6	812	1 AXN2_BRARE	P57095 brachydanio
5	420.5	65.8	835	1 AXN1_BRARE	P57094 brachydanio
6	420	65.7	842	1 AXN1_XENLA	Q9Y9Y0 xenopus lae
7	407	63.7	893	1 AXN1_RAT	070239 ratu
8	407	63.7	992	1 AXN1_MOUSE	035625 mus musculu
9	406	63.5	841	1 AXN1_CHICK	042400 gallu
10	401	62.8	900	1 AXN1_HUMAN	015169 homo sapien
11	172.5	27.0	519	1 RGS2_HUMAN	P49796 homo sapien
12	167.5	26.2	211	1 RGS2_HUMAN	P41220 homo sapien
13	162.5	25.4	211	1 RGS2_MOUSE	008849 mus musculu
14	160	25.0	167	1 RGS4_HUMAN	043665 mus sapien
15	158.5	24.8	745	1 AXN1_MOUSE	094407 drosophila
16	158	24.7	196	1 RGS1_HUMAN	008116 homo sapien
17	155.5	24.3	205	1 RGS4_HUMAN	P49798 homo sapien
18	154.5	24.2	181	1 RGS5_HUMAN	015539 homo sapien
19	152.5	23.9	205	1 RGS4_RAT	P49799 ratu
20	150.5	23.6	180	1 RGS8_HUMAN	P57771 homo sapien
21	149.5	23.4	180	1 RGS8_RAT	P49604 ratu
22	149.5	23.4	205	1 RGS4_MOUSE	008899 mus musculu
23	148.5	23.2	202	1 RGS6_BOVIN	046471 bos tauru
24	147.5	23.1	199	1 RGS6_RAT	P56700 ratu
25	145.5	22.8	181	1 RGS5_MOUSE	008850 mus musculu
26	143.5	22.5	181	1 RGS5_RAT	P49800 ratu
27	140.5	22.0	201	1 RGS6_MOUSE	P97428 mus musculu
28	140.5	22.0	216	1 GAIP_RAT	070321 ratu
29	139.5	21.8	217	1 GAIP_HUMAN	070321 ratu
30	136.5	21.4	159	1 RGS4_HUMAN	014921 homo sapien
31	136.5	21.4	202	1 RGS4_HUMAN	015492 homo sapien
32	133	20.8	284	1 YTN3_CAEEL	018312 caenorhabd
33	130	20.3	544	1 RGS6_RAT	008773 ratu

ALIGNMENTS

RESULT ID	AXN2_RAT	STANDARD	PRT	838 AA.
AC	070240			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)			
DE	(AXIL)			
GN	AXIN2			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98226558; PubMed=9566905;			
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.;			
RT	"Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos."			
RL	Mol. Cell. Biol. 18:2867-2875(1998).			
CC	-1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).			
CC	-1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARADILLO REPEATS CONTAINED IN BETA-CATENIN.			
CC	TERMINAL COMPLEX.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.			
CC	-1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY PP2A.			
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: AF017757; AAC40089.1; -			
DR	HSSP: P49799; JAGR.			
DR	InterPro: IPR000342; -			
DR	InterPro: IPR001158; -			
DR	PFam: PF00615; RGS; 1.			
DR	PFam: PF00778; DIX; 1.			
DR	PROSITE: PS50132; RGS; 1.			
KW	Developmental protein; Phosphorylation.			
FT	DOMAIN 81 200 RGS			
FT	DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).			

Query Match
Best Local Similarity 100.0%; Score 639; DB 1; Length 838;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 469 474 POLY-HIS.
FT DOMAIN 756 838 DIX.
SQ SEQUENCE 838 AA: 92947 MW: 45B825C13BA07F37 CRC64;

1 WTKSHSLGDDGAYLFRTEFLEREKCVDTLDFWFCNGFROMLKDKTTLRVAKAIYKR 60
78 WTKSHSLGDDGAYLFRTEFLEREKCVDTLDFWFCNGFROMLKDKTTLRVAKAIYKR 137
61 YIENNSVSVSKOLKPKATKYIRDGIRKQOIGSYMFDOATEIOAVNEENAYQVFLTSIDYL 120
138 YIENNSVSVSKOLKPKATKYIRDGIRKQOIGSYMFDOATEIOAVNEENAYQVFLTSIDYL 197

121 EYV 123
198 EYV 200

RESULT 2
AXN2_MOUSE STANDARD: PRT: 840 AA.

ID AXN2_MOUSE STANDARD: PRT: 840 AA.

AC 088566; Q80XJ6; (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXINL).
CN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Asbrand C.,
RA Wirtz R., Kuehl M., Wedlich D., Birchmeier W.;
RA "Functional interaction of an axin homolog, conductin, with beta-
catenin, APC, and GSK3beta.";
RT Science 280:596-599(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RA "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
axis formation.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CAENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PPA (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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or send an email to license@isb.ch.

CC -----
CC EMBL: AF073788; AAC26047.1; -
CC DR EMBL: AF205889; AAF22800.1; -
CC DR MGI: 1270862; Axin2.
CC DR HSSP: P49799; IAGR.
CC DR InterPro: IPR000342; -
CC DR InterPro: IPR001158; -
CC DR Pfam: PF00615; RGS: 1.
CC DR Pfam: PF00778; DIX: 1.
CC DR PRINTS: PR01301; RGS-PROTEIN.
CC DR PROSITE: PS50132; RGS: 1.
CC KW Anti-Oncogene; Phosphorylation.
CC FT DOMAIN 81 200 RGS.
CC FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
CC FT DOMAIN 413 478 SIMILARITY).
CC FT DOMAIN 469 476 POLY-HIS.
CC FT DOMAIN 758 840 DIX.
CC FT CONFLICT 101 101 R -> K (IN REF. 2).
CC FT CONFLICT 474 474 H -> Y (IN REF. 2).
CC FT CONFLICT 484 484 S -> P (IN REF. 2).
CC FT CONFLICT 503 503 F -> S (IN REF. 2).
CC FT CONFLICT 603 603 G -> A (IN REF. 2).
CC SQ SEQUENCE 840 AA: 92934 MW: A07D5EF825DE7277 CRC64;

Query Match
Best Local Similarity 100.0%; Score 639; DB 1; Length 840;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WTKSHSLGDDGAYLFRTEFLEREKCVDTLDFWFCNGFROMLKDKTTLRVAKAIYKR 60
78 WTKSHSLGDDGAYLFRTEFLEREKCVDTLDFWFCNGFROMLKDKTTLRVAKAIYKR 137
61 YIENNSVSVSKOLKPKATKYIRDGIRKQOIGSYMFDOATEIOAVNEENAYQVFLTSIDYL 120
138 YIENNSVSVSKOLKPKATKYIRDGIRKQOIGSYMFDOATEIOAVNEENAYQVFLTSIDYL 197

121 EYV 123
198 EYV 200

RESULT 3
AXN2_HUMAN STANDARD: PRT: 843 AA.

ID AXN2_HUMAN STANDARD: PRT: 843 AA.

AC 091211; Q8UH84; (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXINL).
CN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RA "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24.";
RL Genomics 55:341-344(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain, and Lymphoblast;
RC Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RA "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
axis formation.";

```

NS AXN2.
OC Brachydanio rerio (zebrafish) (Zebra danio).
OC Euarystia, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; PubMed=10704853;
RA Shimizu T., Yamataka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish."
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL; PLASMA MEMBRANE (BY SIMILARITY).
CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; AB032263; BAA92440.1; -
DR HSSP; P49799; IAGR.
DR InterPro; IPR000342; -
DR InterPro; IPR001158; -
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
DR Developmental protein; Phosphorylation.
FW DOMAIN 84 203 RGS.
FW DOMAIN 329 415 GSK-3B BINDING SITE (BY SIMILARITY).
FW DOMAIN 415 467 BETA-CATENIN BINDING SITE (BY
FW DOMAIN 415 467 SIMILARITY).
FW POLY-SER.
FT DOMAIN 412 419
FT DOMAIN 730 812 DIX.
SQ SEQUENCE 812 AA; 91496 MW; 46E5ADA6DE2240CC CRC64;

Query Match 87.6%; Score 560; DB 1; Length 812;
Best Local Similarity 86.2%; Pred. No. 2.2e-45;
Matches 106; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 WTKSHSLGGDDGAYLERTFLERKCYVDTLDEFWACNGFRMNLIKDKRTLKVAKAIKR 60
Db 81 WTKSHSLFLGGDDGAYLERTFLERKCYVDTLDEFWACNGFRMNLIKDKRTLKVAKAIA 140
QY 61 YIENNSVYSKOLKPAATKTYIRDGIRKQOIGSYVMFDOAQTEIOAVNEENAYOVFLTS 120
Db 141 YIENNSIYAKOLKPAATKTYIRDNIRKQOIGSYVMFDOAQMEIOGTAMEENAYOVFL 200
QY 121 EYV 123
Db 201 EYV 203

RESULT 5
AXNL_BRARE STANDARD; PRT; 835 AA.
AC P57094;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIN INHIBITION PROTEIN 1).

```

GN AXIN1.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; PubMed=10704853;
RA Shimizu T., Yamamoto Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
Bae Y.-K., Hibi M., Hirano T.,
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB032262; BAA92439.1; -
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 92 214 RGS.
FT DOMAIN 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 753 835 DIX.
FT SEQUENCE 835 AA; 94351 MW; 1C62FCF1F5937C87 CRC64;
Query Match 65.8%; Score 420.5; DB 1; Length 835;
Best Local Similarity 63.2%; Pred. No. 3.2e-32;
Matches 79; Conservative 20; Mismatches 23; Indels 3; Gaps 2;
OY 1 WTKSLSLDGGDGYLFRFTLEERKCVDTLDFWFCNGFROMLKDK--TKTLRVAKAIY 58
DB 89 WAESLHSLDDDDGHLHRTFTLQECADMLDFWFCNGFROMLKDK--TKTLRVAKAIY 148
OY 59 KRYI-ENNSVSVSKQJLKPATKTYIRDGIRKQKQIGSVMDQACTEIOAVENAYQVFLTS 117
DB 149 KYIILDNNGIYSROIKPATKSFIRKQCVKMLHIDPAMFDQAEIQTMEENYPIFLKSD 208
OY 118 IYLEY 122
DB 209 IYLEY 213
RESULT 6
AXIN_XENLA STANDARD; PRT; 842 AA.
AC OYGYO;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (XAXIN).
GN AXIN OR AXN.

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; PubMed=10072781;
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: WEAKLY AND UBICUOUSLY EXPRESSED THROUGHOUT
EARLY DEVELOPMENT. AND HIGHLY EXPRESSED IN THE ANTERIOR
MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL; AF097313; AAC71036.1; -
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 88 211 RGS.
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 760 842 DIX.
FT SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64;
Query Match 65.7%; Score 420; DB 1; Length 842;
Best Local Similarity 61.1%; Pred. No. 3.6e-32;
Matches 77; Conservative 25; Mismatches 20; Indels 4; Gaps 2;
OY 1 WTKSLSLDGGDGYLFRFTLEERKCVDTLDFWFCNGFROMLKDK--TKTLRVAKAIY 57
DB 85 WAESLHSLDDDDGHLHRTFTLQECADMLDFWFCNGFROMLKDK--TKTLRVAKAIY 144
OY 58 KRYI-ENNSVSVSKQJLKPATKTYIRDGIRKQKQIGSVMDQACTEIOAVENAYQVFLTS 116
DB 145 YKYYLDNSNGIYSROIKPATKSFIRKQCVKMLHIDPAMFDQAEIQTMEENYPIFLKSD 204
OY 117 IYLEY 122
DB 205 IYLEY 210
RESULT 7
AXIN_XENLA STANDARD; PRT; 893 AA.
AC OYGYO;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (XAXIN) (FRAGMENT).
GN AXIN OR AXN.

GN AXIN1 OR AXIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCB1_TaxID=10116;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=98151361; PubMed=9482734;
 RA Ikeda S., Kishida S., Yamamoto H., Murali H., Koyama S., Kikuchi A.;
 RT "Axin, a negative regulator of the Wnt signaling pathway, forms a
 RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
 RT dependent phosphorylation of beta-catenin.";
 RL EMBL J. 17:1371-1384(1998).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
 CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
 CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
 CC PLAGIOLOBIN (GAMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
 CC FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
 CC SPLEEN AND LIVER.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF017756; AAC40066.1; ALT_INIT.
 DR HSSP: P49799; IAGR.
 DR Interpro: IPR000342; -
 DR Interpro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein; Phosphorylation.
 KW NON_TER 1
 FT DOMAIN 154 277 RGS.
 FT DOMAIN 414 498 GSK-3B BINDING SITE.
 FT DOMAIN 499 567 BETA-CATENIN BINDING SITE.
 FT DOMAIN 811 893 DIX.
 SQ SEQUENCE 893 AA; 99188 MW; 3CDBD2224EDD384C CRC64;
 Query Match 63.7%; Score 407; DB 1; Length 893;
 Best Local Similarity 61.9%; Pred. No. 6.4e-31;
 Matches 78; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

ID AXIN1_MOUSE STANDARD; PRT; 992 AA.
 AC 035625;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
 GN AXIN1 OR AXIN OR FU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCB1_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
 RA Lee J.J., Tillman S.M., Gumbiner B.M., Costantini F.;
 RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
 CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
 CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
 CC PLAGIOLOBIN (GAMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
 CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF090011; AAC53285.1; -
 DR HSSP: P49799; IAGR.
 DR MGD: MGI:1096327; Axin.
 DR Interpro: IPR000342; -
 DR Interpro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein; Phosphorylation; Alternative splicing.
 KW NON_TER 1
 FT DOMAIN 10 18 POLY-ALA.
 FT DOMAIN 217 340 RGS.
 FT DOMAIN 477 561 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 562 630 BETA-CATENIN BINDING SITE (BY
 FT SIMILARITY).
 FT DOMAIN 910 992 DIX.
 FT VARSPLIC 860 895 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 992 AA; 109917 MW; 70EB53D387BD26F CRC64;
 Query Match 63.7%; Score 407; DB 1; Length 992;
 Best Local Similarity 61.9%; Pred. No. 7.2e-31;
 Matches 78; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

Db 274 YRKYLDSNGVSGKQKPKATKSFITKDCVMKQOIDPAMEDOAQTEIQTMEENTYPSFLKS 333
OY 117 DILEY 122
Db 334 DILEY 339

RESULT 9

AXN_CHICK STANDARD: PRT: 841 AA.
ID AXN_CHICK
AC 042400;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN).
GN AXIN OR AXN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
CC -1- PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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CC EMBL; AF009012; AAC60245.1; -
DR HSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 88 211 RGS.
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DIX.
SQ SEQUENCE 841 AA; 94931 MW; 400DC90E72506FE CRC64;

Query Match 63.5%; Score 406; DB 1; Length 841;
Best Local Similarity 61.1%; Pred. No. 7.5e-31;
Matches 77; Conservative 22; Mismatches 23; Indels 4; Gaps 2;

OY 1 WTKSHSLGODDGAIVLPTELEREKCVTLDPFACNGEFGMN--LKDTEIRAKAI 57
Db 85 WAESHSLDQDDGINTLPFTLKQDCADLDLDFWACSGFRLEPCVNEERLKLAKAI 144

OY 58 YKRRI-ENNSVSKQKPKATKSFITKDCVMKQOIDPAMEDOAQTEIQTMEENTYPSFLKS 116
Db 145 YRKYLDSNGVSGKQKPKATKSFITKDCVMKQOIDPAMEDOAQTEIQTMEENTYPSFLKS 204
OY 117 DILEY 122
Db 205 DILEY 210

RESULT 10

AXN1_HUMAN STANDARD: PRT: 900 AA.
ID AXN1_HUMAN
AC 015163;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B.
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC -1- TERNARY COMPLEX. MAY ALSO BINDS TO PLACOGLOBIN (GAMA-CATENIN),
APC, DVL AND PP2A.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UNIQUTOUSLY EXPRESSED.
CC -1- PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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CC EMBL; AF009674; AAC51624.1; -
DR HSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 125 248 RGS.
FT DOMAIN 385 470 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DIX.
SQ SEQUENCE 900 AA; 99803 MW; EEF990B11FC7B3B CRC64;

Query Match 62.8%; Score 401; DB 1; Length 900;
Best Local Similarity 62.7%; Pred. No. 2.4e-30;

Matches 79; Conservative 17; Mismatches 26; Indels 4; Gaps 2;

OY 1 WPKSLHSLGDDGAVLFPFLERKCVDTLDFWACNGFROMLKDT---KTLVAKAI 57
 DB 122 WAKSLHSLDDDDGISTLFTFLKQEGCADLDFWFACTGSRKLEPCDSNEERKLARAI 181
 OY 58 YKRII-ENNSVSVSKOLPARKTYIRDIGKQIGSVFQAOQTEIOAVNEENAYQVELTS 116
 DB 182 YKRIILDNNGIYSROTKPATKSFIRKICIMKQOLIDPAMFQAOQTEIOATMEENYPSFLKS 241
 OY 117 DYLEY 122
 DB 242 DYLEY 247

RESULT 11
 RGS2_HUMAN STANDARD; PRT; 519 AA.
 AC P49796;
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DE REGULATOR OF G-PROTEIN SIGNALING 3 (RGS3). (RGP3).
 GN RGS3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96178495; PubMed=8602223;
 RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.:
 RT "Inhibition of G-protein-mediated MAP kinase activation by a new
 RT mammalian gene family."
 RT Nature 379:742-746(1996).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -----
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 CC -----
 CC EMBL: U27655; AAC50394.1; -
 CC DR HSSP: P49799; IAGR.
 CC DR MIM: 602189; -
 CC DR InterPro: IPR000342; -
 CC DR Pfam: PF00615; RGS; 1.
 CC DR PRINTS: PRO1301; RGS-PROTEIN.
 CC DR PROSITE: PS50132; RGS; 1.
 CC KW Signal transduction inhibitor.
 CC FT DOMAIN 394 510
 CC FT SEQUENCE 519 AA; 56601 MW; FICFE3F27D4673A0 CRC64;

Query Match 27.0%; Score 172.5; DB 1; Length 519;
 Best Local Similarity 32.5%; Pred. No. 4.5e-09;
 Matches 40; Conservative 24; Mismatches 56; Indels 3; Gaps 2;

OY 1 WPKSLHSLGDDGAVLFPFLERKCVDTLDFWACNGFROMLKDTKTLVAKAIYKR 60
 DB 391 WGSLEKLVLVHKGLAVFOFLTERSEENLEWMLACEDPKKYK-SQSKASAKAKIFAE 449
 OY 61 YIENNSVSVSKOLPARKTYIRDIGKQIGSVFQAOQTEIOAVNEENAYQVELTS 120
 DB 450 YIAIOACKEVNLDSTYRHTKML--QSVTRGCFDLAOKRIFGLMEKDSYPRFLRSPLYL 507
 OY 121 EVY 123

DB 508 DLI 510

RESULT 12
 RGS2_HUMAN STANDARD; PRT; 211 AA.
 AC P41220;
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DE REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2) (G0/G1 SWITCH REGULATORY
 DE PROTEIN 8).
 GN RGS2 OR G0S8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94235158; PubMed=8179820;
 RA Siderovski D.P., Heximer S.P., Forsdyke D.R.;
 RT "A human gene encoding a putative basic helix-loop-helix
 RT phosphoprotein whose mRNA increases rapidly in cycloneximide-treated
 RT blood mononuclear cells."
 RT DNA Cell Biol. 13:125-147(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Baguley C.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=95371353; PubMed=7643615;
 RA Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W.,
 RA Minden M.D., Siderovski D.P.;
 RT "Differential expression of a basic helix-loop-helix phosphoprotein
 RT gene, G0S8, in acute leukemia and localization to human chromosome
 RT 1q31."
 RT Leukemia 9:1291-1298(1995).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML)
 CC AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).
 CC -1- PTM: COULD BE PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY
 CC PROTEIN KINASE(S).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -----
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 CC -----
 CC EMBL: L13391; AAA20680.1; -
 CC DR EMBL: L13463; AAC37587.1; -
 CC DR EMBL: AL035407; CAB62512.1; -
 CC DR HSSP: P49799; IAGR.
 CC DR MIM: 600861; -
 CC DR InterPro: IPR000342; -
 CC DR Pfam: PF00615; RGS; 1.
 CC DR PRINTS: PRO1301; RGS-PROTEIN.
 CC DR PROSITE: PS50132; RGS; 1.
 CC KW Signal transduction inhibitor; Cell cycle; Phosphorylation.
 CC FT DOMAIN 83 199
 CC FT SEQUENCE 211 AA; 24382 MW; EFFE4A47EP9AD8F CRC64;

Query Match 26.2%; Score 167.5; DB 1; Length 211;
 Best Local Similarity 32.8%; Pred. No. 4.8e-09;

Matches 39; Conservative 20; Mismatches 57; Indels 3; Gaps 2;

OY 1 WTKSHSLGDDGAYLFTFLERKCVDTLDFWFCNGFRONMLKDTLTKLVAKAIYKR 60
 DB 80 WSEAFDELLAKYGAARAFPLKSECEENIEFWLACEDFKTK-SPOKLSKARKITVD 138
 OY 61 YIENNSVSKOLKPAKTYIRDGIRKQOIGSVMPDOATEIOAVMEENAYOVFLSDIY 119
 DB 139 FIEKAPKEINIDPOTKILIAONI--QATSCGCTTAAKRYVSLMENNISYPRFLESEFY 195

RESULT 13
 RGS2_MOUSE STANDARD; PRT; 211 AA.

AC 008849; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2).
 GN RGS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97236828; PubMed=9079700;
 RA Chen C., Zheng B., Han J., Lin S.C.;
 RT "Characterization of a novel mammalian RGS protein that binds to
 RT Galpha proteins and inhibits pheromone signalling in yeast."
 RL J. Biol. Chem. 272:8679-8685(1997).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -----
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 CC -----
 CC EMBL; U67187; AAB50617.1; -
 DR HSEF; P49799; IACR.
 DR MGD; MGI:1098271; Rgs2.
 DR InterPro; IPR000342; -
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPPROTEIN.
 DR PROSITE; PS0132; RGS; 1.
 KM Signal transduction inhibitor; Cell cycle.
 FT DOMAIN 83 199 RGS.
 FT SEQUENCE 211 AA; 24297 MW; 61FAA2DC9B0C4DF9 CRC64;

Query Match 25.4%; Score 162.5; DB 1; Length 211;
 Best Local Similarity 31.9%; Pred. No. 1.4e-08;
 Matches 38; Conservative 20; Mismatches 58; Indels 3; Gaps 2;

AC 043665; 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 10 (RGS10).
 GN RGS10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chatterjee T.K., Fisher R.A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. ASSOCIATES SPECIFICALLY WITH THE
 CC ACTIVATED FORMS OF THE G PROTEIN SUBUNITS G-ALPHA(1) AND G-
 CC ALPHA(2) BUT FAILS TO INTERACT WITH THE STRUCTURALLY AND
 CC FUNCTIONALLY DISTINCT G-ALPHA(S) SUBUNIT.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AF045229; AAC03783.1; -
 DR MIM; 602856; -
 DR InterPro; IPR000342; -
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPPROTEIN.
 DR PROSITE; PS0132; RGS; 1.
 KM Signal transduction inhibitor
 FT DOMAIN 27 142 RGS.
 FT SEQUENCE 167 AA; 19608 MW; EF36915F1AA23F3B CRC64;

Query Match 25.0%; Score 160; DB 1; Length 167;
 Best Local Similarity 32.0%; Pred. No. 1.9e-08;
 Matches 39; Conservative 30; Mismatches 49; Indels 4; Gaps 3;

OY 1 WTKSHSLGDDGAYLFTFLERKCVDTLDFWFCNGFRONMLKDTLTKLVAKAIYKR 60
 DB 24 WAAISLENLEDEGVKRRRFLKFESEENVLFWLACEDFKMDK-TQOMKAKEIYWT 82
 OY 61 YIENNSVSKOLKPAKTYIRDGIRKQOIGSVMPDOATEIOAVMEENAYOVFLSDIYL 120
 DB 83 FL--SSKASSQVNVGOSRLNEKILEEP-HPLMFQKLDQIFNLMKYDSYRFLKSDLFL 139
 OY 121 EV 122
 DB 140 KH 141

RESULT 15
 AXN_DROME STANDARD; PRT; 745 AA.

AC Q9V407; Q9XYC1; 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN (AXIS INHIBITION PROTEIN) (DAXIN) (D-AXIN).
 GN AXN OR CG7926.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:02:17 ; Search time 81.06 Seconds
(without alignments)
177.851 Million cell updates/sec

Title: US-09-587-574-2

Perfect score: 639
Sequence: 1 WTSLSLSLGDGDGAYLFRF.....VMEENAYOVLTSDIYLEYV 123Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

SPTREMBL.15:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639	100.0	838	11 070240	070240 rattus norv
2	639	100.0	840	11 088366	088366 mus musculu
3	636	99.5	840	11 090XJ6	090XJ6 mus musculu
4	624	97.7	777	4 090H84	090H84 homo sapien
5	624	97.7	843	4 09Y2T1	09Y2T1 homo sapien
6	420	65.7	842	13 09YGYO	09YGYO xenopus lae
7	407	63.7	832	11 070239	070239 rattus norv
8	407	63.7	992	11 035625	035625 mus musculu
9	406	63.5	841	13 042400	042400 gallus gall
10	401	62.8	900	4 015169	015169 homo sapien
11	336	52.6	706	13 09PTP2	09PTP2 xenopus lae
12	186.5	29.2	235	4 09NS28	09NS28 homo sapien
13	167.5	26.2	192	11 09JL23	09JL23 mus musculu
14	167.5	26.2	297	11 09JL22	09JL22 mus musculu
15	166.5	26.1	211	11 09JHX0	09JHX0 rattus norv
16	163	25.5	196	11 09JL25	09JL25 mus musculu
17	162.5	25.4	211	11 09JL24	09JL24 mus musculu
18	161.5	25.3	204	13 09I909	09I909 xenopus lae
19	158.5	24.8	533	5 022998	022998 caenorhabd

20	158.5	24.8	743	5 09XYC1	09XYC1 drosophila
21	158.5	24.8	745	5 09Y407	09Y407 drosophila
22	144.5	22.6	829	5 09UB06	09UB06 drosophila
23	144.5	22.6	872	5 09NG00	09NG00 drosophila
24	144.5	22.6	1175	5 09YXX8	09YXX8 drosophila
25	144.5	22.6	1175	5 09VCX2	09VCX2 drosophila
26	143.5	22.5	181	11 09JKD7	09JKD7 rattus norv
27	127.5	20.0	208	4 09JUS8	09JUS8 homo sapien
28	127.5	20.0	218	4 09UGC6	09UGC6 homo sapien
29	126.5	19.8	210	11 09QZB0	09QZB0 mus musculu
30	126.5	19.8	239	11 09QZB2	09QZB2 mus musculu
31	126.5	19.8	239	11 09QZB1	09QZB1 mus musculu
32	123.5	19.3	210	13 09PWA0	09PWA0 gallus gall
33	123.5	19.3	217	4 076081	076081 homo sapien
34	123.5	19.3	218	13 09PWA1	09PWA1 gallus gall
35	122.5	19.2	271	5 09V888	09V888 drosophila
36	122	19.0	438	11 09Z2H1	09Z2H1 mus musculu
37	121.5	19.0	181	5 09YVK0	09YVK0 caenorhabd
38	115.5	18.1	108	13 09W7I6	09W7I6 gallus gall
39	115	18.0	443	4 075573	075573 homo sapien
40	112.5	17.6	244	5 096842	096842 drosophila
41	112	17.5	346	4 075577	075577 homo sapien
42	112	17.5	472	4 09Y245	09Y245 homo sapien
43	112	17.5	490	4 09Y647	09Y647 homo sapien
44	109	17.1	409	11 09Z2H2	09Z2H2 mus musculu
45	107.5	16.8	201	5 09NHP9	09NHP9 caenorhabd

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	838 AA.
070240	070240	070240		
AC	070240	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	AXIL.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID-10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-98226558; PubMed-9566905;			
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.;			
RT	*Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos.*;			
RL	Mol. Cell. Biol. 18:2867-2875(1998).			
DR	EMBL: AF017757; AAC40089.1; -			
DR	HSSP: P49799; IAGR.			
DR	INTERPRO: IPR000342; -			
DR	INTERPRO: IPR001158; -			
DR	PFAM: PF00615; RGS; 1.			
DR	PFAM: PF00778; DIX; 1.			
DR	PRODOM: PD001580; -; 1.			
DR	PRODOM: PD003639; -; 1.			
SO	SEQUENCE 838 AA; 92947 MW; 458825C13BA07F37 CRC64;			
Query Match	100.0%; Score 639; DB 11; Length 838;			
Best Local Similarity	100.0%; Pred. No. 7.7e-53;			
Matches 123; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 WTSLSLSLGDGDGAYLFRFLEKRCVDTLDFWFCNGFRONKMDTKLRYAKAYKR 60			
DB	78 WTSLSLSLGDGDGAYLFRFLEKRCVDTLDFWFCNGFRONKMDTKLRYAKAYKR 137			
OY	61 YINNSVSVSKOLKPAKTYTRDGIKKQOIGSVMEFDAOTETQAVMEENAYOVLTSDIYL 120			

Db 138 YIENNSVSVKOLKPKATYIRIDGIRKQOIGSVMPDQOTEIOAVMEENAYOVFLTSDIYL 197
 QY 121 EYV 123
 198 EYV 200

RESULT 2
 ID 088566 PRELIMINARY; PRT: 840 AA.
 AC 088566;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE CONDUCTIN.
 GN AXIN2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98221239; PubMed=9554852;
 RA Behrens J., Jerschow B.-A., Wurttele M., Grimm J., Asbrand C., Wirtz R.,
 RA Kuhl M., Wedlich D., Birchemer W.,
 RT "Functional interaction of an axin homolog, conductin, with beta-
 RL catenin, APC, and GSK3beta."
 RT Science 280:596-599(1998).
 DR EMBL: AF073788; AAC26047.1; -.
 DR HSSP: P49799; IAGR.
 DR MGD: MGI:1270862; Axin2.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRODOM: PD001580; -; 1.
 DR PRODOM: PD003639; -; 1.
 SO SEQUENCE 840 AA; 92934 MW; A07D5FEB25DE7277 CRC64;

Query Match 100.0%; Score 639; DB 11; Length 840;
 Best Local Similarity 100.0%; Pred. No. 7.8e-53;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLHSLGDODGAYLFTFLERKCVDTLDFWFCNGFRQNLKDKTKLRVAKAIYKR 60
 |||||||
 Db 78 WTKSLHSLGDODGAYLFTFLERKCVDTLDFWFCNGFRQNLKDKTKLRVAKAIYKR 137
 |||||||

QY 61 YIENNSVSVKOLKPKATYIRIDGIRKQOIGSVMPDQOTEIOAVMEENAYOVFLTSDIYL 120
 |||||||
 Db 138 YIENNSVSVKOLKPKATYIRIDGIRKQOIGSVMPDQOTEIOAVMEENAYOVFLTSDIYL 197
 |||||||

QY 121 EYV 123
 198 EYV 200

RESULT 3
 ID 090XJ6 PRELIMINARY; PRT: 840 AA.
 AC 090XJ6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE AXIN2.
 GN AXIN2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,

RA Jenkins N.A., Warburton D., Costantini F.;
 RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
 RT expression pattern, interaction with Axin and effects on embryonic
 RT axis formation."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF205889; AAF22800.1; -.
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGSPPROTEIN.
 SO SEQUENCE 840 AA; 92896 MW; 767D546B43C921C5 CRC64;

Query Match 99.5%; Score 636; DB 11; Length 840;
 Best Local Similarity 99.2%; Pred. No. 1.5e-52;
 Matches 122; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTKSLHSLGDODGAYLFTFLERKCVDTLDFWFCNGFRQNLKDKTKLRVAKAIYKR 60
 |||||||
 Db 78 WTKSLHSLGDODGAYLFTFLERKCVDTLDFWFCNGFRQNLKDKTKLRVAKAIYKR 137
 |||||||

QY 61 YIENNSVSVKOLKPKATYIRIDGIRKQOIGSVMPDQOTEIOAVMEENAYOVFLTSDIYL 120
 |||||||
 Db 138 YIENNSVSVKOLKPKATYIRIDGIRKQOIGSVMPDQOTEIOAVMEENAYOVFLTSDIYL 197
 |||||||

QY 121 EYV 123
 198 EYV 200

RESULT 4
 ID 09UH84 PRELIMINARY; PRT: 777 AA.
 AC 09UH84;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE AXIN2.
 GN AXIN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN, LYMPHOBLAST;
 RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
 RA Jenkins N.A., Warburton D., Costantini F.;
 RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
 RT expression pattern, interaction with Axin and effects on embryonic
 RT axis formation."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF205888; AAF22799.1; -.
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGSPPROTEIN.
 SO SEQUENCE 777 AA; 86857 MW; 3A4943ABF430BBD3 CRC64;

Query Match 97.7%; Score 624; DB 4; Length 777;
 Best Local Similarity 95.9%; Pred. No. 1.9e-51;
 Matches 118; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTKSLHSLGDODGAYLFTFLERKCVDTLDFWFCNGFRQNLKDKTKLRVAKAIYKR 60
 |||||||
 Db 77 WTKSLHSLGDODGAYLFTFLERKCVDTLDFWFCNGFRQNLKDKTKLRVAKAIYKR 136
 |||||||

QY 61 YIENNSVSVKOLKPKATYIRIDGIRKQOIGSVMPDQOTEIOAVMEENAYOVFLTSDIYL 120
 |||||||

Db 137 YIENNSIVSKOLKPKATKYIRGDIKQOIDSIMFDQAOTIEIOSVMEENAYQVFLTSDIYL 196
QY 121 EYV 123
Db 197 EYV 199
RESULT 5
Q9Y2T1 PRELIMINARY: PRT: 843 AA.
ID 09Y2T1
AC 09Y2T1
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CONDUCTIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99168905; PubMed-10049590;
RA Mal M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24.";
RL Genomics 55:341-344(1999).
DR EMBL: AF078165; AAD20976.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PFAM: PF00778; DIX; 1.
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A664D CRC64;

Query Match 97.7%; Score 624; DB 4; Length 843;
Best Local Similarity 95.9%; Pred. No. 2.1e-51;
Matches 118; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 WTKSLHSLGDGDGAYLFTFLERKCVDTLDFWFCNGFRQNLKDTTLRYAKAIYKR 60
Db 78 WTKSLHSLGDGDGAYLFTFLERKCVDTLDFWFCNGFRQNLKDTTLRYAKAIYKR 137
QY 61 YIENNSIVSKOLKPKATKYIRGDIKQOIGSVFDOAOTIEIOAVMEENAYQVFLTSDIYL 120
Db 138 YIENNSIVSKOLKPKATKYIRGDIKQOIGSVFDOAOTIEIOAVMEENAYQVFLTSDIYL 197
QY 121 EYV 123
Db 198 EYV 200
RESULT 6
Q9Y2T1 PRELIMINARY: PRT: 842 AA.
ID 09Y2T1
AC 09Y2T1
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99173782; PubMed-10072781;
RA Hedgpeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RT expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).

DR EMBL: AF097313; AAC71036.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 65.7%; Score 420; DB 13; Length 842;
Best Local Similarity 61.1%; Pred. No. 5.9e-32;
Matches 77; Conservative 25; Mismatches 20; Indels 4; Gaps 2;

QY 1 WTKSLHSLGDGDGAYLFTFLERKCVDTLDFWFCNGFRQNLKDTTLRYAKAI 57
Db 85 WTKSLHSLGDGDGAYLFTFLERKCVDTLDFWFCNGFRQNLKDTTLRYAKAI 144
QY 58 YKRYT-ENNSIVSKOLKPKATKYIRGDIKQOIGSVFDOAOTIEIOAVMEENAYQVFLTS 116
Db 145 YKRYT-ENNSIVSKOLKPKATKYIRGDIKQOIGSVFDOAOTIEIOAVMEENAYQVFLTS 204
QY 117 DITLEY 122
Db 205 DITLEY 210

RESULT 7
Q70239 PRELIMINARY: PRT: 832 AA.
ID 070239
AC 070239
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE RAXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98151361; PubMed-9482734;
RA Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
RT "Axin, a negative regulator of the Wnt signaling pathway, forms a
RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin.";
RL EMBO J. 17:1371-1384(1998).
DR EMBL: AF017756; AAC40066.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 832 AA; 92856 MW; B489504C7E594347 CRC64;

Query Match 63.7%; Score 407; DB 11; Length 832;
Best Local Similarity 61.9%; Pred. No. 1e-30; Indels 4; Gaps 2;
Matches 78; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

QY 1 WTKSLHSLGDGDGAYLFTFLERKCVDTLDFWFCNGFRQNLKDTTLRYAKAI 57
Db 90 WTKSLHSLGDGDGAYLFTFLERKCVDTLDFWFCNGFRQNLKDTTLRYAKAI 149
QY 58 YKRYT-ENNSIVSKOLKPKATKYIRGDIKQOIGSVFDOAOTIEIOAVMEENAYQVFLTS 116
Db 150 YKRYT-ENNSIVSKOLKPKATKYIRGDIKQOIGSVFDOAOTIEIOAVMEENAYQVFLTS 209
QY 117 DITLEY 122
Db 205 DITLEY 210

Db	210	DIVLEY	215
RESULT	8		
ID	035625	PRELIMINARY;	PRT; 992 AA.
AC	035625;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	AXIN (FRAGMENT).		
GN	AXIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97373830; PubMed=9230313;		
RA	Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,		
RA	Yi Lee J.J., Tilgman S.M., Gumbiner B.M., Costantini F.;		
RT	"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling		
RT	pathway that regulates embryonic axis formation.";		
RL	Cell 90:181-192(1997).		
DR	EMBL: AF009011; AAC53285.1; -;		
DR	HSSP: P49799; 1AGR.		
DR	MCD; MGI:1096327; Axin.		
DR	INTERPRO: IPR000342; -;		
DR	INTERPRO: IPR001158; -;		
DR	PFAM: PF00615; RGS; 1.		
DR	PFAM: PF00778; DIX; 1.		
DR	PRINTS: PRO1301; RGSPROTEIN.		
FT	NON_TER	1	1
EQ	SEQUENCE	992 AA; 109917 MW; 70EBB53D387BD26F CRC64;	

Query Match	63.7%	Score 407	DB 11	Length 992
Best Local Similarity	61.9%	Pred. No. 1.2e-30		
Matches 78	Conservative 21	Mismatches 23	Indels 4	Gaps
Qy	1	WTKSLHSILDIDOGAYLFFRTFLERKCVPTLDFWPFACNGFRMONLKD.T--KTLRVAKAI 57		
Db	214	WASLSHSLDDQDGISLFRFLFKQEGCADLDFWFCSCFRFLRLEPDSNEERKLARAI 273		
Qy	58	YKRYI-ENNSVSQKLCPATKYIIRDGKIQQIGSVMEQAOETEIOAVMEENAYOVFLTS 116		
Db	274	YRKRIILDSNGIVSNQTFKPKATRSFKICQVCMKQOIDPAMFQAOETEIOSTWEENTYSPFLKS 333		
Qy	117	DIYLEY 122		
Db	334	DIYLEY 339		
RESULT	9			
ID	042400	PRELIMINARY;	PRT;	841 AA.
AC	042400;			
DT	01-JAN-1998 (TREMblrel. 05, Created)			
DT	01-JAN-1998 (TREMblrel. 05, Last sequence update)			
DT	01-OCT-2000 (TREMblrel. 15, Last annotation update)			
DE	AXIN.			
GN	AXIN.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
NCBI_TaxID	9031;			
RM	(1)			
SEQUENCE	FROM N.A.			
RP	MDMLINE=97373830; PubMed=9230313;			
RX	zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,			
RA	III Lee J.U., Tilghman S.M., Gumbiner B.M., Costantini F.;			
RT	"The mouse fused locus encodes Axlin, an inhibitor of the Wnt signalling			

RT pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 DR EMBL, AF009012; AAC0245.1; -.
 DR HSSP; P49799; IAGR.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM; PF00615; RGS; 1.
 DR PFAM; PF00778; DIX; 1.
 DR PRODOM; PD001580; -. 1.
 DR PRODOM; PD003639; -. 1.
 SO SEQUENCE 841 AA; 94931 MW; 400D0C90E72506FE CRC64;

Query Match	63.5%;	Score 406;	DB 13;	Length 841;
Best Local Similarity	61.1%;	Pred. No. 1.3e-30;		
Matches 77;	Conservative 22;	Mismatches 23;	Indels 4;	Gaps 2;
QY	1	WTKSLHSLLGDGDGAYLFTFLERKCVDTLDWFACNGFRQMN--LKDTKTLNVAKAI	57	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	85	WAESHSLLDLDQDGGINLFTFLKQDCADLLDFWACSGFRLEPCVSNEEKRLKAI	144	
QY	58	YKRYI-ENNSVSVSKOLKPAIKTYINDGIIKKOIGSVMEQDAOTELQAVMEANAQVELTS	116	
		: : : : : : : : : : : : : : : : : : : : : : : : : : : :		
Db	145	YKKYITLDNNGIYSVRQIKPATKSFKIDCVMKQLQIDPMFQDAOTELQCMIEDNTYFLFRS	204	
QY	117	DIYLEY 122		
		: : : :		
Db	205	DIYLEY 210		

RESULT	10			
015169				
ID	015169	PRELIMINARY;	PRT;	900 AA.
AC	015169;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)		
DE	AXIN (FRAGMENT).			
GN	AXIN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=973738303; PubMed=9230313;			
RA	Zeng L., Fagotto F., Zhang T., Hsu W., Vasioek T.J., Perry W.L.,			
RT	Tit Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;			
RL	"The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation.";			
RL	Cell 90:181-192(1997).			
DR	EMBL; AF009674; AAC51624.1; .			
DR	HSSP; P49799; IAGR.			
DR	INTERPRO; IPR000342; .			
DR	INTERPRO; IPR001158; .			
DR	PFAM; PF00615; RGS; 1.			
DR	PFAM; PF00778; DGS; 1.			
DR	PRINTS; PR01301; RGSPPROTEIN.			
FT	NON_TER	1		
SEQUENCE	900 AA;	99803 MW;	EESF990B11FC7B3B	CRC64;

	Query Match	62.8%	Score 401;	DB 4;	Length 900;
	Best Local Similarity	62.7%;	Pred. No. 4.2e-30;		
	Matches	79;	Conservative 17;	Mismatches 26;	Indels 4; Gaps 2;
Oy	1	WTKSHSLIGDODGAYLRTPFLERKCVDTLDFWACNGEROMLNKDR--KTLRVAKAI	57		
		:			
Db	122	WAESHSLILDODDGISLPRTFLKGCGADLLDFWACTGEFKRLPCODSWEERKLIAARI	181		
Oy	58	YKRYI-EUNNSVSKOLKPATKYIRIDGJIKKOIGSMVFQOATEIOAVNEANAQVFLTS	116		
		:			
Db	182	YKKYLDDNNGIVSRQTRPAITSFIIKGCTMKLLDPDMPEQOATEIOAMVEENTYSFLKS	241		

RA Reif K., Cyster J.G.;
RT "RGS molecule expression in murine B lymphocytes and ability to down-
RT regulate chemotaxis to lymphoid chemokines."
RL J. Immunol. 164:4720-4723(2000).
DR EMBL: AF215670; AAF34627.1; -.
FT NON_TER 1
SO SEQUENCE 297 AA; 33683 MW; ADF80985150B525C CRC64;

Query Match 26.2%; Score 167.5; DB 11; Length 297;
Best Local Similarity 31.7%; Pred. No. 2.2e-08;

Matches 39; Conservative 19; Mismatches 55; Indels 3; Gaps 2;

OY 1 WTKSLHSLIGDGDGAYLRFLEEREKCVDTLDFWACNGFRQNLKDTKTLRVAKAIYKR 60
169 WSESLKLLHKYGLVFAQLFTEFESENELEFWLACEDFKRK-SOSKMAKAKKIFAE 227
DB 61 YIENNSVYSKQIKPATKYIRNGIKKQOIGSVMPDQOTEIQAVMENAYOVFLTSDIYL 120
228 FTAIQACEVNLDSYTRHTKENTL-QSITRGCFDLAQKRIFGLMKDSYRFLRSDIYL 285
OY 121 EYV 123
DB 286 DLI 288

RESULT 15

O9JHXO PRELIMINARY; PRT: 211 AA.

AC 09JHXO; 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=THORACIC AORTA SMOOTH MUSCLE;
RA Grant S.L., Lasegue B., Griendling K.K.;
RT "RGS2 regulates angiotensin II signaling in vascular smooth muscle."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279918; AAF85981.1; -.
SO SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;

Query Match 26.1%; Score 166.5; DB 11; Length 211;
Best Local Similarity 32.8%; Pred. No. 1.8e-08;

Matches 39; Conservative 19; Mismatches 58; Indels 3; Gaps 2;

OY 1 WTKSLHSLIGDGDGAYLRFLEEREKCVDTLDFWACNGFRQNLKDTKTLRVAKAIYKR 60
80 WEAEDDELLAKYGLAARAFRLKSECEENLEFWLACEDFKRK-SPQKLSKARKIYTD 138
OY 61 YIENNSVYSKQIKPATKYIRNGIKKQOIGSVMPDQOTEIQAVMENAYOVFLTSDIY 119
139 FTEKEAPKEINIDFQTKLIAONT--QDATSGCFTTAOKRVYSIMENNSYRFLSESEY 195
DB

Search completed: June 7, 2001, 02:09:39
Job time: 442 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:01:15 ; Search time 80.96 Seconds
(without alignments)
38.128 Million cell updates/sec

Title: US-09-587-574-3
Sequence: 1 ANGVSLPHPRTRHRLPKEM.....RLEKIKLELSRHSLSIERLQ 54

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401.*
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22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	100.0	840	20	W93570 Human conductin pr
2	272	100.0	840	20	W93569 Human conductin pr
3	142.5	52.4	992	20	W96265 Mus
4	141.5	52.0	900	20	W96264 Human axin. Homo
5	65	23.9	462	16	K78230 Candida antarctica
6	65	23.9	463	15	R48084 C. antarctica lipas
7	61.5	22.6	995	20	Y04658 L.lactis Hsdr subu
8	58	21.3	1816	21	Y95440 Caenorhabditis ele
9	57	21.0	115	21	B27999 Human secreted pro
10	57	21.0	260	21	G56044 Arabidopsis thalia
11	57	21.0	260	21	G61383 Arabidopsis thalia

12	57	21.0	306	21	G56043 Arabidopsis thalia
13	57	21.0	306	21	G61382 Arabidopsis thalia
14	57	21.0	321	21	G56042 Arabidopsis thalia
15	57	21.0	321	21	G61381 Arabidopsis thalia
16	56.5	20.8	534	17	R91309 Fungal signal reco
17	56.5	20.8	535	17	R91310 Fungal signal reco
18	56	20.6	349	19	W78102 Chimeric receptor
19	55	20.2	856	21	B40894 Human ORF ORF658
20	54.5	20.0	398	19	W98441 H. pylori GHPO 511
21	54	19.9	578	18	W10422 Penicillium chrys
22	53.5	19.7	267	18	B42487 Human ORF ORF2251
23	53.5	19.7	439	20	W88235 Human ORF ORF2251
24	53.5	19.7	626	20	Y06292 Human transcriptio
25	53.5	19.7	824	19	W68093 Human transcriptio
26	53	19.5	347	17	W05394 Human SH3p13 prote
27	53	19.5	406	20	Y23627 Human fibronogen d
28	53	19.5	406	20	Y23627 A human growth fac
29	53	19.5	406	20	Y05393 Human TIE ligand N
30	53	19.5	406	21	B28212 Human TIE ligand N
31	53	19.5	406	21	B12426 Human TIE ligand N
32	53	19.5	406	21	Y54496 Human muscle angio
33	53	19.5	406	21	Y86289 Human secreted pro
34	53	19.5	453	22	B53070 Human angiogenesis
35	53	19.5	758	21	B11540 SEN virus protein
36	53	19.5	900	17	R88615 TNF-R p55IC-Bindin
37	53	19.5	908	18	W15473 Human P100 protein
38	53	19.5	1257	20	Y06427 Mouse circadian re
39	52.5	19.3	1047	18	W01535 Cellular homologue
40	52	19.1	422	14	R39819 ZMPK1 homologue pr
41	52	19.1	478	10	W92950 WO9905287 Seq ID 1
42	52	19.1	722	19	W55104 Streptococcus pneu
43	52	19.1	803	21	B00066 KIAA0160 polypept
44	52	19.1	2234	21	Y81502 Streptococcus pneu
45	51.5	18.9	149	14	R39358 rZPP.149. Sus scr

ALIGNMENTS

RESULT 1	W93570	standard; Protein: 840 AA.
ID	W93570	
XX	W93570;	
AC		
XX		
DT	17-JUN-1999 (first entry)	
XX		
DE	Human conductin protein.	
XX		
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW	therapy: cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;	
KW	tumour suppressor.	
OS		
XX	Homo sapiens.	
XX		
PN	W09911780-A2.	
XX		
PD	11-MAR-1999.	
XX		
PE	01-SEP-1998; 98WO-DE02621.	
XX		
PR	02-SEP-1997; 97DE-1038205.	
XX		
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
PI	Behrens J, Birchmeier W;	
XX		
DR	WPI: 1999-214706/18.	
DR	N-PSDB; X23370.	
XX		
PT	Tumor-suppressing protein conductin - used for treatment and	
PT	diagnosis of tumors	

XX Claim 11; Fig 3; 22pp; German.
 PS This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 XX Sequence 840 AA;
 SQ
 Query Match 100.0%; Score 272; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 4.9e-25;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ANGOVSLPHFPTHRLEPKEMTPVEPAFAFAELISRLKIKLESLERHSLEERLQ 54
 DB 343 angvslphfptrhlrpkemtpvepafaafaelsrlkikleslshsleerlq 396
 RESULT 2
 ID W93569 standard; Protein; 840 AA.
 XX W93569;
 AC
 XX 17-JUN-1999 (first entry)
 DT
 XX Human conductin protein.
 DE
 XX Conductin: tumour; diagnosis; treatment; beta-catenin; anti-tumour;
 KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
 KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
 KW tumour suppressor.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 78..200
 FT /note= "Regulator of G protein signalling domain as
 FT described in claim 12"
 FT Binding-site 343..396
 FT /note= "GSK-3-beta binding region as described in
 FT claim 13"
 FT Binding-site 397..465
 FT /note= "Beta-catenin binding domain as described in
 FT claim 14"
 FT Region 783..833
 FT /note= "Dishevelled homology region as described in
 FT claim 15"
 FT
 XX WO9911780-A2.
 PN
 XX 11-MAR-1999.
 PD
 XX 01-SEP-1998; 98WO-DE02621.
 PF
 XX 02-SEP-1997; 97DE-1038205.
 PR
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PA
 XX Behrens J, Birchmeier W;
 PI
 XX WPI: 1999-214706/18.
 DR
 XX N-PSDB; X23369.
 XX Tumor-suppressing protein conductin - used for treatment and
 PT diagnosis of tumors
 XX

PS Claim 11; Fig 1; 22pp; German.
 XX This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 XX Sequence 840 AA;
 SQ
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 Best Local Similarity 100.0%; Pred. No. 4.9e-25;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 343 angvslphfptrhlrpkemtpvepafaafaelsrlkikleslshsleerlq 396
 RESULT 3
 ID W96265 standard; Protein; 992 AA.
 XX W96265;
 AC
 XX 14-JUN-1999 (first entry)
 DT
 XX Murine axlin.
 DE
 XX Axlin: cancer; breast cancer; colorectal cancer;
 KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin.
 XX Mus musculus.
 OS
 XX WO9902179-A1.
 PN
 XX 21-JAN-1999.
 PD
 XX 09-JUL-1998; 98WO-US14414.
 PF
 XX 10-JUL-1997; 97US-0890865.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Constantini F, Zeng L;
 PI
 XX WPI: 1999-120510/10.
 DR
 XX N-PSDB; X09013.
 XX Newly isolated nucleic acid encoding "axis inhibition" protein
 PT (Axlin) - useful for detecting, diagnosing and treating cancer
 XX
 XX Claim 8; Figure 8; 95pp; English.
 PS
 XX Nucleic acids encoding mutant and wild type Axlin and
 CC oligonucleotides derived from them are useful for detecting
 CC mutations in the Axlin gene and for determining whether a subject is
 CC likely to develop cancer (including breast, colorectal,
 CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
 CC type Axlin and homologues of Axlin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axlin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions
 CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axlin acts through

PR	22-JUN-1999:	9905-0140415.
XX		
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.	
XX		
PI	Scharenberg AM:	
XX		
DR	WPI: 2000-465957/40.	
XX		
PT	New SOC/CRCAC calcium channel polynucleotides and polypeptides used to	
PT	diagnose and treat proliferative disorders associated with the channel,	
PT	and to screen for novel modulators of the channel -	
XX		
PS	Example; Page 72-76; 108bp; English.	
CC		
CC	The present sequence is that of a <i>Caenorhabditis elegans</i>	
CC	polypeptide at the <i>c05c12.3</i> locus. The polypeptide was identified	
CC	in a database search for putative calcium channel proteins. The	
CC	<i>c05c12.3</i> protein was notable cause its central pore region had	
CC	some similarity to, but was clearly distinct from, members of the	
CC	TRP family of calcium channels. The polypeptide was used in	
CC	BLAST screening to isolate 2 other <i>C. elegans</i> homologues (see	
CC	<i>y95441-42</i>) and mouse <i>melastatin-1</i> (see <i>y95438</i>). These were used	
CC	to screen EST databases for lymphocyte homologues. Human clones	
CC	(see <i>A49927-23</i>) encoding members (see <i>y95435-37</i>) of a new family of	
CC	SOC (store operated channel) or CRCAC (calcium release activated	
CC	channel) calcium channel polypeptides were identified.	
XX		
Sequence	1816 AA;	

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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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XX AC G61383;  

XX DT 18-OCT-2000 (first entry)  

DE Arabidopsis thaliana protein fragment SEQ ID NO: 79611.  

XX XX  

XX Protein identification: signal transduction pathway; metabolic pathway;  

XX hybridisation assay; genetic mapping; gene expression control; promoter;  

XX termination sequence.  

XX OS Arabidopsis thaliana.  

XX PN EP1033405-A2.  

XX PD 06-SEP-2000.  

XX PE 25-FEB-2000; 2000EP-0301439.  

XX PR 25-FEB-1999; 99US-0121825.  

PR 05-MAR-1999; 99US-0123180.  

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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RESULT 2
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Sequence 2, Application US/09111556A
Patent No. 6020180
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Pathar, Shamkant A
APPLICANT: Egel-Miltani, Michi
APPLICANT: Borch, Kim
APPLICANT: Clausen, Ib G
APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6020180 of No. 6020180th America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,556A
FILING DATE: 22-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3748, 214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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Query Match 23.9%; Score 65; DB 3; Length 463;
Best Local Similarity 48.3%; Pred. No. 1.6;
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Patent No. 6074863
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Pathar, Shamkant A
APPLICANT: Egel-Miltani, Michi
APPLICANT: Borch, Kim
APPLICANT: Clausen, Ib G
APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6074863 of No. 6074863th America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,758
FILING DATE: 22-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3748, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-360-758-2

Query Match 23.9%; Score 65; DB 3; Length 463;
Best Local Similarity 48.3%; Pred. No. 1.6;
Matches 14; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 1 ANGOVSLPHPR--THRLPKEMTVERPA 27
|: ||: ||| | : | : | : |||
Db 336 ASYTVSVKFRFTWHAIPDEIVYQPPA 364

RESULT 4
US-08-317-401E-2
Sequence 2, Application US/08317401E
Patent No. 5922561
GENERAL INFORMATION:
APPLICANT: Thompson, Sheryl Ann
APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE OF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5922561 of No. 5922561th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711

REFERENCE/DOCKET NUMBER: 4248.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM SOURCE:
ORGANISM: Aspergillus niger
US-08-317-401E-2

Query Match 20.8%; Score 56.5; DB 2; Length 534;
Best Local Similarity 33.3%; Pred. No. 21;
Matches 13; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

OY 20 MTPVPAFAFAELISRLKLEL-----ESRHSLEERL 53
DB 164 LTQTPAIVAAAGVAKFKRERREIIVDTSGRHKQEEEL 202

RESULT 5
US-08-317-401E-4
Sequence 4, Application US/08317401E
Patent No. 5922561

GENERAL INFORMATION:
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE OF
TITLE OF INVENTION: ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59225610 No. 5922561disk of No. 5922561th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317.401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4248.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
US-08-317-401E-4

Query Match 20.8%; Score 56.5; DB 2; Length 552;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 13; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

OY 20 MTPVPAFAFAELISRLKLEL-----ESRHSLEERL 53
DB 160 LTQTPAIVAAAGVAKFKRERREIIVDTSGRHKQEEEL 218

RESULT 6
US-08-936-135-4
Sequence 4, Application US/08936135
Patent No. 6054293

GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936.135
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 0097-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2584 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-936-135-4

Query Match 20.6%; Score 56; DB 3; Length 2584;
Best Local Similarity 47.8%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 2 NCQVSLPFPRTTRLPKENTPVE 24
DB 1790 NSERGLPHEPRTTRRYRGLYPHE 1812

RESULT 7
US-08-936-135-2
Sequence 2, Application US/08936135
Patent No. 6054293

GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA

Query Match 20.8%; Score 56.5; DB 2; Length 552;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 13; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

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ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2588 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-936-135-2

Query Match                20.6%; Score 56; DB 3; Length 2588;
Best Local Similarity      47.8%; Pred. NO. 1.5e+02;
Matches    11; Conservative   3; Mismatches     9; Indels    0; Gaps    0;

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RESULT 8
 US-08-785-310A-7
 Sequence 7, Application US/08785310A
 Patent No. 5840532
 GENERAL INFORMATION:
 APPLICANT: McKnight, Steven L.
 APPLICANT: Russell, David W.
 TITLE OF INVENTION: Neuronal PAS Domain Protein
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/785,310A
 FILING DATE: 21-JAN-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UTSD:1226
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 824 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

```

;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-08-785-310A-7

```

Query Match	19.7%;	Score 53.5;	DB 2;	Length 824;
Best Local Similarity	20.0%;	Pred. No. 84;		
Matches	20;	Conservative	12;	Mismatches 51;
				Gaps 3;

4 QVSLPRHPRTTHRLPKEM	-----TPVEPAAF 28
QY	

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QY      29 AELISRLKLEKLELSR-----HSLERL 53
      :|: | : : | | | | | | | | | |
Db      496 SAQ-FSMQRTKDLEQRTRIQANIRWQEEELHKIQEQL 534

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RESULT 9
US-08-816-693A-52
; Sequence 52, Application US/08816693A

APPLICANT: Takahashi, Joseph S
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrence H
TITLE OF INVENTION: Clock Gene and Gene Product
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
CITY: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: 05/08/816,693A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5874241thrup, Thomas E
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 824 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
OS-08-816-693A-52

Query Match	19.7%	Score 53.5	DB 2	Length 824
Best Local Similarity	20.0%	Pred. No. 84		
Matches 20	Conservative 12	Mismatches 17	Indels 51	Gaps 3

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QY      4 QVSLPHFPRTHLRLEKEM-----TPVEPAAF 28
      : | | | | :
Db    436 EASIPALPRATLPQELLVPGLSQAATWPAFLPSPLSCDLTQQLLPQTVLQSTPAPMAQF 495

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QY      29 AAELISRLKLEKLELESR-----HSLTEERL 53
      :|: | : : | | | | | | | | | | | | | | |
Db      496 SAQ-FSMFQTIKDQLEQRTIRILQANIRWQGEELHKIQEQL 534

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RESULT 10
US-08-885-291-52
; Sequence 52, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A
; EARLIER FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 52
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-885-291-52

```

```

Query Match          19.7%: Score 53.5; DB 3; Length 824;
Best Local Similarity 20.0%: Pred. No. 84;
Matches 20; Conservative 12; Mismatches 17; Indels 51; Gaps 3;

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OY 4 QVSLPHPRHRLPKEM-----TPVEPAF 28
DB 436 EASTPALPSRATLPGLSQAATMPALPSPLSCDTQQLPQTVLQSTPAPMAOF 495
OY 29 AAEILSRLEKLESLR-----HSLEERL 53
DB 496 SAO-FSMFOTIKDLEORTRILOANTRMOOEELHKTQEL 534

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RESULT 11
US-08-934-494-2
; Sequence 2, Application US/08934494
; Patent No. 6030831
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatln (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,494
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-934-494-2

```

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Query Match          19.5%: Score 53; DB 3; Length 406;
Best Local Similarity 34.1%: Pred. No. 42;
Matches 14; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

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OY 12 RTRHLPKEMTPVEPAFAAEILSRLEKLEKLESLRSLER 52
DB 161 RRRRLPEMAQVPDP----AHNVSRHLRPLPDCELFQVGER 197

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RESULT 12
US-09-143-068-2
; Sequence 2, Application US/09143068
; Patent No. 6074873
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth
; APPLICANT: Williams, Mickey
; TITLE OF INVENTION: Tie Ligand Homologues
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatln (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,068
; FILING DATE: 28-Aug-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1078P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-143-068-2

```

```

Query Match          19.5%: Score 53; DB 3; Length 406;
Best Local Similarity 34.1%: Pred. No. 42;
Matches 14; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

```

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OY 12 RTRHLPKEMTPVEPAFAAEILSRLEKLEKLESLRSLER 52
DB 161 RRRRLPEMAQVPDP----AHNVSRHLRPLPDCELFQVGER 197

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RESULT 13
US-08-699-103B-10
; Sequence 10, Application US/08699103B
; Patent No. 6107462
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper D.
; APPLICANT: Hampton, Randolph
; TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING

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```

1      TITLE OF INVENTION:  CHOLESTEROL SYNTHESIS
2      NUMBER OF SEQUENCES:  25
3      CORRESPONDENCE ADDRESS:
4      ADDRESSEE:  Fish & Richardson P.C.
5      STREET:  2200 Sand Hill Road, Suite 100
6      City:  Menlo Park
7      STATE:  CA
8      COUNTRY:  USA
9      ZIP:  94025
10     COMPUTER READABLE FORM:
11     MEDIUM TYPE:  Diskette
12     COMPUTER:  IBM Compatible
13     OPERATING SYSTEM:  DOS
14     SOFTWARE:  FASTSEQ for Windows Version 2.0
15     CURRENT APPLICATION DATA:
16     APPLICATION NUMBER:  US/08/699,103B
17     FILING DATE:  16- AUG-1996
18     PRIOR APPLICATION DATA:
19     APPLICATION NUMBER:  60/002,581
20     FILING DATE:  17-AUG-1995
21     ATTORNEY/AGENT INFORMATION:
22     NAME:  Green, Grant D
23     REGISTRATION NUMBER:  31,259
24     REFERENCE/DOCKET NUMBER:  09272/005001
25     TELECOMMUNICATION INFORMATION:
26     TELEPHONE:  650/322-5070
27     TELEFAX:  650/854-0875
28     INFORMATION FOR SEQ ID NO:  10:
29     SEQUENCE CHARACTERISTICS:
30     LENGTH:  853 amino acids
31     TYPE:  amino acid
32     TOPOLOGY:  linear
33     MOLECULE TYPE:  protein
34     OS-08-699-103B-10

```

Query Match	19.5%;	Score 53;	DB 3;	Length 853;
Best Local Similarity	37.9%;	Pred. No. 1e+02;		
Matches 11; Conservative	6;	Mismatches 12;	Indels 0;	Gaps 0;

QY 8 PHFPRTHRLPKEMTPVEPAFAEALISRL 36
|| : : | | | ||| : || |
Db 44 PHYGLKEIYENMAPGENKRFADIIISVL 72

RESULT 14
 US-08-699-103B-12
 Sequence 12, Application US/08699103B
 Patent No. 6107462
 GENERAL INFORMATION:
 APPLICANT: Rine, Jasper D.
 APPLICANT: Hampton, Randolph
 TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING
 TITLE OF INVENTION: CHOLESTEROL SYNTHESIS
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/699,103B
 FILING DATE: 16-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/002,581
 FILING DATE: 17-AUG-1995

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Green, Grant D.
3 REGISTRATION NUMBER: 31,259
4 REFERENCE/DOCKET NUMBER: 09272/005001
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: 650/322-5070
7 TELEFAX: 650/854-0875
8 INFORMATION FOR SEQ ID NO: 12:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 908 amino acids
11 TYPE: amino acid
12 TOPOLOGY: linear
13 MOLECULE TYPE: protein
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Query Match	19.5%;	Score 53;	DB 3;	Length 908;
Best Local Similarity	37.9%;	Pred. No. 1,1e+02;		
Matches	11;	Conservative	6;	Mismatches 12;
				Indels 0;
				Gaps 0;

QY 8 PHEPRTHRLPKEMTPVEPAFAAELISRL 36
||: : : ||| : |||
Db 101 PHYGLKEIYENMAPGENKRFADIIISVL 129

```

RESULT 15
US-09-220-641-3
? Sequence 3, Application US/09220641
? Patent No. 6210923
? GENERAL INFORMATION:
? APPLICANT: Lee, Cheng-Chi
? APPLICANT: Sun, Zhong Sheng
? APPLICANT: Albrecht, Urs
? APPLICANT: Eichele, Gregor
? TITLE OF INVENTION: Mammalian Circadian Regulator M-RICU12 (M-PER2
? FILE REFERENCE: D6067
? CURRENT APPLICATION NUMBER: US/09/220,641
? CURRENT FILING DATE: 1998-12-24
? EARLIER APPLICATION NUMBER: US 60/068,886
? EARLIER FILING DATE: 1997-12-26
? NUMBER OF SEQ ID NOS: 5
? SEQ ID NO 3
? LENGTH: 1257
? TYPE: prt
? ORGANISM: Mus musculus
? FEATURE:
? OTHER INFORMATION: m-ricu12 predicted amino acid sequence.
US-09-220-641-3

```

	Query Match	Best Local	Similarity	Score	DB	Length
Matches	11	Conservative	47.8%	Pred. No. 1.6e+02		
				Mismatches	11	Indels
						Gaps
QY	6	SLPHFPTRLPKEMTPVEPAAF	28			
Db	921	SQPHFAHPTLASELTPASQAEF	943			

```
QY      6 SLPHFPRTHRLPKEMTPVEPAAF 28
          | | | | | : | | | |
Db      921 SQPHFPAHPTLASEITPASQAEF 943
```

Search completed: June 7, 2001, 02:02:10
Job time: 5403 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2001, 02:03:20 ; Search time 56.43 Seconds
(without alignments)
65.764 Million cell updates/sec

Title: US-09-587-574-3

Perfect score: 272
Sequence: 1 ANGVSLPHRPRTIRLPEKM.....RLKLTLELSRHSLEERLQ 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR 67:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	100.0	838	2 T08423	Axin homolog Axll
2	142.5	52.4	832	2 T08422	negative regulator
3	64.5	23.7	268	2 C83442	hypothetical prote
4	63	23.2	141	2 D69857	conserved hypotet
5	62.5	23.0	251	2 T12864	probable antitrepre
6	62	22.8	333	2 C48423	homeotic protein e
7	61.5	22.6	539	2 S55190	hypothetical prote
8	60	22.1	377	2 T46149	protein kinase ATN
9	59.5	21.9	369	2 S56638	mitogen-activated
10	59.5	21.9	964	2 E70826	probable membrane
11	59.5	21.9	7862	2 T38346	elastic titin - hu
12	59	21.7	231	2 S30438	homeotic protein e
13	58.5	21.5	601	2 A82561	hypothetical prote
14	58.5	21.5	725	2 T19994	hypothetical prote
15	58	21.3	171	2 S35638	homeotic protein E
16	58	21.3	1707	2 T18951	hypothetical prote
17	57.5	21.1	254	2 D70406	DMSO reductase cha
18	57.5	21.1	978	2 A70387	conserved hypotet
19	57	21.0	392	2 B48423	homeotic protein e
20	57	21.0	401	2 A48423	engrailed homodom
21	57	21.0	722	2 T26297	hypothetical prote
22	56.5	20.8	526	2 T39748	probable ser/thr p
23	56.5	20.8	534	2 UC4572	signal recognition
24	56	20.6	261	2 S30437	homeotic protein e
25	56	20.6	489	1 SYBSES	glutamate--tRNA 11
26	56	20.6	501	2 T39801	hypothetical sh3-c
27	56	20.6	545	2 C83379	probable dehydroge
28	56	20.6	840	2 D82615	hypothetical prote
29	56	20.6	1258	2 D75453	5-methyltetrahydro

30	55.5	20.4	349	2 S32040	homeotic protein e
31	55.5	20.4	1325	2 S16129	dyneln-associated
32	55.5	20.4	1364	2 T40839	hypothetical prote
33	55	20.2	239	2 T02984	myb-related prote
34	55	20.2	416	2 T30946	hypothetical prote
35	55	20.2	1553	2 T09361	hypothetical prote
36	54.5	20.0	312	2 C71136	hypothetical prote
37	54.5	20.0	324	2 S44956	lmbi protein - str
38	54.5	20.0	370	2 C64645	hypothetical prote
39	54.5	20.0	510	2 PC4054	cardiac C-protein
40	54.5	20.0	662	2 T36792	hypothetical prote
41	54.5	20.0	1063	2 T03743	bifocal protein -
42	54	19.9	375	2 T01468	hypothetical prote
43	54	19.9	591	2 F82234	aspartyl-tRNA synt
44	54	19.9	602	2 T29386	hypothetical prote
45	53.5	19.7	183	2 D81296	hypothetical prote

ALIGNMENTS

RESULT 1
T08423
Axin homolog Axll - rat
N:Alternate names: Axll
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A:Title: Axll, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: Z16414; MIMD:98226558
A:Accession: T08423
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:93080758; PIDD:AC40089.1; PID:93080759
A:Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 272; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 7.1e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANGVSLPHRPRTIRLPEKMPVPPAFALISRLKLTLELSRHSLEERLQ 54
Db 343 ANGVSLPHRPRTIRLPEKMPVPPAFALISRLKLTLELSRHSLEERLQ 396

RESULT 2
T08422
negative regulator axin [Imported] - rat
N:Alternate names: rAxin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Mural, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A:Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: Z16413; MIMD:98151361
A:Accession: T08422
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IK>
A:Cross-references: EMBL:AF017756; NID:92982197; PIDD:AC40066.1; PID:92982198
A:Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Query Match 52.4%; Score 142.5; DB 2; Length 832;
Best Local Similarity 56.6%; Pred. No. 9.2e-09;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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OY      2  NGVSYSLPHEPTHTSLPKEMTPEVPAFAELISRLKEKTLISRHSSLEKQ 54
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      368  NGRVPLPHIPTTTPMPKEIR-VEFQKFAEELIHRLEAVQRTREAEKLEERLK 419

RESULT      3
C83442
hypothetical protein PA1624 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83442
R:Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laribig, K.; Lim,
..; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: AB2950; MUID:20437337
A:Accession: C83442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <STO>
A:Cross-references: GB:AE004590; GB:AE004091; NID:g9947587; PIDN:AG05013.1; GSPDB:GN001
A:Experimental source: strain PAO1
A:Genetics
:Gene: PA1624

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Query Match	33.7%	Score 64.5	DB 2	Length 268
Best Local Similarity	23.1%	Pred. No. 3.3		
Matches	18	Conservative	9	Mismatches 14; Indels 15; Gaps 2;

OY	1	ANGOVSLHPFRTRHLPKEMTPVPSAAALISLSEKL----	KLELSRHSLEER	52
db	195	ANGGTTTSH-----	VPAPFGSMLELTVTRLRIDGCVRELKSGKHAQENR	239

RESULT **4**

D69857
conserved hypothetical protein yk1A - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence.revision 05-Dec-1997 #text.change 20-Jun-2000
C:Accession: D69857

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertin, A.M.; Alloni, G.; Azevedo, V.; Bertelezi, C.; Bron, S.; Brönnlitz, S.; Bruschi, C.V.; Caldwell, B.; Caprano, V.; Carter, N.M.; Chakrabarty, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Furuta, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hujo, M.F.; Iech, J.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardiniois, K.; Koetter, P.; Konigstein, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, A.; Y. M.; Ogawa, K.; Oglivar, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli, R.; Riiger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, J.; Sato, T.; Scanlon, T.; A:Authors: Schlach, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akenchil, M.; Tamakoshi, A.; Tanaka, T.; Terpeira, P.; Toignon, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipit, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A:Authors: Yoshioka, H.F.; Zundstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033

A:Accession: D69857

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-141 <KUN>

A:Cross-references: GB:D99110; GB:AL009126; NID:g2633472; PIDN:CAB13171.1; PID:g2633668

A:Experimental source: strain 168

C:Genetics:

A:Gene: yk1A

A:Superfamily: hypothetical protein yk1A

Query Match	23.28;	Score 63;	DB 2;	Length 141;
Best Local Similarity	33.38;	Pred. No. 2.4;		
Matches	16;	Conservative	11;	Mismatches 13;
				Indels 8;
				Gaps 2;

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QY      5 VSLPFRTHRLPKEMTPVE--PAFAA-----ELISRLKLEKLE 44
      ||:| ||:| :| | :| | :| | :| | :| | :| |
Db     31 VAMGCPRAKKLEKATNPQFLAAGYAACFDSALQLVARTERVKVETE 78

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RESULT 5
T12864
probable antirepressor - *Bacillus subtilis* phage SPBc2

C:\Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000

Rilazarevic, V.; Diestelhoeft, A.; Soldo, B.; Hilbert, H.; MaueI, C.; Karamata, D submitted to the EMBL Data Library, August 1997

A:Description: The complete nucleotide sequence of the *Bacillus subtilis* SPbetac2 protease gene.
A:Reference number: Z17583

A:Accession: T12864
A:Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA
A: Residues: 1-251 <LAZ>
1. C. 2000 reference. EMBL: AF020713. NID: G3025478. STD: G3025578. PTDN: AAC13073 1

C. Rönk, S. Arouillet, S. Brusch, C.V. Caldwell, B. Capuano, V.; Cater, N.M.; R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bert
Alcoss-terferes; EMDL07013; HJG9022870; FLG9022870; LBN9022870

A.; Enhllich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A.; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.

A; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, S.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Mau, A.; Authors: Lauber, J.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Mau, A.;

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parlo, V.; Poll, I.M.; Poltelet, C.; Rivoita, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, P.; Schabert, G.; Schreiber, D.; Scofield, F.; Sakimichi, T.; Sekuska, A.; Senise, J.

T. Winters, P. Winant, A. Yamamoto, H. Yanane,
T. Yano, K. Yasumoto, K. Yata, K. Yoshida,
T. Yotsuyanagi, M. Zaitsev

Article: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*

A:Reference number: A69580; MUID:98044033
A:Accession: D69919

A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA

A,Residues: 1251 <KUN>
A,Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:92634478; PIDN:CAB13985.1;

A: Experimental source: strain 106
C: Genetics:
A: Genes: none

a/genre: yoju
c: Superfamily: phage P1 kila protein

Query Match 23.08; Score 62.5; DB 2; Length 251;

Best Local Similarity 32.18; Pred. No. 5.3;
Matches 17; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

QY 1 ANGQVSLPHFPRTH---LPKEMTPEVEPAFAELISRIEKLKLEESHSI 49

Db 62 ATGR-SLKHEILTRKCDMVANKMTGAKGVLTADQVYSKEEEMENALKKRPRL 113

6 RESULT

C48423
homeotic protein engrailed 1 - chicken

C.Species: Gallus gallus (chicken)
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Oct-1997

C:\Accession: C48423
Rloggan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner,

Dev. Genet. 13, 345-358, 1992

A:Accession: C48423
A:Reference number: A40423; MUID:5510333
A>Status: preliminary; not compared with conceptual translation

A:Residues: 1-333 <106>
A:Molecule type: DNA
A:Status: predicted,1) not compared with conserved sequences

C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:245-301/Domain: homeobox homology <HOX>

Query Match 22.8%; Score 62; DB 2; Length 333;
 Best Local Similarity 38.8%; Pred. No. 8.2;
 Matches 19; Conservative 9; Mismatches 13; Indels 8; Gaps 3;

OY 11 PRTNRLPKEMTPVEP---AAFAELISRLKLELE-SRHSLEPRLO 54
 DB 230 PRTNRLPKEMTPVEP---AAFAELISRLKLELE-SRHSLEPRLO 54

RESULT 7
 S55190

hypothetical protein YJR003C - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein J1415; hypothetical protein YJR03.30
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Mar-2000

R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S55183

A:Accession: S55190
 A:Molecule type: DNA

A:Residues: 1-539 <DEH>
 A:Cross-references: EMBL:X87611; NID:g854567; PIDN:CAA60924.1; PID:g854575

R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
 submitted to the Protein Sequence Database, September 1995

A:Reference number: S56771
 A:Accession: S57018

A:Molecule type: DNA
 A:Residues: 1-539 <ZAG>

A:Cross-references: EMBL:Z49503; NID:g1015623; PIDN:CAA89525.1; PID:g1015624; MIPS:YJR003C

C:Genetics:
 A:Map position: 10R

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YJR003C

Query Match 22.6%; Score 61.5; DB 2; Length 539;
 Best Local Similarity 34.3%; Pred. No. 16;
 Matches 12; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

OY 8 PHE-PRTHRLPKEMTPVEPAAFAELISRLKLE 41
 DB 56 PHE-PRTHRLPKEMTPVEPAAFAELISRLKLE 41

RESULT 8
 T46149
 protein kinase ATN1-like protein - Arabidopsis thaliana
 N:Alternate names: protein T3A5.100
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000

C:Accession: T46149
 R:Blöcker, H.; Mewes, H.W.; Meyer, K.F.X.; Lemcke, K.; Schueller, C.; Quetler, F.; Sala
 submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23024
 A:Accession: T46149

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-377 <BLD>
 A:Cross-references: EMBL:AL12979

A:Experimental source: cultivar Columbia; BAC clone T3A5
 C:Genetics:

A:Map position: 3
 A:Introns: 66/2; 111/3; 177/1; 217/3; 269/3

A:Note: T3A5.100
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

Query Match 22.1%; Score 60; DB 2; Length 377;
 Best Local Similarity 30.6%; Pred. No. 16;
 Matches 15; Conservative 11; Mismatches 15; Indels 8; Gaps 2;

OY 5 VSLPHE-----PRTNRLPKEMTPVEPAAFAELISRLKLELES 45
 DB 261 ISIPYFVNOGKRPSLSNIDPEVYPILECCWADSKRTLEFDITLSLES 309

RESULT 9
 S56638

mitogen-activated protein kinase 1 homolog (clone AspK9) - oat
 N:Alternate names: MAP1 kinase
 C:Species: Avena sativa (oat)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999

C:Accession: S56638
 R:Huntley, A.K.; Phillips, A.L.

Plant Mol. Biol. 27, 1043-1052, 1995
 A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that s

A:Reference number: S56638; MUID:95284341
 A:Accession: S56638

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-369 <HUT>
 A:Cross-references: EMBL:X79993; NID:g871983; PIDN:CAA56314.1; PID:g871984

C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; protein kinase

F:33-322/Domain: protein kinase homology <KIN>
 F:42-50/Region: protein kinase ATP-binding motif

Query Match 21.9%; Score 59.5; DB 2; Length 369;
 Best Local Similarity 35.8%; Pred. No. 18;
 Matches 19; Conservative 7; Mismatches 18; Indels 9; Gaps 3;

OY 7 LPHFPRTHRLPKEMTPVEPAAFAELISRLKLELESNHSLEERL 53
 DB 276 LPHFPRTHRLPKEMTPVEPAAFAELISRLKLELESNHSLEERL 53

RESULT 10
 E70826
 probable membrane protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: E70826
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98293987
 A:Accession: E70826

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-964 <COI>
 A:Cross-references: GB:AL021943; GB:AL123456; NID:g3261530; PIDN:CA17459.1; PID:el25

A:Experimental source: strain H37Rv
 C:Genetics:

A:Gene: mmpL5

Query Match 21.9%; Score 59.5; DB 2; Length 964;
 Best Local Similarity 31.2%; Pred. No. 53;
 Matches 15; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

OY 7 LPHFPRTHRLPKEMTPVEPAAFAELISRLKLELESNHSLEERLQ 54
 DB 621 LPHFPRTHRLPKEMTPVEPAAFAELISRLKLELESNHSLEERLQ 663

RESULT 11

138346
 elastic titin - human (fragment)
 C:Species: Homo sapiens (man)

R.; Simpson, A. J. G.; Reinach, F. C.; Arruda, P.; Abreu, F. A.; Acencio, M.; Alvarenga, R.;

C;Superfamily: unassigned homeobox proteins

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:10:29 ; Search time 39.03 Seconds

(without alignments)
47.394 Million cell updates/sec

Title: US-09-587-574-3

Perfect score: 272
Sequence: 1 ANGVSLPRFRTHRLPRK.....RLKLEKLESLRSLERLQ 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SWISSPROT_39:*
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	100.0	838	1 AXN2_RAT	070240 rattus norv
2	272	100.0	840	1 AXN2_MOUSE	088566 mus musculi
3	268	98.5	843	1 AXN2_HUMAN	097211 homo sapien
4	204	75.0	812	1 AXN2_BRARE	P57095 brachydanto
5	157.5	57.9	841	1 AXN2_CHICK	042400 gallus galli
6	150.5	55.3	835	1 AXN1_BRARE	P57094 brachydanto
7	142.5	52.4	893	1 AXN1_RAT	070239 rattus norv
8	141.5	52.0	992	1 AXN1_MOUSE	035625 mus musculi
9	141.5	52.0	900	1 AXN1_HUMAN	015169 homo sapien
10	136.5	50.2	842	1 AXN1_XENLA	097970 xenopus lae
11	66	24.3	333	1 HME1_CHICK	005916 gallus galli
12	63	23.2	141	1 YKLA_BACSU	034762 bacillus su
13	61.5	22.6	539	1 VJX3_YEAST	P47084 saccharomyc
14	61	22.4	391	1 HME1_HUMAN	005925 homo sapien
15	59.5	21.9	410	1 TX28_HUMAN	015482 homo sapien
16	59.5	21.9	964	1 MML5_MYCTU	053784 mycobacteri
17	59	21.7	231	1 HME1_BRARE	004896 brachydanto
18	58.5	21.5	725	1 SYTC_CAEEL	P57093 caenorhabdi
19	58	21.3	171	1 HME1_XENLA	P31538 xenopus lae
20	57	21.0	401	1 HME1_MOUSE	P09065 mus musculi
21	57	21.0	714	1 HUNK_MOUSE	088866 mus musculi
22	56.5	20.8	534	1 SR54_ASPIRG	Q00179 aspergillus
23	56	20.6	261	1 HME3_BRARE	P31533 brachydanto
24	56	20.6	310	1 TH14_HALNI	Q91mc7 halobacteri
25	56	20.6	489	1 SYE_BACST	P22240 bacillus st
26	55.5	20.4	349	1 HME1_ARTSF	005640 artemia san
27	55.5	20.4	1280	1 DYNA_RATM	P28023 rattus norv
28	54.5	20.0	662	1 MYPC_AMBME	Q90203 ambystoma m
29	54.5	20.0	662	1 V663_HSV11	Q00195 icalaurid h
30	54	19.9	288	1 HME2_CHICK	Q05917 gallus galli
31	54	19.9	332	1 HME2_HUMAN	P19622 homo sapien
32	53.5	19.7	258	1 RS3_METTH	026116 mechanobact
33	53.5	19.7	339	1 PCB3_HUMAN	P57721 homo sapien

34	53.5	19.7	339	1 PCB3_MOUSE	P57722 mus musculi
35	53.5	19.7	439	1 FGL2_HUMAN	Q14314 homo sapien
36	53.5	19.7	745	1 AXN1_DROME	Q97407 drosophila
37	53.5	19.7	824	1 NPA2_HUMAN	Q99743 homo sapien
38	53	19.5	325	1 YB93_MYCTU	Q10552 mycobacteri
39	53	19.5	347	1 SH33_MOUSE	Q62421 mus musculi
40	53	19.5	354	1 CD72_MOUSE	P21855 mus musculi
41	53	19.5	908	1 PSD2_HUMAN	Q13200 homo sapien
42	53	19.5	1257	1 PER2_MOUSE	Q54943 mus musculi
43	52.5	19.3	93	1 HME1_SCHAM	P14150 schistosom
44	52.5	19.3	254	1 FRI_PPAVU	P23699 phaseolus v
45	52.5	19.3	338	1 SCAL_HUMAN	Q15126 homo sapien

ALIGNMENTS

RESULT	ID	AXN2_RAT	STANDARD:	PRT:	838 AA.
AC	070240:				
DT	01-OCT-2000 (Rel. 40, Created)				
DT	01-OCT-2000 (Rel. 40, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)				
DE	(AXIL).				
GN	AXIN2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98226558; PubMed=9566905;				
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.;				
RT	"Axil", a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos.;				
RT	Mol. Cell. Biol. 18:2867-2875(1998).				
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).				
CC	- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX.				
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.				
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY P2A.				
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.				
CC	- SIMILARITY: CONTAINS 1 DIX DOMAIN.				
CC	-----				
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CC	-----				
DR	EMBL; AF017757; AAC40089.1; ..				
DR	HSSP; P49799; IAGR.				
DR	InterPro; IPR000342; ..				
DR	InterPro; IPR001158; ..				
DR	Pfam; PF00778; DIX; 1.				
DR	Pfam; PF00778; DIX; 1.				
DR	PROSITE; PS50132; RGS; 1.				
KW	Developmental protein; Phosphorylation.				
FT	DOMAIN 81 200 RGS.				
FT	DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).				

FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 SIMILARITY).
FT DOMAIN 756 838 POLY-HIS.
SQ SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;

Query Match 100.0%; Score 272; DB 1; Length 838;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGVSLPFPFTRHLPKEMTPVEPAFAAEILISRLKLESLERHSLEERTQ 54
DQ 343 ANGVSLPFPFTRHLPKEMTPVEPAFAAEILISRLKLESLERHSLEERTQ 396

RESULT 2
ID AXN2_MOUSE STANDARD; PRT; 840 AA.
AC 088566; 090XJ6;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Asbrand C.,
Wirtz R., Kuehl M., Wedlich D., Birchmeier W.;
RT "Functional interaction of an axin homolog, conductin, with beta-
catenin, APC, and GSK3beta.";
RL Science 280:596-599(1998).
[2]
RN SEQUENCE FROM N.A.
RP Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATEININ. THE INTERACTION CONTAINED IN BETA-CATEININ.
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEININ.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF073788; AAC26047.1; -
DR EMBL: AF205889; AAR22860.1; -
DR MGD: MG1:1270862; AXIN2.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -

DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PS01301; RGS-PROTEIN.
DR PROSITE: PS00332; RGS; 1.
KW Anti-oncogene; Phosphorylation.
FT DOMAIN 81 200
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 469 476 POLY-HIS.
FT DOMAIN 758 840 DIX.
FT CONFLICT 101 101 R -> K (IN REF. 2).
FT CONFLICT 474 474 H -> Y (IN REF. 2).
FT CONFLICT 484 484 S -> P (IN REF. 2).
FT CONFLICT 503 503 F -> S (IN REF. 2).
FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA; 92934 MW; A07DSEFB25DE7277 CRC64;

Query Match 100.0%; Score 272; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGVSLPFPFTRHLPKEMTPVEPAFAAEILISRLKLESLERHSLEERTQ 54
DQ 343 ANGVSLPFPFTRHLPKEMTPVEPAFAAEILISRLKLESLERHSLEERTQ 396

RESULT 3
ID AXN2_HUMAN STANDARD; PRT; 843 AA.
AC 09Y2T1; 09UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24.";
RL Genomics 55:341-344(1999).
[2]
RN SEQUENCE FROM N.A.
RP Tissue-Brain, and Lymphoblast;
RC Tissue-Brain, and Lymphoblast;
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATEININ. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATEININ. THE INTERACTION CONTAINED IN BETA-CATEININ.
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEININ.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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DR EMBL: AF078165; AAD0976.1; -
DR EMBL: AF205888; AAF22799.1; -
DR MIM: 604025; -
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 81 200 RGS.
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 469 474 DIX.
FT DOMAIN 761 843 DIX.
FT CONFLICT 37 62 OPGVKGQVTRKPMYSVSNTRNEDGL -> HHGCGPGHOT
FT CONFLICT 346 346 Q -> R (IN REF. 2).
FT CONFLICT 572 636 MISSING (IN REF. 2).
FT CONFLICT 687 687 P -> S (IN REF. 2).
FT CONFLICT 696 696 Q -> H (IN REF. 2).
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A6664D CRC64;

Query Match 98.5%; Score 268; DB 1; Length 843;
Best Local Similarity 98.1%; Pred. No. 5.2e-24;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPPTTHRLPKEMTPVEPAFAELISRLKLELSHSLERLQ 54
DB 343 ANGOVSLPFPPTTHRLPKEMTPVEPAFAELISRLKLELSHSLERLQ 396

RESULT 4
AXN2_BRAE STANDARD; PRT: 812 AA.
AC P57093;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2).
GN AXIN2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20171051; PubMed-10704853;
RA Shintzu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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DR EMBL: AB032263; BAA92440.1; -
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 84 203 RGS.
FT DOMAIN 329 415 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 415 467 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 412 419 POLY-SER.
FT DOMAIN 730 812 DIX.
SQ SEQUENCE 812 AA; 91496 MW; 46E5ADA6DE2240CC CRC64;

Query Match 75.0%; Score 204; DB 1; Length 812;
Best Local Similarity 79.2%; Pred. No. 1.8e-16;
Matches 42; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 NGOVSLPFPPTTHRLPKEMTPVEPAFAELISRLKLELSHSLERLQ 54
DB 346 NGOVSLPFPPTTHRLPKEMTPVEPAFAELISRLKLELSHSLERLQ 398

RESULT 5
AXN2_CHICK STANDARD; PRT: 841 AA.
AC 042400;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN).
GN AXIN OR AXN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Embryo;
RA MEDLINE-97373830; PubMed-9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L. III,
RA Lee J.J., Tildeman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL: AF009012; AAC60245.1; -
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 88 211 RGS.
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY SIMILARITY).
FT DOMAIN 759 841 DIX.
SQ SEQUENCE 841 AA; 94931 MW; 400DCC90E72506FE CRC64;

Query Match 57.9%; Score 157.5; DB 1; Length 841;
Best Local Similarity 59.3%; Pred. No. 5.5e-11;
Matches 32; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANGVSLPFRPTRLRPEKMPVEPAFAELISRLKLESLERHSLEERLQ 54
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 ANGRVPLPHIRPTNRPKDI-HVEPEKFAELINLRLEQKEREAEKLEERLK 414

RESULT 6
AXNL_BRARE STANDARD; PRT; 835 AA.
AC P57094;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITOR PROTEIN 1).
GN AXIN1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; PubMed=10704853;
RA Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
BAE Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL: AB032262; BAA92439.1; -
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 154 277 RGS.

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FT DOMAIN 92 214 RGS.
FT DOMAIN 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY SIMILARITY).
FT DOMAIN 753 835 DIX.
SQ SEQUENCE 835 AA; 94351 MW; 1C62FCF1F5937C87 CRC64;

Query Match 55.3%; Score 150.5; DB 1; Length 835;
Best Local Similarity 60.4%; Pred. No. 3.7e-10;
Matches 32; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 NGVSLPFRPTRLRPEKMPVEPAFAELISRLKLESLERHSLEERLQ 54
|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 366 NGRVPLPHIRPTNRPKDI-HVEPEKFAELISRLKLESLERHSLEERLK 417

RESULT 7
AXNL_RAT STANDARD; PRT; 893 AA.
AC Q70239;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 PROTEIN (AXIS INHIBITOR PROTEIN 1) (RAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP TISSUE=Brain;
RC MEDLINE=98151361; PubMed=9482734;
RA Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;
RX "Axin, a negative regulator of the Wnt signaling pathway, forms a
complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
dependent phosphorylation of beta-catenin.";
RL EMBO J. 17:1371-1384(1998).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
FOLLOVED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
SPLEEN AND LIVER.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL: AF017756; AAC40066.1; ALT_INIT.
DR HSSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 154 277 RGS.

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FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 818 900 SIMILARITY).
SQ SEQUENCE 900 AA; 99803 MW; EESF990B11FC7B3B CRC64;

Query Match 52.0%; Score 141.5; DB 1; Length 900;
Best Local Similarity 56.6%; Pred. No. 4.6e-09;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 2 NGQVSLPHPRTHRLPKEMTPVEPAFAAELISRLKLELSRHSLEERQ 54
Db 400 NGKVPPLPHPRTHRLPKEMTPVEPAFAAELISRLKLELSRHSLEERL 451

RESULT 10
AXN_XENLA STANDARD: PRT; 842 AA.

ID AXN_XENLA STANDARD: PRT; 842 AA.
AC 091G10;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (AXIN).
CN AXIN OR AXN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;

RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; PubMed=10072781;
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RL Mech. Dev. 80:147-151(1999)."
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: WEAKLY AND UBQUITOUSLY EXPRESSED THROUGHOUT
CC EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR
CC MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.

CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.

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DR EMBL; AF097313; AAC71036.1; -
DR HSP; P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam; PF00615; RGS; 1.
DR PROSITE; PS50132; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KM Developmental protein; Phosphorylation.

FT DOMAIN 88 211 RGS
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
SIMILARITY).

SO SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64;

Query Match 50.2%; Score 136.5; DB 1; Length 842;

Best Local Similarity 53.7%; Pred. No. 1.7e-08;
Matches 29; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

OY 1 ANGQVSLPHPRTHRLPKEMTPVEPAFAAELISRLKLELSRHSLEERQ 54
Db 362 ANGKVPPLPHPRTHRLPKEMTPVEPAFAAELISRLKLELSRHSLEERL 414

RESULT 11
HMEI_CHICK STANDARD: PRT; 333 AA.

ID HMEI_CHICK STANDARD: PRT; 333 AA.
AC 005916;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HOMEOBOX PROTEIN ENGRAILED-1 (GG-EN-1).
CN EN1 OR EN-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93185339; PubMed=1363401;
RA Logan C., Hanks M.C., Noble-Topham S., Nallathattan D.,
RA Provart N.J., Joyner A.L.;
RT "Cloning and sequence comparison of the mouse, human, and chicken
RT engrailed genes reveal potential functional domains and regulatory
RT regions."
RL Dev. Genet. 13:345-358(1992).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- SIMILARITY: BELONGS TO THE ENGRAILED FAMILY OF HOMEOBOX PROTEINS.

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DR EMBL; L12694; AAA53435.1; -

DR EMBL; L12695; AAA53436.1; -

DR HSP; P02836; 1HDD.

DR TRANSFAC; T02014; -

DR InterPro: IPR000747; -

DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00024; HOMEOBOX.

DR PRINTS; PR00026; ENGRAILED.

DR PROSITE; PS00027; HOMEOBOX_1; 1.

DR PROSITE; PS50071; HOMEOBOX_2; 1.

DR PROSITE; PS00033; ENGRAILED; 1.

FT HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein.

FT DOMAIN 22 29 POLY-GLY.

FT DOMAIN 36 65 PRO-RICH.

FT DOMAIN 59 65 POLY-PRO.

FT DOMAIN 97 104 POLY-GLY.

FT DNA_BIND 244 303 HOMEOBOX.

SO SEQUENCE 333 AA; 34515 MW; DQFLIF917ELFBAD CRC64;

Query Match 24.3%; Score 66; DB 1; Length 333;
Best Local Similarity 38.5%; Pred. No. 1.2; Length 333;
Matches 20; Conservative 9; Mismatches 15; Indels 8; Gaps 3;

OY 8 PHPRTHRLPKEMTPVEPAFAAELISRLKLELSRHSLEERQ 54
Db 227 PSSPRTKLKKKTEKEDKPRFAFAE--QLQRLAEPQANNYITEGRQ 275

RESULT 12

YKLA_BACSU
ID YKLA_BACSU STANDARD: PRT: 141 AA.
AC 034762;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE HYPOTHEMETICAL 14.9 KDA PROTEIN IN PROA-METC INTERGENIC REGION.
GN YKLA.
OS Bacillus subtilis.
CC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16;
RA Devine K.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE OSMC/OHR FAMILY.

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CC EMBL: AJ002571; CAA05593.1; -
DR EMBL: 299110; CAB13171.1; -
DR Subtilist: BG13238; YKLA.
KW Hypothetical protein.
SQ SEQUENCE 141 AA: 14868 MW: 764A32D0619D2233 CRC64:

Query Match 23.2%; Score 63; DB 1; Length 141;
Best Local Similarity 33.3%; Pred. No. 1;
Matches 16; Conservative 11; Mismatches 13; Indels 8; Gaps 2;

OY 5 VSLPFRTHRLPKEMTPVE--PAAFAA-----ELISRLKLEKLE 44
DB 31 VAMPCTPRAKLLEKATNPQLPAAGYACFDSALQIVARTENVKETE 78

RESULT 13
YJX3_YEAST
ID YJX3_YEAST STANDARD: PRT: 539 AA.
AC P47084;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHEMETICAL 62.2 KDA PROTEIN IN MPPI0-SAG1 INTERGENIC REGION.
GN YJR003C OR J1415 OR YJR83.30.
OS Saccharomyces cerevisiae (Baker's Yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RA de Haan M., Smits P.H.M., Grievell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

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CC EMBL: X87611; CAA60924.1; -
DR EMBL: 249503; CAA89525.1; -
DR SCD: S0003763; YJR003C.

KW Hypothetical protein.
SQ SEQUENCE 539 AA: 62214 MW: A20DA32241625B8B CRC64:

Query Match 22.6%; Score 61.5; DB 1; Length 539;
Best Local Similarity 34.3%; Pred. No. 7;
Matches 12; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

OY 8 PHEFRTHRLPKEMTPVEPAFAELISRLKLEK 41
DB 56 PSEDFIRHLLPEDITTDYSLSONVIESLNKLEV 90

RESULT 14
HME1_HUMAN
ID HME1_HUMAN STANDARD: PRT: 391 AA.
AC Q05925;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).
GN EN1.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93185339; PubMed=1363401;
RA Logan C., Hanks M.C., Noble-Topham S., Nallathathan D.,
RA Provart N.J., Joyner A.L.;
RT Cloning and sequence comparison of the mouse, human, and chicken
RT engrailed genes reveal potential functional domains and regulatory
RT regions."
RT Dev. Genet. 13:345-358(1992).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ENGRAILED FAMILY OF HOMEBOX PROTEINS.

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CC EMBL: L12698; AAA53501.1; -
DR EMBL: L12699; AAA53502.1; -
DR HSSP: P02836; 1ENH.
DR TRANSFAC: T02015; -
DR MIM: 131290; -
DR InterPro: IPR000747; -
DR InterPro: IPR001356; -
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00026; ENGRAILED.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR PROSITE: PS00033; ENGRAILED; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT DOMAIN 199 218
FT DOMAIN 224 231
FT DNA_BIND 302 361
FT SEQUENCE 391 AA: 40044 MW: 30DA29BF0995956F CRC64;

Query Match 22.4%; Score 61; DB 1; Length 391;
Best Local Similarity 36.5%; Pred. No. 5.6;
Matches 19; Conservative 9; Mismatches 16; Indels 8; Gaps 3;

OY 8 PHEFRTHRLPKEMTPVEP---AAFAELISRLKLEKLE-SRHSLEERTQ 54
DB 285 PSSPRTKLKKKKNEKEDKRPRTAFTE--QLORLKAERQANRYITTEORRO 333

RESULT 15

TX28_HUMAN STANDARD; PRT; 410 AA.
 ID O15482;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TESTIS-SPECIFIC PROTEIN TEX28.
 CN CXORF2 OR TEX28.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97422617; PubMed=9268643;
 RA Hanna M.C., Platts J.T., Kirkness E.F.;
 RT "Identification of a gene within the tandem array of red and green
 color pigment genes."
 RL Genomics 43:384-386(1997).
 CC -1- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
 CC -1- SIMILARITY: SOME, TO HUMAN KIAA0481.
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 CC -----
 DR EMBL: U93720; AAB71379.1; -
 DR MIM: 300092; -
 SQ SEQUENCE 410 AA; 46131 MW; 8E455A761D52A660 CRC64;

Query Match 21.9%; Score 59.5; DB 1; Length 410;

Best Local Similarity 32.4%; Pred. No. 8.9;

Matches 22; Conservative 9; Mismatches 20; Indels 17; Gaps 2;

QY 2 NGQVSLPFPFTRRLP-----KMTPEVPAFAFAELISRLKLEL-----E 44
 Db 162 DGPVNLPHASRPFLFSFQSLQGTCTLEFDVAQQNLLQKAKALEEAKRHISLQE 221
 QY 45 SRHSLER 52
 Db 222 SYHSLKER 229

Search completed: June 7, 2001, 02:10:31
 Job time: 419 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:09:39 ; Search time 81.06 seconds
(without alignments)
78.081 Million cell updates/sec

Title: US-09-587-574-3

Perfect score: 272
Sequence: 1 ANGVSLPHPRTRHRLPKEM.....RLKIKLELSRHSLSERLQ 54

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.unclassified:*
14: sp.vertebrate:*
15: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	100.0	838	11 070240	070240 rattus norv
2	272	100.0	840	11 088566	088566 mus musculu
3	272	100.0	840	11 090XU6	090XU6 mus musculu
4	268	98.5	843	4 09Y2T1	09Y2T1 homo sapien
5	264	97.1	777	4 09UH84	09UH84 homo sapien
6	157.5	57.9	841	13 042400	042400 gallus gall
7	144	52.9	706	13 09PTP2	09PTP2 xenopus lae
8	142.5	52.4	832	11 070239	070239 rattus norv
9	142.5	52.4	992	11 035625	035625 mus musculu
10	141.5	52.0	900	4 015169	015169 homo sapien
11	136.5	50.2	842	13 09YGY0	09YGY0 xenopus lae
12	68	25.0	2590	13 09W7R4	09W7R4 brachydanio
13	64	23.5	226	2 09RR10	09R10 acinetobact
14	62.5	23.0	251	2 034449	034449 bacillus su
15	62.5	23.0	251	9 064113	064113 bacterioph
16	61.5	22.6	234	5 096565	096565 junonia coe
17	61.5	22.6	234	5 068167	068167 lactococcus
18	60.5	22.2	369	10 081599	081599 tritricum ae
19	60	22.1	377	10 09SC04	09SC04 arabidopsis

20	59.5	21.9	129	8 047954	047954 trypanosoma
21	59.5	21.9	369	10 043379	043379 avena sativ
22	59.5	21.9	442	4 09NZJ2	09NZJ2 homo sapien
23	59.5	21.9	2715	11 09WTS6	09WTS6 mus musculu
24	59.5	21.9	7962	4 010465	010465 homo sapien
25	59.5	21.7	363	2 09ZG07	09ZG07 myxococcus
26	59	21.7	884	4 09UXP6	09UXP6 homo sapien
27	59	21.7	1327	2 09PKX4	09PKX4 streptomyces
28	58.5	21.5	601	2 09PAT1	09PAT1 xylella fas
29	58.5	21.5	883	4 09ULI9	09ULI9 homo sapien
30	58.5	21.5	1061	4 09NOV6	09NOV6 homo sapien
31	58	21.3	259	13 09YGU2	09YGU2 brachydanio
32	58	21.3	1707	5 017652	017652 caenorhabdl
33	57.5	21.1	254	2 067279	067279 aquifex aeo
34	57.5	21.1	978	2 067124	067124 aquifex aeo
35	57.5	21.1	1454	10 09X1I7	09X1I7 arabidopsis
36	57	21.0	156	5 022757	022757 caenorhabdl
37	57	21.0	287	10 09SSL8	09SSL8 caenorhabdl
38	57	21.0	435	5 09V539	09V539 drosophila
39	57	21.0	722	5 09XU77	09XU77 caenorhabdl
40	56.5	20.8	90	14 074750	074750 human immun
41	56.5	20.8	207	10 09M8W6	09M8W6 arabidopsis
42	56.5	20.8	483	2 087270	087270 bartonella
43	56.5	20.8	526	3 09USX7	09USX7 schizosacch
44	56.5	20.8	1100	10 09XIM3	09XIM3 arabidopsis
45	56	20.6	501	3 09UUD0	09UUD0 schizosacch

ALIGNMENTS

RESULT 1
ID 070240 PRELIMINARY; PRT; 838 AA.
AC 070240;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE AXIL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98226558; PubMed=9566905;
RA Yamanoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,
RA Kikuchi A.;
RT "Axil, a member of the Axin family, interacts with both glycogen
RT synthase kinase 3beta and beta-catenin and inhibits axis formation of
RT Xenopus embryos.";
RL MOL. Cell. Biol. 18:2867-2875(1998).
DR EMBL; AF017757; AAC40089.1; -;
DR HSSP; P49799; IAGR.
DR INTERPRO; IPR000342; -;
DR INTERPRO; IPR001158; -;
DR PFM; PF00615; RGS; 1.
DR PFM; PF00778; DIX; 1.
DR PRODOM; PD001580; -; 1.
DR PRODOM; PD003639; -; 1.
SQ SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;

Query Match 100.0%; Score 272; DB 11; Length 838;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANGVSLPHPRTRHRLPKEMTPVPAFAELISRLKIKLELSRHSLSERLQ 54
DB 343 ANGVSLPHPRTRHRLPKEMTPVPAFAELISRLKIKLELSRHSLSERLQ 396
RESULT 2

088566
ID 088566 PRELIMINARY; PRT; 840 AA.
AC 088566;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CONDUCTIN.
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.-A., Wuttele M., Grimm J., Asbrand C., Wirtz R.,
Kuhl M., Medlich D., Birchmeier W.,
RT "Functional interaction of an axin homolog, conductin, with beta-
catenin, APC, and GSK3beta."
RL Science 280:596-599(1998).
DR EMBL: AF073788; AAC26047.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1270862; Axin2.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SQ SEQUENCE 840 AA; 92934 MW; A07D5FEB25DE7277 CRC64;

Query Match 100.0%; Score 272; DB 11; Length 840;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPFTRHLPKEMTPVEPAFAELISRLKLELSRHSLSERRIQ 54
Db 343 ANGOVSLPFPFTRHLPKEMTPVEPAFAELISRLKLELSRHSLSERRIQ 396
|||||
RESULT 3
ID 090XJ6 PRELIMINARY; PRT; 840 AA.
AC 090XJ6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN2.
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF205889; AAF22800.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPTOTEN.
SQ SEQUENCE 840 AA; 92896 MW; 767D546B43C921C5 CRC64;

Query Match 100.0%; Score 272; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPFTRHLPKEMTPVEPAFAELISRLKLELSRHSLSERRIQ 54
Db 343 ANGOVSLPFPFTRHLPKEMTPVEPAFAELISRLKLELSRHSLSERRIQ 396
|||||
RESULT 4
ID 09Y2T1 PRELIMINARY; PRT; 843 AA.
AC 09Y2T1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CONDUCTIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.,
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24."
RL Genomics 55:341-344(1999).
DR EMBL: AF078165; AAD20976.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A464D CRC64;

Query Match 98.5%; Score 268; DB 4; Length 843;
Best Local Similarity 98.1%; Pred. No. 8.6e-23;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANGOVSLPFPFTRHLPKEMTPVEPAFAELISRLKLELSRHSLSERRIQ 54
Db 343 ANGOVSLPFPFTRHLPKEMTPVEPAFAELISRLKLELSRHSLSERRIQ 396
|||||
RESULT 5
ID 09UH84 PRELIMINARY; PRT; 777 AA.
AC 09UH84;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE AXIN2.
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, LYMPHOBLAST.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF205888; AAF22799.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.

DR PRINTS: PRO1301: RGSPROTEIN.
SO SEQUENCE 777 AA: 86857 MW: 3A4943ABF430BBD3 CRC64:

Query Match 97.1%; Score 264; DB 4; Length 777;
Best Local Similarity 96.3%; Pred. No. 2,3e-22;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANGOVSLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 54
DB 342 ANGRVPLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 395

RESULT 6
ID 042400 PRELIMINARY; PRT: 841 AA.
AC 042400;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE AXIN.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

NCBI_TaxID=9031;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=97373830; PubMed=9230313;
Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
Rii Lee J.J., Tligman S.M., Gumbiner B.M., Costantini F.,
The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation."

RL Cell 90:181-192(1997).
DR EMBL: AF009012; AAC60245.1; -
DR HSSP: P49799; IAGR.

DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFM: PF00778; DIX; 1.
DR PFM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.

DR SEQUENCE 841 AA: 94931 MW: 4000DC90E72506FE CRC64;
SQ

Query Match 57.9%; Score 157.5; DB 13; Length 841;
Best Local Similarity 59.3%; Pred. No. 4,8e-10;
Matches 32; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

OY 1 ANGOVSLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 54
DB 362 ANGRVPLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 414

RESULT 7
ID 09PTP2 PRELIMINARY; PRT: 706 AA.
AC 09PTP2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE AXIN-RELATED PROTEIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodidae; Xenopus.

NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Itoh K., Antipova A., Ratcliffe M., Sokol S.;
RT "Dishevelled transduces a signal by displacing GSK3 from axin-GSK3

RT complex."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF140243; AA022574.1; -
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFM: PF00778; DIX; 1.
DR PRINTS: PRO1301: RGSPROTEIN.
SO SEQUENCE 706 AA: 79196 MW: C3D0AF0D9540F162 CRC64:

Query Match 52.9%; Score 144; DB 13; Length 706;
Best Local Similarity 55.6%; Pred. No. 1,5e-08;
Matches 30; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANGOVSLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 54
DB 303 ANGRVPLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 356

RESULT 8
ID 070239 PRELIMINARY; PRT: 832 AA.
AC 070239;

DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;

SEQUENCE FROM N.A.
MEDLINE=96151361; PubMed=9482734;
Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
"Axin, a negative regulator of the Wnt signaling pathway, forms a
complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
dependent phosphorylation of beta-catenin."

RL EMBL: AF017756; AAC40066.1; -
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFM: PF00778; DIX; 1.
DR PFM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.

DR SEQUENCE 832 AA: 92856 MW: B489504C7E594347 CRC64;
SQ

Query Match 52.4%; Score 142.5; DB 11; Length 832;
Best Local Similarity 55.6%; Pred. No. 2,6e-08;
Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 2 NGOVSLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 54
DB 368 NGRVPLPHFPRTTHRLPKEMTPVEPAFAAELISRLKLESLRHSLEERLQ 419

RESULT 9
ID 035625 PRELIMINARY; PRT: 992 AA.
AC 035625;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE AXIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

NCBI_TaxID=10090;
RN [1]

RP	SEQUENCE FROM N.A.
RX	MEDLINE=97373830; PubMed=9230313;
RA	Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
RA	Iii Lee J.J., Tilgman S.M., Gumbiner B.M., Costantini F.;
RT	"The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT	pathway that regulates embryonic axis formation.";
RL	Cell 90:181-192(1997).
DR	EMBL; AF009011; AAC53285.1; -
DR	HSSP; A49799; IAGR.
DR	MGI; MGI:1096327; Axln.
DR	INTERPRO; IPRO00342; -
DR	INTERPRO; IPRO01158; -
DR	PFAM; PF00615; RGS: 1.
DR	PEAM; PF00778; DIX: 1.
DR	PRINTS; PRO1301; RGSPROTEIN.
FT	NON_TER
SQ	SEQUENCE 992 AA; 109917 MW; 70EEB5D387BD26F CRC64;
OY	Query Match 52.4%; Score 142.5; DB 11; Length 992; Best Local Similarity 56.6%; Pred. No.3.le-08; Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
Dn	2 NGVSLPHPTHRRLPKEMTPVEPAFAAEIISRLKLEIESRHSLEERLQ 54 : : : Db 492 NGRVPLPIPRITRYMPKEIR-VEPQKFAELIHRLNAVQRTRAEAKLERLK 543
RESULT 10	
ID	015169 PRELIMINARY; PRT; 900 AA.
AC	015169;
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	AXIN (FRAGMENT).
CN	AXIN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97373830; PubMed=9230313;
RA	Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
RA	Iii Lee J.J., Tilgman S.M., Gumbiner B.M., Costantini F.;
RT	"The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT	pathway that regulates embryonic axis formation.";
RL	Cell 90:181-192(1997).
DR	EMBL; AF009674; AAC51624.1; -
DR	HSSP; A49799; IAGR.
DR	INTERPRO; IPRO00342; -
DR	INTERPRO; IPRO01158; -
DR	PFAM; PF00615; RGS: 1.
DR	PEAM; PF00778; DIX: 1.
DR	PRINTS; PRO1301; RGSPROTEIN.
FT	NON_TER
SQ	SEQUENCE 900 AA; 99803 MW; EE5F990B11FC7B3B CRC64;
OY	Query Match 52.0%; Score 141.5; DB 4; Length 900; Best Local Similarity 56.6%; Pred. No.3.6e-08; Matches 30; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
Dn	2 NGVSLPHPTHRRLPKEMTPVEPAFAAEIISRLKLEIESRHSLEERLQ 54 : : : Db 400 NGRVPLPIPRITRYMPKEIR-VEPQKFAELIHRLNAVQRTRAEAKLERLK 451
RESULT 11	
ID	09YGYO PRELIMINARY; PRT; 842 AA.
AC	09YGYO;

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DE AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; Pubmed=10072781;
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
   expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).
DR EMBL; AF097313; AAC71036.1; -.
DR HSSP; P49799; IAGR.
DR INTERPRO; IPR003442; -.
DR INTERPRO; IPR001158; -.
DR PFAM; PF00615; RGS; 1.
DR PFAM; PF00778; DIX; 1.
DR PRODOM; PD001580; -. 1.
DR PRODOM; PD003639; -. 1.
SQ SEQUENCE 842 AA; 94459 MW; BDAl52734C97191E CRC64;

OY 1 ANGVSLPHPRTRHLRPEKMTVPEPAFAFAELISRLKLTLESHLSLEERLQ 54
   |||:|||||:||||:|:| |||||||:|:|:|||||
Db 362 ANGRSPLPHPRTRHMPKDT-HVDEKFAAELISRLKGLVDRDRAEQKLERLK 414

RESULT 12
O9W7R4 PRELIMINARY; PRT; 2590 AA.
AC Q9W7R4;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TEN-M3.
DE TEN-M3.
GN TEN-M3.
OS Brachydonto reio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasboridae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Mieda M., Kikuchi Y., Hirate Y., Aoki M., Okamoto H.;
RT "Compartmentalized expression of zebrafish ten-m3 and ten-m4,
   homologues of the Drosophila tenm /odd Oz gene, in the central nervous
   system.";
RL Mech. Dev. 0:0-0(1999).
DR EMBL; AB026979; BAA81892.1; -.
DR HSSP; P02468; IKLO.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR002049; -.
DR PFAM; PF00008; EGF; 5.
DR PRINTS; PRO0011; EGFAMININ.
DR PROSITE; PS00022; EGF_1; UNKNOWN_8.
DR PROSITE; PS01186; EGF_2; 7.
SQ SEQUENCE 2590 AA; 288587 MW; 597592866219148D CRC64;

Query Match 25.0%; Score 68; DB 13; Length 2590;
Best Local Similarity 31.0%; Pred. No. 33;
Matches 22; Conservative 6; Mismatches 19; Indels 24; Gaps 2.
3 GOVSLPHPRTRHLRPEKMT-----VPEPAFAFAELISRLKLTLE----- 42

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DB 76 GGGTLPVPPPHNQPSVVALNHNLSRRNVPAPPALPALPQLTPPSVPLQDSWVLG 135
OY 43 -----LESRHS 49
DB 136 SNVPLESRHFL 146

RESULT 13
OY 09RB10 PRELIMINARY; PRT; 226 AA.
AC 09RB10;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PUTATIVE 2-COMPONENT REGULATORY PROTEIN.
OS Acinetobacter sp. ADP1.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OX Acinetobacter.
RN NCBI_Taxid=62977;
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RA Jones R.M., Collier L.S., Neidie E.L., Williams P.A.;
RT "arabC genes determine the catabolism of aryl esters in Acinetobacter
sp. strain ADP1."
RL J. Bacteriol. 181:4568-4575(1999).
DR EMBL; AF150928; AAF04314.1; -.
DR HSSP; P08402; 1B00.
DR INTERPRO: IPR001789; -.
DR PFAM; PF00072; response_reg.1.
DR PFAM; PF00486; trans_reg_C.1.
SQ SEQUENCE 226 AA: 26423 MW: B3C1E64105C74DB CRC64;

Query Match 23.5%; Score 64; DB 2; Length 226;
Best Local Similarity 31.4%; Pred. No. 7.6;
Matches 16; Conservative 11; Mismatches 22; Indels 2; Gaps 1;

OY 3 GOVSLPHFPRTHR---LPKEMTPVEPAFAFAELISRLKLESLERHSLEERT 53
DB 135 GOVOL--PNTNRLILKDGOPINLSTKEWSTLEPMMVMMYPMQIFSKMLEERT 183

RESULT 14
OY 034449 PRELIMINARY; PRT; 251 AA.
AC 034449;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE YOOD. PROTEIN.
GN YOOD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OX Bacillus/Staphylococcus group; Bacillus.
RN NCBI_Taxid=1423;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA MEDLINE-98044033; PubMed-9384377;
RA Kunze F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchart S.,
RA Borries R., Bourcier L., Brans A., Braun M., Bignelli S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Ertlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallion N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Hatach J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

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RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koertter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigne C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetlelle D., Portolillo S., Prescott A.M.,
RA Presacan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Serio S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsita P., Toognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler E., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
subtilis."
RL Nature 390:249-256(1997).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunze F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z89114; CAB13959.1; -.
DR EMBL; Z89115; CAB13985.1; -.
SQ SEQUENCE 251 AA: 28593 MW: BE79F500A3A0E3C8 CRC64;

Query Match 23.0%; Score 62.5; DB 2; Length 251;
Best Local Similarity 32.1%; Pred. No. 13;
Matches 17; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

OY 1 ANGVSLPHFPRTHR---LPKEMTPVEPAFAFAELISRLKLESLERHS 49
DB 62 AIGR-SLKHHILRKGDWANKMTGAKGVLFPAQVYSKREEMKALKARPSL 113

RESULT 15
OY 064113 PRELIMINARY; PRT; 251 AA.
AC 064113;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE PUTATIVE ANTIREPRESSOR.
GN YOOD.
OS Bacteriophage SPBc2.
OC viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
OX NCBI_Taxid=66797;
RN (1)
RP SEQUENCE FROM N.A.
RA Lazarevic V., Dusterhoft A., Soldo B., Hilbert H., Mauel C.,
RA Karamata D.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020713; AAC13073.1; -.
SQ SEQUENCE 251 AA: 28593 MW: BE79F500A3A0E3C8 CRC64;

Query Match 23.0%; Score 62.5; DB 9; Length 251;
Best Local Similarity 32.1%; Pred. No. 13;
Matches 17; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

OY 1 ANGVSLPHFPRTHR---LPKEMTPVEPAFAFAELISRLKLESLERHS 49
DB 62 AIGR-SLKHHILRKGDWANKMTGAKGVLFPAQVYSKREEMKALKARPSL 113

```

Search completed: June 7, 2001, 02:09:41
 Job time: 444 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:01:17 ; Search time 80.96 Seconds
(without alignments)
48.719 Million cell updates/sec

Title: US-09-587-574-4
Perfect score: 360
Sequence: 1 QHEDDEKEGSEQALSSRDG.....VLKTPCGQSPGVGRSPSR 69

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq-0401:*

1:	/SID52/gcgdata/geneseq/geneseq/AA1980.DAT:*
2:	/SID52/gcgdata/geneseq/geneseq/AA1981.DAT:*
3:	/SID52/gcgdata/geneseq/geneseq/AA1982.DAT:*
4:	/SID52/gcgdata/geneseq/geneseq/AA1983.DAT:*
5:	/SID52/gcgdata/geneseq/geneseq/AA1984.DAT:*
6:	/SID52/gcgdata/geneseq/geneseq/AA1985.DAT:*
7:	/SID52/gcgdata/geneseq/geneseq/AA1986.DAT:*
8:	/SID52/gcgdata/geneseq/geneseq/AA1987.DAT:*
9:	/SID52/gcgdata/geneseq/geneseq/AA1988.DAT:*
10:	/SID52/gcgdata/geneseq/geneseq/AA1989.DAT:*
11:	/SID52/gcgdata/geneseq/geneseq/AA1990.DAT:*
12:	/SID52/gcgdata/geneseq/geneseq/AA1991.DAT:*
13:	/SID52/gcgdata/geneseq/geneseq/AA1992.DAT:*
14:	/SID52/gcgdata/geneseq/geneseq/AA1993.DAT:*
15:	/SID52/gcgdata/geneseq/geneseq/AA1994.DAT:*
16:	/SID52/gcgdata/geneseq/geneseq/AA1995.DAT:*
17:	/SID52/gcgdata/geneseq/geneseq/AA1996.DAT:*
18:	/SID52/gcgdata/geneseq/geneseq/AA1997.DAT:*
19:	/SID52/gcgdata/geneseq/geneseq/AA1998.DAT:*
20:	/SID52/gcgdata/geneseq/geneseq/AA1999.DAT:*
21:	/SID52/gcgdata/geneseq/geneseq/AA2000.DAT:*
22:	/SID52/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	100.0	840	20	W93570 Human conductin pr
2	360	100.0	840	20	W93569 Human conductin pr
3	139.5	38.8	992	20	W96265 Murine axlin. Mus
4	113.5	31.5	900	20	W96264 Human axlin. Homo
5	68.5	19.0	441	14	R41875 Steroid hormone re
6	68.5	19.0	441	17	R89214 Peroxisome prolif
7	68.5	19.0	441	20	Y05472 Human PPAR-delta p
8	68.5	19.0	1132	16	R77417 Human cell cycle p
9	68.5	19.0	397	19	W29659 Homo sapiens BP202
10	63.5	17.6	382	19	W44865 Human TPC3 telomer
11	63.5	17.6	434	20	W73959 Human TPC3 protein

12	63.5	17.6	605	21	Y57950 Human transmembran
13	62.5	17.4	1042	21	B11732 Cryptosporidium pa
14	62.5	17.4	1837	21	B11726 Cryptosporidium pa
15	62	17.2	303	21	G59725 Arabidopsis thalia
16	62	17.2	348	17	W01437 Murine cyclin-depe
17	62	17.2	375	21	G59724 Arabidopsis thalia
18	62	17.2	390	21	G59723 Arabidopsis thalia
19	61.5	17.1	144	21	G27248 Zee mays protein f
20	61.5	17.1	172	21	G21146 Zee mays protein f
21	61.5	17.1	917	21	Y53920 Human Bcl-2 associ
22	61	16.9	95	20	Y76563 Human ovarian tumo
23	61	16.9	138	21	G10503 Arabidopsis thalia
24	61	16.9	202	21	G10502 Arabidopsis thalia
25	61	16.9	204	21	G10501 Arabidopsis thalia
26	61	16.9	1490	22	B65644 Novel protein kina
27	60.5	16.8	474	20	Y40494 T. pallidum yael p
28	59.5	16.5	181	21	G33818 Arabidopsis thalia
29	59.5	16.5	186	21	G33817 Arabidopsis thalia
30	59.5	16.5	192	21	G33816 Arabidopsis thalia
31	59.5	16.5	216	21	G24174 Arabidopsis thalia
32	59.5	16.5	221	21	G24173 Arabidopsis thalia
33	59	16.4	700	12	R11354 Cellular Receptor
34	59	16.4	1498	16	R77085 Hamster sulphonylu
35	59	16.4	1582	16	R77088 Hamster sulphonylu
36	58	16.1	214	21	Y93216 Amino acid sequenc
37	58	16.1	567	16	R71700 Spleen necrosis vi
38	58	16.1	1498	16	R77084 Rat sulphonylurea
39	58	16.1	1582	16	R77087 Rat sulphonylurea
40	57.5	16.0	104	21	G40674 Zee mays protein f
41	57.5	16.0	104	21	G40680 Zee mays protein f
42	57.5	16.0	105	21	G12626 Zee mays protein f
43	57.5	16.0	129	21	G12625 Zee mays protein f
44	57.5	16.0	129	21	G40672 Zee mays protein f
45	57.5	16.0	138	21	Y79574 Human calpain 10n.

ALIGNMENTS

RESULT 1					
ID W93570 standard; Protein: 840 AA.					
XX	W93570;				
XX	17-JUN-1999 (first entry)				
XX	Human conductin protein.				
DE	Human conductin protein.				
XX	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;				
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;				
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;				
KW	tumour suppressor.				
XX					
OS	Homo sapiens.				
XX					
PN	W09911780-A2.				
XX					
PD	11-MAR-1999.				
XX					
PF	01-SEP-1998; 98MO-DE02621.				
XX					
PR	02-SEP-1997; 97DE-1038205.				
XX					
PA	(DELB-) DELBRUECK CENT MOLECULAR MEDIZIN MAX.				
XX					
PI	Behrens J, Birchmeier W;				
XX					
DR	WPI; 1999-214706/18.				
XX					
DR	N-PSDB; X23370.				
XX					
PT	Tumor-suppressing protein conductin - used for treatment and				
PT	diagnosis of tumors				

XX Claim 11; Fig 3; 22pp; German.
PS
XX This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
CC
XX Sequence 840 AA:
SQ
Query Match 100.0%; Score 360; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 2.9e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QIREDEKEGSEQALSRDGAPOHPLALPSSGYEDPQTITLDDHLSRVLTGCGSPG 60
DB 397 qiredeekesqalsrdgapvqphlallpsgsyedpqtllldhlsrvlktgpcgspg 456
OY 61 VGRYSPRSR 69
DB 457 vgrysprsr 465
RESULT 2
W93569
ID W93569 standard; Protein; 840 AA.
XX
AC W93569;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human conductin protein.
XX
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW tumour suppressor.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FT Key 78..200
FT Domain /note= "Regulator of G protein signalling domain as
FT Binding-site 343..396 described in claim 12"
FT Binding-site /note= "GSK 3-beta binding region as described in
FT Binding-site 397..465 claim 13"
FT Binding-site /note= "Beta-catenin binding domain as described in
FT Region 783..833 claim 14"
FT /note= "Dishevelled homology region as described in
FT claim 15"
XX
XX W09911780-A2.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-DE02621.
XX
XX 02-SEP-1997; 97DE-1038205.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX Behrens J, Birchmeier W;
XX WPI: 1999-214706/18.
XX
XX N-PSDB: X23369.
XX

XX Tumor-suppressing protein conductin - used for treatment and
PT diagnosis of tumors
PS
XX Claim 11; Fig 1; 22pp; German.
XX
XX This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
CC
XX Sequence 840 AA:
SQ
Query Match 100.0%; Score 360; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 2.9e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QIREDEKEGSEQALSRDGAPOHPLALPSSGYEDPQTITLDDHLSRVLTGCGSPG 60
DB 397 qiredeekesqalsrdgapvqphlallpsgsyedpqtllldhlsrvlktgpcgspg 456
OY 61 VGRYSPRSR 69
DB 457 vgrysprsr 465
RESULT 3
W96265
ID W96265 standard; Protein; 992 AA.
XX
AC W96265;
XX
DT 14-JUN-1999 (first entry)
XX
DE Murine axin.
XX
KW Axin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW beta-catenin.
XX
OS Mus musculus.
XX
XX Mus musculus.
XX W09902179-A1.
XX
XX 21-JAN-1999.
XX
XX 09-JUL-1998; 98WO-US14414.
XX
XX 10-JUL-1997; 97US-0890865.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Constantini F, Zeng L;
XX WPI: 1999-120510/10.
XX N-PSDB: X09013.
XX
XX Newly isolated nucleic acid encoding "axis inhibition" protein
XX (Axin) - useful for detecting, diagnosing and treating cancer
XX
XX Claim 8; Figure 8; 95pp; English.
XX
XX Nucleic acids encoding mutant and wild type Axin and
XX oligonucleotides derived from them are useful for detecting
XX mutations in the axin gene and for determining whether a subject is
XX likely to develop cancer (including breast, colorectal,
XX gastrointestinal, esophageal, carcinomas or melanomas). The wild
XX

CC type Axin and homologues of Axin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions
 CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axin acts through
 CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
 XX
 SQ Sequence 992 AA:

Query Match 38.8%; Score 139.5; DB 20; Length 992;
 Best Local Similarity 35.3%; Pred. No. 2,4e-08;
 Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIRDEDEKESQALSSRDGAPVQHPLALPS-----GSYEEDPQTIL 43
 Db 544 ryrmeeegedgemp-----sgymashkliprvpawhfprryvdmgscglrdahempesll 599
 OY 44 DDLHSRLVLTGCGSPGVGRYSPRS 68
 Db 600 dehvgrvmrtgpcgspgphrpsds 624

RESULT 4
 W96264
 W96264 standard; Protein: 900 AA.

AC W96264;
 DT 14-JUN-1999 (first entry)

XX Human axin.

XX Axin: cancer; breast cancer; colorectal cancer;
 KM gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KM diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin.

XX Homo sapiens.

XX W09902179-A1.

XX 21-JAN-1999.

XX 09-JUL-1998; 98WO-US14414.

XX 10-JUL-1997; 97US-0890865.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Constantini F, Zeng L;

XX WPI: 1999-120510/10.

XX N-PSDB; X09012.

XX Newly isolated nucleic acid encoding "axis inhibition" protein
 PT (Axin) - useful for detecting, diagnosing and treating cancer

XX Disclosure: Figure 11; 95pp; English.

XX Nucleic acids encoding mutant and wild type Axin and
 CC oligonucleotides derived from them are useful for detecting
 CC mutations in the axin gene and for determining whether a subject is
 CC likely to develop cancer (including breast, colorectal,
 CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
 CC type Axin and homologues of Axin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions

CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axin acts through
 CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
 XX
 SQ Sequence 900 AA:

Query Match 31.5%; Score 113.5; DB 20; Length 900;
 Best Local Similarity 34.4%; Pred. No. 3.1e-05;
 Matches 33; Conservative 10; Mismatches 22; Indels 31; Gaps 3;

OY 3 REDEEK-----ESQALSSRDGAPVQHPLALPS----- 32
 Db 440 reeeekleerlkvrmeeeegedgdpssgppgc-hklppapawhfprrlcwtacaglr 498
 OY 33 GSYEDDPQTILDDLHSRLVLTGCGSPGVGRYSPRS 68
 Db 499 dahempeslldehvgrvrlrttgrrgspgphrpsds 534

RESULT 5
 R41875
 ID R41875 standard; Protein: 441 AA.

XX R41875;

XX 13-APR-1994 (first entry)

XX Steroid hormone receptor (NUC1).

XX Steroid; hormone; receptor; osteosarcoma; superfamily.

XX Homo sapiens.

XX GB2265376-A.

XX 29-SEP-1993.

XX 23-MAR-1993; 93GB-0006043.

XX 24-MAR-1992; 92US-0857055.

XX (MERI) MERCK & CO INC.

XX Rodan GA, Rutledge SJ, Schmidt A, Vogel RJ;

XX WPI: 1993-305586/39.

XX N-PDSB; Q48939.

XX New human steroid hormone receptor NUC1 - used to assay and
 PT evaluate ligands binding to the receptor

XX Claim 5; Page 39-40; 62pp; English.

XX The steroid hormone receptor (designated NUC1) is used in assays to
 CC identify and evaluate chemical entities that bind to it.

XX Sequence 441 AA:

Query Match 19.0%; Score 68.5; DB 14; Length 441;
 Best Local Similarity 30.3%; Pred. No. 3.8;
 Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIRDEDEKESQALSSRDGAPVQH--PLALPSGYEE-----DPQTILDDLHSRLVLT 53
 Db 10 evreeekkeevaa-----egapelnsgpqhlpssytdlstrsspslldq-----1q 59

OY 54 PGCQSPGVGRYSPRSR 69
 Db 60 mcdgagascgslnmecr 75

```
RESULT 6
R89214
ID R89214 standard; Protein; 441 AA.
XX
AC R89214;
XX
DT 03-APR-1996 (first entry)
XX
DE Peroxisome proliferator activated receptor hNUC1B.
XX
KM hNUC1B; peroxisome proliferator activated receptor; hyperlipidemia;
KW hypercholesterolemia; hyperlipoproteinemia.
XX
OS Homo sapiens.
XX
PN M09601430-A2.
XX
PD 18-JAN-1996.
XX
PF 29-JUN-1995; 95MO-US08328.
XX
PR 01-JUL-1994; 94US-0270635.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Mukherjee R;
XX
DR WPI: 1996-087756/09.
DR N-PSDB; T10583.
XX
PT Screening methods for identifying NUC protein inhibitors - for use
PT as potential agents for the treatment of hyperlipidemia,
PT hypercholesterolemia and hyperlipoproteinemia
XX
PS Claim 44; Page 29-31; 45pp; English.
XX
CC A novel human peroxisome proliferator activated receptor (PPAR),
CC designated hNUC1B (R89214), is expressed from a cDNA clone (T10583)
CC isolated from a human kidney cDNA library. hNUC1B is a member of
CC the PPAR family and can be used to screen NUC protein inhibitors.
XX
SQ Sequence 441 AA;

Query Match 19.0%; Score 68.5; DB 17; Length 441;
Best Local Similarity 30.3%; Pred. No. 3.8;
Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIREDEKEGSEQALSSRDGAPVQH--PLALLPSGSYE-----DPQITLDDHLSRVLKT 53
DB 10 evreeeekveavae---egapelngpqpahlpsssyldlrrssppslldq-----1q 59
OY 54 PGQSPGVGRYSPRSR 69
DB 60 mgcdgascgslnmeqr 75

RESULT 7
Y05472
ID Y05472 standard; Protein; 441 AA.
XX
AC Y05472;
XX
DT 07-JUL-1999 (first entry)
XX
DE Human PPAR-delta protein sequence.
XX
KM Nuclear receptor agonist; antagonist; identification; PPAR;
KW peroxisome proliferator activated receptor.
XX
OS Homo sapiens.
XX
```

```
PN M09918124-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98MO-US21049.
XX
PR 07-OCT-1997; 97US-0061385.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Cummings RT, Hermes JD, Moller DE, Zhou G;
XX
DR WPI: 1999-263998/22.
DR N-PSDB; X36523.
XX
PT Identifying nuclear receptor agonists and antagonists
XX
PS Disclosure; Fig 10a; 60pp; English.
XX
CC This sequence is the human peroxisome proliferator activated
CC receptor delta (PPAR-delta).
CC The invention relates to a method for identifying nuclear receptor
CC agonists and antagonists comprises measuring fluorescent resonance energy
CC transfer between fluorescent-labelled nuclear receptors and
CC co-activators. The method can be used for identifying agonists and
CC antagonist of nuclear receptors.
XX
SQ Sequence 441 AA;

Query Match 19.0%; Score 68.5; DB 20; Length 441;
Best Local Similarity 30.3%; Pred. No. 3.8;
Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIREDEKEGSEQALSSRDGAPVQH--PLALLPSGSYE-----DPQITLDDHLSRVLKT 53
DB 10 evreeeekveavae---egapelngpqpahlpsssyldlrrssppslldq-----1q 59
OY 54 PGQSPGVGRYSPRSR 69
DB 60 mgcdgascgslnmeqr 75

RESULT 8
R77417
ID R77417 standard; Protein; 1132 AA.
XX
AC R77417;
XX
DT 08-AUG-1996 (first entry)
XX
DE Human cell cycle protein min1.
XX
KM Human; MIN1; cell cycle; G2/M border; progression; cdc2 kinase; yeast;
KW functional complementation; weel; mik1; mutant; cancer; development;
KW antimitotic factor; mitosis.
XX
OS Homo sapiens.
XX
PN JF07274971-A.
XX
PD 24-OCT-1995.
XX
PF 05-APR-1994; 94JP-0093033.
XX
PR 05-APR-1994; 94JP-0093033.
XX
PA (SHKJ ) SHINGIJUTSU JIGYODAN.
XX
KM WPI: 1995-399339/51.
DR N-PSDB; T05406.
XX
PT Human derived cell cycle gene encoding an anti-mitotic factor - used
```


Pr In the control of the G2/M phase of the cell cycle.

XX Claim 1: Page 4; 5pp: Japanese.

CC This is the amino acid sequence of the human MINI gene product. The
CC protein has a mol. wt. about 129 kD. The gene is expressed at the G2/M
CC border of the cell cycle and can inactivate the cell cycle progression
CC protein cdc2 kinase. The gene was isolated by functional complementation
CC of a yeast weel/mik1 mutant strain. The gene and protein can be used in
CC the determination of cancer cell development and as an antimitotic
CC factor.

XX Sequence 1132 AA;

Query Match 19.0%; Score 68.5; DB 16; Length 1132;

Best Local Similarity 31.5%; Pred. No. 12;

Matches 23; Conservative 9; Mismatches 26; Indels 15; Gaps 3;

OY 1 QIREDEKESQALSSRDGAPVQHPLALPSGSEEDPQTILDDH-----LSRV 50

Db 976 qtleqlpkdhdhdfst---tpiqhqrlllpsfqgseddddlipmdknpptpsvlfpl 1032

OY 51 LKTPGCO--SPGV 61

Db 1033 vktpqghvpsgm 1045

RESULT 9

W29659 W29659 standard; Protein; 397 AA.

XX W29659;

DT 18-FEB-1999 (first entry)

DE Homo sapiens BP202_3 clone secreted protein.

XX secreted protein; BP202_3.

XX Homo sapiens.

PN W09830695-A2.

PD 16-JUL-1998.

PF 09-JAN-1998; 98WO-US00543.

PR 08-JAN-1998; 98US-0004684.

PR 09-JAN-1997; 97US-0780814.

PA (GENY) GENETICS INST INC.

PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;

PI Racie LA, Spaulding V, Treacy M;

DR WPI: 1998-413686/35.

DR N-PSDB: V40520.

PT New isolated nucleic acids and secreted proteins - obtained from
PT human adult ovary, human foetal kidney, human foetal brain and human
PT adult brain cDNA libraries

PS Disclosure: Page 67-68; 113pp; English.

XX The sequence is that of a novel, isolated secreted protein.

XX Sequence 397 AA;

Query Match 18.9%; Score 68; DB 19; Length 397;

Best Local Similarity 32.9%; Pred. No. 3.9;

Matches 25; Conservative 10; Mismatches 23; Indels 18; Gaps 4;

OY 1 QIREDE---KESQALSSRDGAPVQHPLALPSGSEEDPQTILDDH-----L 47

Db 238 gmrefleqlpkdhdhdfst---tpiqhqrlllpsfqgseddddlipmdknpptpsvlfpl 294

OY 48 SRVLKTPGCO--SPGV 61

Db 295 flvktpqghvpsgm 310

RESULT 10

W44865 W44865 standard; Protein; 382 AA.

XX W44865;

DT 28-AUG-1998 (first entry)

DE Human TPC3 telomere length and telomerase regulatory protein.

KW TPC3; telomere length; telomerase; human; cancer; gene therapy;

KW diagnosis; vaccine.

XX Homo sapiens.

PN W09811204-A1.

PD 19-MAR-1998.

PF 13-SEP-1996; 96WO-US14679.

PR 13-SEP-1996; 96WO-US14679.

PA (GERO-) GERON CORP.

PI Adams RR, Andrews WH, Feng J, Villeponteau B;

DR WPI: 1998-207373/18.

DR N-PSDB: V19480.

PT Human TPC2, TPC3 and TR genes - regulate telomere length or modulate

PT telomerase activity

PS Disclosure: Fig 6A-C; 86pp; English.

XX This polypeptide comprises human TPC3, a protein that regulates

CC telomere length or modulates telomerase activity. Its amino acid

CC sequence was deduced from a cDNA clone (see V19480) obtained from a

CC human 293 cell library. TPC3 and TPC2 (see W44864) proteins can be

CC obtained by purification from natural sources, by in vitro

CC synthesis or by purification from recombinant host cells. They

CC have application in methods for reconstituting in vitro telomerase

CC or other enzymatic activities that maintain telomeres and regulate

CC telomere length. These methods have application in screens for

CC therapeutic agents, and for diagnostic tests. In addition,

CC peptides corresponding to TPC2 or TPC3 proteins can also be used to

CC regulate telomere length and telomerase activity in mammalian

CC cells. Immunogenic peptides and proteins of the invention can also

CC be used in therapeutic immunisation and vaccination procedures.

CC Antibodies that specifically bind to TPC2 or TPC3 proteins can

CC be used in screening, diagnosing and monitoring diseases and other

CC conditions, such as cancer, pregnancy or fertility.

XX Sequence 382 AA;

Query Match 17.6%; Score 63.5; DB 19; Length 382;

Best Local Similarity 35.0%; Pred. No. 13;

Matches 21; Conservative 9; Mismatches 17; Indels 13; Gaps 4;

OY 11 SEQALSSRDGAPVQHPLALPSGSEEDPQTILDDHLSRVLKTPGCO--SPGV 68

Db 184 seq--sasesapddqp-----dreedpraged--pkexspgadskglygckrgspka 232

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RESULT 11
W73959
ID W73959 standard; Protein; 434 AA.
XX
XX AC W73959;
XX
XX DT 29-APR-1999 (first entry)
XX
XX DE Human TPC3 protein.
XX
XX TPC2; TPC3; human; telomere length regulation; cancer; pregnancy;
XX fertility; diagnosis; therapy.
XX
XX OS Homo sapiens.
XX
XX PN US5858777-A.
XX
XX PD 12-JAN-1999.
XX
XX PF 13-SEP-1996; 96US-0710249.
XX
XX PR 08-SEP-1995; 95US-0003492.
XX 05-JAN-1996; 96US-0583808.
XX 13-SEP-1996; 96US-0710249.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Adams RR, Andrews WH, Feng J, Villeponteau B;
XX
XX DR WPI: 1999-152104/13.
XX
XX DR N-PSDB: X01534.
XX
XX PT DNA encoding proteins TPC2 and TPC3 - useful for regulating telomere
XX length or modulating telomerase activity
XX
XX PS Disclosure; Fig 6; 59pp; English.
XX
XX CC This sequence is the human TPC3 protein, which is contained within
XX the recombinant mammalian host cell of the invention. The invention
XX provides methods and reagents for regulating telomere length and
XX modulating telomerase activity in mammalian cells as well as for
XX detecting, diagnosing, and treating related diseases and conditions such
XX as cancer, pregnancy, or fertility in humans and other mammals.
XX
XX SQ Sequence 434 AA;

Query Match 17.6%; Score 63.5; DB 20; Length 434;
Best Local Similarity 35.0%; Pred. No. 15;
Matches 21; Conservative 9; Mismatches 17; Indels 13; Gaps 4;

OY 11 SEQALSSRDGAPVQHPLALPSSGYEDDPQTILDHLSRYLKTGPCQSPGVG--RYSPRS 68
    ||| | : | | | | | | | | | | | | | | | | | | | | | | | | | |
    ||| | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 236 seq--sasesapedgp-----dreedpragaed--pkaekspgadsdkygcrtgspka 284

RESULT 12
Y57950
ID Y57950 standard; Protein; 605 AA.
XX
XX AC Y57950;
XX
XX DT 23-MAR-2000 (first entry)
XX
XX DE Human transmembrane protein HTPMN-74.
XX
XX KW Human; transmembrane protein; HTPMN; diagnosis; immunospecific;
XX antiproliferative; neuroprotective; immune disorder;
XX reproductive disorder; smooth muscle disorder; neurological disorder;
XX gastrointestinal disorder; developmental disorder;
XX cell proliferative disorder.

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XX
XX OS Homo sapiens.
XX
XX PN W09961471-A2.
XX
XX PD 02-DEC-1999.
XX
XX PF 28-MAY-1999; 99WO-US11904.
XX
XX PR 29-MAY-1998; 98US-0087260.
XX 02-JUL-1998; 98US-0091674.
XX 02-OCT-1998; 98US-0102954.
XX 24-NOV-1998; 98US-0109869.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;
XX Au-Young J;
XX
XX DR WPI: 2000-072605/06.
XX
XX DR N-PSDB: Z56771.
XX
XX PT Proteins, polynucleotides, vectors, host cells and antibodies used to
XX diagnose, treat or prevent immune, reproductive, smooth muscle,
XX neurological, gastrointestinal, developmental and cell proliferative
XX disorders -
XX
XX PS Claim 1; Page 172-174; 229pp; English.
XX
XX SQ Sequence 605 AA;

Query Match 17.6%; Score 63.5; DB 21; Length 605;
Best Local Similarity 33.9%; Pred. No. 23;
Matches 19; Conservative 10; Mismatches 24; Indels 3; Gaps 2;

OY 3 REDEKEGSEQUALSSR--DGAPVQHPLALP-SGSYEDDPQTILDHLSRYLKTGP 55
    ||| | | | : | : | : | | | | | | | | | | | | | | | | | | |
    ||| | | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db 161 reeeeeeekemeekveekqdvveeeelipvngsqeakpqvdfststssqtpg 216

RESULT 13
B11732
ID B11732 standard; Protein; 1042 AA.
XX
XX AC B11732;
XX
XX DT 28-OCT-2000 (first entry)
XX
XX DE Cryptosporidium parvum Iowa isolate GP900, domain 5.
XX
XX KW GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
XX competitive inhibition; attachment; invasion; ligand binding; sporozoite;
XX merozoite; diarrhoea; protozoacide; domain 5; transmembrane domain;
XX cytoplasmic domain.
XX
XX OS Cryptosporidium parvum.
XX
XX PN US6071518-A.
XX
XX PD 06-JUN-2000.

```

XX 12-SEP-1997: 97US-0928361.
PF 13-SEP-1996: 96US-0026062.
XX 01-JUN-1993: 93US-0071880.
PR 29-MAY-1992: 92US-0891301.
PR 03-APR-1995: 95US-0415751.
PR 14-AUG-1996: 96US-0700651.
XX (RECC) UNIV CALIFORNIA.
XX Peteresen C;
PI WPI: 2000-422065/36.
XX
XX New GP900 protein fragments and fusion proteins of Cryptosporidium
PT parvum, useful for detecting the presence of the parasite, and
PT diagnosing or treating Cryptosporidium infections by competitive
PT inhibition of the function of GP900 -
XX
XX Claim 3; Column 73-80; 59pp; English.
XX
XX The invention relates to the GP900 glycoprotein of the protozoan
CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
CC proteins comprising GP900 fragments. The invention also relates to the
CC administration of GP900 or fragments thereof to a host to elicit anti-
CC GP900 antibody production, and to a method of cryptosporidiosis treatment
CC or prophylaxis comprising administration of anti-GP900 antibodies to an
CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
CC competitively inhibit sporozoite or merozoite attachment or invasion, and
CC are also useful for the generation of anti-GP900 antibodies. The
CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
CC additionally inhibit the binding of GP900 ligands to GP900. GP900
CC proteins, fragments and antibodies may therefore be used to treat or
CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
CC immunocompromised persons. Cryptosporidiosis can be contracted from
CC contaminated municipal water supplies (e.g., public swimming pools). It
CC is also a cause of disease in animals, resulting in financial losses in
CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
CC used for the diagnosis of Cryptosporidium parvum infections, and for the
CC detection of the parasite in the environment. Sequences B11728-B11732
CC represent the different domains of the Cryptosporidium parvum Iowa
CC isolate GP900 protein (B11726). The present sequence is that of domain 5
CC of GP900, which contains a putative transmembrane domain and a
CC cytoplasmic domain.
CC
CC Sequence 1042 AA;
SQ

Query Match 17.4%; Score 62.5; DB 21: Length 1042;
Best Local Similarity 29.2%; Pred. No. 59;
Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;
OY 8 KEGSEALSSRQCAPVQHLLALPSGSYEEDPQT-----ILDDHLRLVLT-PCG 56
DB 857 kagsgskdsdesnpid-----psctmipydkptgkllidpesgiaidnsygvfatvpgt 910
OY 57 OSPGVGRYSPRS 68
DB 911 aapkgvgvipes 922

RESULT 14
ID B11726 standard; Protein: 1837 AA.
XX B11726;
AC B11726;
XX 28-OCT-2000 (first entry)
DT
XX Cryptosporidium parvum Iowa isolate GP900.
XX

KW GP900: Iowa isolate; glycoprotein; antibody; cryptosporidiosis;
KM competitive inhibition; attachment; invasion; ligand binding; sporozoite;
KW merozoite; diarrhoea; protozoacide.
XX
XX Cryptosporidium parvum.
XX
XX Key location/Qualifiers
FH Misc-difference 1785 /note="Encoded by AAC in A61846"
FT
XX
XX US6071518-A.
XX
XX 06-JUN-2000.
XX
XX 12-SEP-1997: 97US-0928361.
XX
XX 13-SEP-1996: 96US-0026062.
PR 01-JUN-1993: 93US-0071880.
PR 29-MAY-1992: 92US-0891301.
PR 03-APR-1995: 95US-0415751.
PR 14-AUG-1996: 96US-0700651.
XX
XX (RECC) UNIV CALIFORNIA.
XX
XX Peteresen C;
PI WPI: 2000-422065/36.
XX
XX N-PSDB; A61846, A61847.
DR
XX
XX New GP900 protein fragments and fusion proteins of Cryptosporidium
PT parvum, useful for detecting the presence of the parasite, and
PT diagnosing or treating Cryptosporidium infections by competitive
PT inhibition of the function of GP900 -
XX
XX Claim 2; Column 51-60; 59pp; English.
XX
XX The invention relates to the GP900 glycoprotein of the protozoan
CC Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion
CC proteins comprising GP900 fragments. The invention also relates to the
CC administration of GP900 or fragments thereof to a host to elicit anti-
CC GP900 antibody production, and to a method of cryptosporidiosis treatment
CC or prophylaxis comprising administration of anti-GP900 antibodies to an
CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to
CC competitively inhibit sporozoite or merozoite attachment or invasion, and
CC are also useful for the generation of anti-GP900 antibodies. The
CC antibodies also inhibit sporozoite or merozoite attachment/invasion and
CC additionally inhibit the binding of GP900 ligands to GP900. GP900
CC proteins, fragments and antibodies may therefore be used to treat or
CC prevent cryptosporidiosis. Infection with Cryptosporidium is a common
CC cause of diarrhoea in humans and causes life-threatening diarrhoea in
CC immunocompromised persons. Cryptosporidiosis can be contracted from
CC contaminated municipal water supplies (e.g., public swimming pools). It
CC is also a cause of disease in animals, resulting in financial losses in
CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
CC used for the diagnosis of Cryptosporidium parvum infections, and for the
CC detection of the parasite in the environment. The present sequence
CC represents the GP900 protein of the Iowa isolate of Cryptosporidium
CC parvum.
CC
CC Sequence 1837 AA;
SQ

Query Match 17.4%; Score 62.5; DB 21: Length 1837;
Best Local Similarity 29.2%; Pred. No. 1,2e+02;
Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;
OY 8 KEGSEALSSRQCAPVQHLLALPSGSYEEDPQT-----ILDDHLRLVLT-PCG 56
DB 1652 kagsgskdsdesnpid-----psctmipydkptgkllidpesgiaidnsygvfatvpgt 1705
OY 57 OSPGVGRYSPRS 68
DB 1706 aapkgvgvipes 1717

RESULT 15
ID G59725 standard; Protein; 303 AA.
XX G59725;
AC
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77283.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 18-JUN-1999; 99US-0139817.
PR 21-JUN-1999; 99US-0139899.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 26-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 06-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147112.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148664.
PR 16-AUG-1999; 99US-0149358.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.

PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149930.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

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Query Match 17.2% Score 62: DB 21; Length 303;
Best Local Similarity 36.0% Pred. No. 15;
Matches 18; Conservative 9; Mismatches 19; Indels 4; Gaps 2.

OY 1 QIREDEKEGSGALSRDGAQFVHPHLLPSSGSEEDBPQ-TILDDHLSR 49
      . . . . . : : : : : : : : : : : : : : : : : : : : :
Db 71 eieseeeseeetcmvearegyvngnlsqg---seameddesilrtletr 117

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Search completed: June 7, 2001, 02:01:18
Job time: 5660 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2001, 02:02:10 ; Search time 40.76 Seconds
(without alignments)
32.521 Million cell updates/sec

Title: US-09-587-574-4

Perfect score: 360
Sequence: 1 QIREDEKRGSEGLSSRDG.....VLKTPCGSPGVGRVSPRR 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63.5	17.6	434	2 US-08-710-249-4	Sequence 4, Appl
2	62.5	17.4	1042	3 US-08-928-361B-11	Sequence 11, Appl
3	62.5	17.4	1837	3 US-08-928-361B-5	Sequence 5, Appl
4	62	17.2	348	3 US-08-415-655-5	Sequence 5, Appl
5	62	17.2	348	3 US-08-415-655-13	Sequence 13, Appl
6	62	17.2	348	3 US-08-415-655-15	Sequence 15, Appl
7	59	16.4	1498	2 US-08-404-531B-29	Sequence 29, Appl
8	59	16.4	1498	2 US-08-476-900A-29	Sequence 29, Appl
9	59	16.4	1498	3 US-08-488-546A-29	Sequence 29, Appl
10	59	16.4	1582	2 US-08-404-531B-9	Sequence 9, Appl
11	59	16.4	1582	2 US-08-476-900A-9	Sequence 9, Appl
12	59	16.4	1582	3 US-08-488-546A-9	Sequence 9, Appl
13	59	16.4	1582	4 US-08-726-320-5	Sequence 5, Appl
14	58	16.1	567	1 US-08-007-282B-14	Sequence 2, Appl
15	58	16.1	1498	2 US-08-404-531B-28	Sequence 28, Appl
16	58	16.1	1498	2 US-08-476-900A-28	Sequence 28, Appl
17	58	16.1	1498	3 US-08-488-546A-28	Sequence 28, Appl
18	58	16.1	1581	2 US-08-404-531B-6	Sequence 6, Appl
19	58	16.1	1581	3 US-08-476-900A-6	Sequence 6, Appl
20	58	16.1	1581	3 US-08-488-546A-6	Sequence 6, Appl
21	58	16.1	1581	4 US-08-726-320-4	Sequence 4, Appl
22	57.5	16.0	1043	3 US-08-928-361B-30	Sequence 30, Appl
23	57.5	16.0	1721	3 US-08-700-651-5	Sequence 3, Appl
24	57.5	16.0	1721	3 US-08-928-361B-6	Sequence 6, Appl
25	57	15.8	352	4 US-09-102-204-1	Sequence 1, Appl
26	57	15.8	416	2 US-09-211-930-11	Sequence 11, Appl
27	57	15.8	416	3 US-09-340-993-11	Sequence 11, Appl

28	56.5	15.7	449	2 US-08-657-392-2	Sequence 2, Appl
29	56.5	15.7	449	5 PCT-US94-02539-2	Sequence 2, Appl
30	56.5	15.7	459	2 US-08-673-332-2	Sequence 2, Appl
31	56.5	15.7	471	2 US-08-657-392-31	Sequence 31, Appl
32	56.5	15.7	471	5 PCT-US94-02539-31	Sequence 31, Appl
33	56.5	15.7	711	1 US-08-235-838-7	Sequence 7, Appl
34	56.5	15.7	711	2 US-08-465-473B-7	Sequence 7, Appl
35	56	15.6	432	1 US-08-522-166-8	Sequence 8, Appl
36	56	15.6	432	1 US-08-488-382A-8	Sequence 8, Appl
37	56	15.6	432	2 US-08-480-912-8	Sequence 8, Appl
38	56	15.6	1162	2 US-08-728-323A-2	Sequence 2, Appl
39	56	15.6	1199	4 US-09-208-742-2	Sequence 2, Appl
40	55.5	15.4	242	2 US-08-845-998-2	Sequence 2, Appl
41	55.5	15.4	242	4 US-09-206-537-2	Sequence 2, Appl
42	54.5	15.1	206	6 5185431-1	Sequence 2, Appl
43	54.5	15.1	222	4 US-09-040-483-3	Patent No. 5185431
44	54.5	15.1	222	6 5185431-4	Patent No. 5185431
45	54	15.0	993	4 US-09-060-410-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-710-249-4
Sequence 4, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00122005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-710-249-4

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-546A-29

Query Match 16.4%; Score 59; DB 3; Length 1498;
Best Local Similarity 36.7%; Pred. No. 84;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;

OY 3 REDEKESGQALSRDGAPOVHPLALPSGYEEDPOTILDHLSRVL 51
Db 948 KASEPSQGLPRAMSSRDG-----LLDEEEEEEAEASEEDNLSVL 990

RESULT 10
US-08-404-531B-9
Sequence 9, Application US/08404531B
Patent No. 5863724
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 5863724
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-404-531B-9

Query Match 16.4%; Score 59; DB 2; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;

OY 3 REDEKESGQALSRDGAPOVHPLALPSGYEEDPOTILDHLSRVL 51
Db 948 KASEPSQGLPRAMSSRDG-----LLDEEEEEEAEASEEDNLSVL 990

RESULT 11
US-08-476-900A-9
Sequence 9, Application US/08476900A
Patent No. 6031150
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of detecting Persistent Hyperinsulinemic Hypogly
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-900A-9

Query Match 16.4%; Score 59; DB 3; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;

OY 3 REDEKESGQALSRDGAPOVHPLALPSGYEEDPOTILDHLSRVL 51
Db 948 KASEPSQGLPRAMSSRDG-----LLDEEEEEEAEASEEDNLSVL 990

RESULT 12
US-08-488-546A-9
Sequence 9, Application US/08488546A
Patent No. 6054313
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6054313
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia

STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-546A-9

Query Match 16.4%; Score 59; DB 3; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;
QY 3 REDEKESQALSRGAPVQHPLALPPSGSYEDPQTITDHLRYL 51
DB 948 KASEPSQGLPRAMSSRDG-----LLDDEEEFEFAESEDDNLSVL 990

RESULT 13
US-08-726-320-5
Sequence 5, Application US/08726320
Patent No. 6171815
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
TITLE OF INVENTION: NOVEL HUMAN SULFONYLUREA RECEPTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,320
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: AF-0001 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 784874
US-08-726-320-5

Query Match 16.4%; Score 59; DB 4; Length 1582;
Best Local Similarity 36.7%; Pred. No. 91;
Matches 18; Conservative 7; Mismatches 18; Indels 6; Gaps 1;
QY 3 REDEKESQALSRGAPVQHPLALPPSGSYEDPQTITDHLRYL 51
DB 948 KASEPSQGLPRAMSSRDG-----LLDDEEEFEFAESEDDNLSVL 990

RESULT 14
US-08-007-282B-2
Sequence 2, Application US/08007282B
Patent No. 5403582
GENERAL INFORMATION:
APPLICANT: NAZERIAN, KEYVAN
APPLICANT: CALVERT, JAY G.
APPLICANT: WITTER, RICHARD L.
APPLICANT: YAMAGUCHI, NOBORU
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF AN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road Suite 500 East
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,282B
FILING DATE: 19930121
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOHETICAL: NO
ANTI-SENSE: NO
US-08-007-282B-2

Query Match 16.1%; Score 58; DB 1; Length 567;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 2 IREDEKEGSEQALSSRDGAPVOHPLALPSSGYEDDPOT 41
||| : | : | : ||||| | : |||||
DB 194 IREESVRELEETIRHSYSPVOYHPLALPSSRGVDDLPOT 233

RESULT 15
US-08-404-531B-28

; Sequence 28, Application US/08404531B
; Patent No. 5863724
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
; APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonilyurea Receptor
; Patent No. 5863724
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 586372415
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404.531B
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-404-531B-28

Query Match 16.1%; Score 58; DB 2; Length 1498;
Best Local Similarity 39.1%; Pred. No. 11+02;
Matches 18; Conservative 6; Mismatches 16; Indels 6; Gaps 1;

OY 6 EEKEGSEQALSSRDGAPVOHPLALPSSGYEDDPOTILDDHLSRVL 51
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DB 951 EPSQGLPRAMSSRDG-----LLIDDEEEEEEAASEEDDNLSSVL 990

Search completed: June 7, 2001, 02:02:11
Job time: 5404 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:03:22 ; Search time 56.43 Seconds

(without alignments)
84.031 Million cell updates/sec

Title: US-09-587-574-4

Perfect score: 360
Sequence: 1 QIREDEKKGSEQALSSRDG.....VLKTPGQSPGVRGPRSR 69Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase :
1: PIR.67:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	100.0	838	2 T08423	Axin homolog Ax11
2	139.5	38.8	832	2 T08422	negative regulator
3	72	20.0	409	2 J70764	translation elonga
4	71	19.7	793	1 KXMSF	furin (EC 3.4.21.7
5	68.5	19.0	441	2 A45360	steroid hormone re
6	68	18.9	206	2 H64410	hypothetical prote
7	66	18.3	409	2 T38487	translation elonga
8	66	18.3	563	2 A69335	succinate dehydrog
9	65	18.1	793	1 KXRTF	furin (EC 3.4.21.7
10	64.5	17.9	262	2 C70648	probable nuclo prot
11	64.5	17.9	414	2 T49459	hypothetical prote
12	64	17.8	907	2 A45560	sporozoite surface
13	63	17.5	619	2 B71559	probable metallopr
14	62.5	17.4	1832	2 T31113	mucin-like glycopr
15	62	17.2	348	2 I49262	cyclin cdk inhibit
16	60.5	16.8	134	2 E57233	complexin II - hum
17	60.5	16.8	134	2 C57233	complexin II - rat
18	60.5	16.8	325	2 H70600	probable transfera
19	60.5	16.8	450	2 B71304	probable zinc prot
20	60	16.7	1544	2 T04464	hypothetical prote
21	59.5	16.5	349	2 T05857	hypothetical prote
22	59	16.4	223	2 D75515	hypothetical prote
23	59	16.4	291	2 C81943	probable integrase
24	59	16.4	291	2 C81943	integrase/recombin
25	59	16.4	970	2 C57282	anryrin-related pr
26	59	16.4	1267	2 S53058	probable membrane
27	59	16.4	1582	2 A56248	sulfonylurea recep
28	59	16.4	1867	2 T15344	anryrin-related un
29	59	16.4	2388	2 J60271	beta spectrin, bet

30	58.5	16.2	280	2 T50554	3-methyl-2-oxobuta
31	58.5	16.2	379	2 A45267	heterocyst pattern
32	58.5	16.2	513	2 T41011	hypothetical prote
33	58.5	16.2	595	1 EDBEMC	immediate-early ph
34	58.5	16.2	929	2 T52517	hypothetical prote
35	58.5	16.2	2219	2 T41547	hypothetical prote
36	58.5	16.2	2219	2 T27684	hypothetical prote
37	58.5	16.2	5105	2 T32650	hypothetical prote
38	58	16.1	226	2 S33024	hypothetical prote
39	58	16.1	300	2 S19560	proline-rich prote
40	58	16.1	413	4 F0H0E2	retrovirus-related
41	58	16.1	471	2 A53711	collagenase 3 (EC
42	58	16.1	567	1 VCFVAS	env polyprotein -
43	58	16.1	606	2 H71065	hypothetical prote
44	58	16.1	897	2 T21688	hypothetical prote
45	58	16.1	1209	2 T13153	brachma associated

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
M:1. Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: 216414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A>Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 360; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 3.9e-32;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIREDEKKGSEQALSSRDGAPVQHPALLPSCGYEDPQTIIIDHLKRVLKTPGQSPG 60
DB 397 QIREDEKKGSEQALSSRDGAPVQHPALLPSCGYEDPQTIIIDHLKRVLKTPGQSPG 456
QY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465

RESULT 2
T08422
negative regulator axin [imported] - rat
N:Alternate names: Axin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
M:1. Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: 216413; MUID:98151361
A:Accession: T08422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IKE>
A:Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A>Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Query Match 38.8%; Score 139.5; DB 2; Length 832;
 Best Local Similarity 35.3%; Pred. No. 1.4e-07;
 Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIREDEKESGSEALSSRDGAPVQHPLALPSGSTE-----GSYEEDPQTLL 43
 Db 420 RYRMEEGEDGEMP-----SGPMASHKLLPSVPMHMFPPRYVDMGSGGLRDHNEHPESTLL 475
 OY 44 DDHLSRVLTPECCSPGGRVSPRS 68
 Db 476 DEHYGVKMTPECCSPGGRVSPRS 500

RESULT 3
 JT0764
 Translation elongation factor eEF-1 gamma chain - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C:Accession: JT0764; P0161
 R:Momoi, H.; Yamada, H.; Ueguchi, C.; Mizuno, T.
 Gene 134, 119-122, 1993
 A:Title: Sequence of a fission yeast gene encoding a protein with extensive homology to
 A:Reference number: JT0764; MUID:94063505
 A:Accession: JT0764
 A:Molecule type: DNA
 A:Residues: 1-409 <MOM>
 A:Cross-references: GB:DJ4606; NID:g457595; PIDN:BA03456.1; PID:g2160329
 A:Accession: P0161
 A:Molecule type: Protein
 A:Residues: 226-244 <MO2>
 A:Note: A 23k fragment beginning at residue 226 appears to be a degradation product of the
 C:Superfamily: translation elongation factor eEF-1 gamma chain
 C:Keywords: protein biosynthesis
 F:226-409/Region: DNA binding #status predicted

Query Match 20.0%; Score 72; DB 2; Length 409;
 Best Local Similarity 35.3%; Pred. No. 2;
 Matches 12; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 3 REDEKESGSEALSSRDGAPVQHPLALPSGSTE 36
 Db 231 KKDEKKNAKPRQARPKPKHPLASAPNGSFD 264

RESULT 4
 KXMSF
 furin (EC 3.4.21.75) precursor - mouse
 N:Alternate names: kexin homolog; paired-basic endopeptidase; prohormone-processing endo
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
 C:Accession: A23679; I49677
 R:Hatsuzawa, K.; Hosaka, M.; Nakagawa, T.; Nagase, M.; Shoda, A.; Murakami, K.; Nakayama
 J. Biol. Chem. 265, 22075-22078, 1990
 A:Title: Structure and expression of mouse furin, a yeast Kex2-related protease. Lack of
 A:Reference number: A23679; MUID:91093035
 A:Accession: A23679
 A:Molecule type: mRNA
 A:Residues: 1-793 <HNT>
 A:Cross-references: GB:X54056; NID:g50996; PIDN:CAA37888.1; PID:g50997
 R:Creemers, J.-J.W.; Roelofs, A.A.J.; van den Ouweland, A.A.M.; van Duinhoven, H.H.L.;
 Mol. Biol. 11, 127-138, 1992
 A:Title: Cloning and functional expression of a 4.3 kbp mouse fur cDNA: Evidence for dif
 A:Reference number: I49677
 A:Accession: I49677
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-745; V, 747-793 <RES>
 A:Cross-references: GB:I26489; NID:g432275; PIDN:AAA37643.1; PID:g432276
 C:Comment: This subtilisin-like endoproteinase removes paired basic residues to process
 C:Genetics:
 A:Gene: FUR

C:Superfamily: kexin; subtilisin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-793/Product: furin #status predicted <MAT>
 F:27-714/Domain: extracellular #status predicted <EXT>
 F:144-382/Domain: subtilisin homology <SBP>
 F:715-735/Domain: transmembrane #status predicted <TM>
 F:736-793/Domain: intracellular #status predicted <INT>
 F:153,194,368/Active site: Asp, His, Ser #status predicted
 F:387,440,553/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 19.7%; Score 71; DB 1; Length 793;
 Best Local Similarity 40.0%; Pred. No. 5.6;
 Matches 20; Conservative 3; Mismatches 27; Indels 0; Gaps 0;

OY 7 EKEGSEALSSRDGAPVQHPLALPSGSTEEDPQTLLDHLRLVLT 56
 Db 672 EQTCSRQSSRSRSPQPPALRPEVMEPRQLQAGLASHLEVIAGLSC 721

RESULT 5
 A45360
 steroid hormone receptor delta - human
 N:Alternate names: nuclear hormone receptor 1 (NUC1); peroxisome proliferator-activat
 C:Species: Homo sapiens (man)
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
 C:Accession: A45360
 R:Schmidt, A.; Endo, N.; Rutledge, S.J.; Vogel, R.; Shinar, D.; Rodan, G.A.
 Mol. Endocrinol. 6, 1634-1641, 1992
 A:Title: Identification of a new member of the steroid hormone receptor superfamily
 A:Reference number: A45360; MUID:93078797
 A:Accession: A45360
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-441 <SCH>
 A:Experimental source: osteosarcoma SAOS-2/B10 cells
 A:Note: Sequence extracted from NCBI database (NCBI:118801)
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc fin
 F:72-359/Domain: erba transforming protein homology <ERBA>

Query Match 19.0%; Score 68.5; DB 2; Length 441;
 Best Local Similarity 30.3%; Pred. No. 5.4;
 Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

OY 1 QIREDEKESGSEALSSRDGAPVQH--PLALPSGSTE-----DPQTLLDHLRLVLT 53
 Db 10 EVREDEKEEVEA-----EGAPELNGGPOHALPSSSYTDLSSSSPPLDQ-----LQ 59

OY 54 PGCGSPGVGRVSPRS 69
 Db 60 MCGDASCGLMECR 75

RESULT 6
 H64410
 hypothetical protein homolog MJ0888 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: H64410
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 R:Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodex,
 rson, J.D.; Sedov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kalne, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
 A:Reference number: A64300; MUID:96337999
 A:Accession: H64410
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-206 <BUL>

A:Cross-references: GB:067532; GB:L77117; NID:g2826344; PIDN:AAB98892.1; PID:g1591566; PID:
C:Genetics:
A:Map position: REV819507-818887
C:Superfamily: glyoxalase

Query Match 18.9%; Score 68; DB 2; Length 206;
Best Local Similarity 32.8%; Pred. No. 2.5;
Matches 19; Conservative 10; Mismatches 21; Indels 8; Gaps 2;

QY 2 IREDEE---KEGSOALSSRDGAPVQHPPLALPSCSYEDPQTLLDHLSPVLTPTG 55
DB 76 IREDEEVLKNGDEVYSSLFCAKLNPKEITPSEIEE---LKSYLEITPTPG 129

RESULT 7
178487
translation elongation factor EF-1 gamma - flsion yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T38487
R:Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997
A:Reference number: 221796
A:Accession: T38487

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-409

A:Cross-references: EMBL:297210; PIDN:CAJ1029.1; GSPDB:GN00066; SPDB:SPAC2994.02C

A:Experimental source: strain 972h-; cosmid c2994

C:Genetics:
A:Gene: SPDB:SPAC2994.02C

A:Map position: 1

A:Insertions: 73/1

C:Superfamily: translation elongation factor eEF-1 gamma chain

Query Match 18.3%; Score 66; DB 2; Length 409;
Best Local Similarity 32.4%; Pred. No. 9.3;

Matches 11; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 3 REDEKEGSEALSSRDGAPVQHPPLALPSCSYE 36
DB 231 KKDEKKNAKPKQAEAPKPKHPLASANGSFD 264

RESULT 8
A69335
succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
C:Accession: A69335

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschess, E.F.
Glocke, A.; Zhou, L.; Overbeek, R.; Goehyne, J.D.; Weidman, J.F.; McDonald, L.
Nature 350, 364-370, 1997

A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343

A:Accession: A69335

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-563 <KLE>

A:Cross-references: GB:AE001057; GB:AE000782; NID:g2689380; PIDN:AAB90557.1; PID:g264993
C:Superfamily: fumarate reductase flavoprotein: 3-oxosteroid 1-dehydrogenase homology; F
C:KeyWords: FAD; flavoprotein; oxidoreductase
F:4-265/Domain: fumarate reductase flavoprotein homology <RRF>
F:297-385/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

Query Match 18.3%; Score 66; DB 2; Length 563;
Best Local Similarity 25.3%; Pred. No. 14;

Matches 19; Conservative 10; Mismatches 12; Indels 34; Gaps 3;

QY 10 GSEALSSRDGAPVQHPPLALPSCSYEDPQTLLDHLSPVLTPTG 60
DB 208 GGLAIVANGIPLKDMERFQHPGLVPSG-----ILMTECRREGGY 251

QY 61 -----VGRYSP 66
DB 252 LUNKGERPMKRYAP 266

RESULT 9
KKRTF
furin (EC 3.4.21.75) precursor - rat

M:Alternate names: kexin homology; paired-basic endopeptidase; prohormone-processing e
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: S13106

R:Mitsumi, Y.; Sohma, M.; Ikehara, Y.

A:Title: Sequence of the cDNA encoding rat furin, a possible propeptide-processing en
Nucleic Acids Res. 18, 6719, 1990

A:Reference number: S13106; MUID:91067492

A:Accession: S13106

A:Molecule type: mRNA

A:Cross-references: EMBL:X55660; NID:956171; PIDN:CAJ9193.1; PID:956172

C:Comment: This subtilisin-like endoprotease removes paired basic residues to proce
C:Superfamily: kexin; subtilisin homology

C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-793/Product: furin #status predicted <MAT>
F:27-714/Domain: extracellular #status predicted <EXT>

F:144-382/Domain: subtilisin homology <SBT>
F:715-735/Domain: transmembrane #status predicted <TM>

F:736-793/Domain: intracellular #status predicted <INT>
F:153,194,368/Active site: Asp, His, Ser #status predicted
F:387,440,553/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.1%; Score 65; DB 1; Length 793;
Best Local Similarity 38.0%; Pred. No. 26;

Matches 19; Conservative 4; Mismatches 27; Indels 0; Gaps 0;

QY 7 EKGSGOALSSRDGAPVQHPPLALPSCSYEDPQTLLDHLSPVLTPTG 56
DB 672 EGYCSKQSSRSRPPQPPALPVEYVPRKAGASHPLVGLGSC 721

RESULT 10
C70648
probable nuoJ protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: C70648

R:Colt, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
Rajandream, M.A.; Rogers, J.; Rutter, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987

A:Accession: C70648

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-262 <COL>

A:Cross-references: GB:Z83867; GB:AL123456; NID:g3261695; PIDN:CAJ06285.1; PID:e29093
A:Experimental source: strain H37RV

Query Match 17.9%; Score 64.5; DB 2; Length 262;
Best Local Similarity 30.6%; Pred. No. 8.2;

Matches 26; Conservative 7; Mismatches 21; Indels 31; Gaps 4;

OY 3 REDEKESQALSRDAPVQH-----LALLPSGYEDPQTILDD 45

Db 179 REDEKRRKQRLSERRPGCHPPLPGVYARNAVDVALLPDGYSY----- 230

OY 46 HLS--RVLT---PCQSPGVGRYS 65

Db 231 -LSVPRMLRTGADGLQRPSPGAVS 254

RESULT 11

T49459

hypothetical protein B14D6.110 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49459

R:Schulte, U.; Allyn, V.; Hohelsel, J.; Brandt, P.; Farimann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49459

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <SCH>

A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.110

A:Experimental source: BAC clone B14D6; strain OR74A

A:Genetics:

A:Gene: NCSP:B14D6.110

A:Map position: 6

A:Introns: 317/2

Query Match 17.9%; Score 64.5; DB 2; Length 414;

Best Local Similarity 34.0%; Pred. No. 14;

Matches 17; Conservative 7; Mismatches 25; Indels 1; Gaps 1;

OY 4 EDEKESQALSRDAPVQHPLALPSGYEDPQTILDDHLSRVLT 53

Db 54 EDEKESQALSRDAPVQHPLALPSGYEDPQTILDDHLSRVLT 102

RESULT 12

A:Accession: A45560

sporozoite surface antigen SPAC-1 - Theileria annulata

C:Species: Theileria annulata

C>Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

C:Accession: A45560

R:Hall, R.; Hunt, P.D.; Carrington, M.; Simmons, D.; Williamson, S.; Meckam, R.P.; Tait, M.; Blochem. Parasitol. 53, 105-112, 1992

A:Title: Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surface A:Reference number: A45560; MUID:92365719

A:Accession: A45560

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-907 <HAL>

A:Cross-references: GB:M63017; NID:g161884; PID:g161885

A>Note: sequence extracted from NCBI backbone (NCBIN:111148, NCBIRP:111150)

C:Keywords: surface antigen

Query Match 17.8%; Score 64; DB 2; Length 907;

Best Local Similarity 26.5%; Pred. No. 39;

Matches 22; Conservative 12; Mismatches 15; Indels 34; Gaps 4;

OY 4 EDEKESQALSRD--GAPVQH-----LALLPSGY-EDP 39

Db 120 DDEDEEDDKSTSKNGSPKAPGVSSSTSSASPTPTTISQTLGSPSGSHAOQDP 179

OY 40 QTILDDHLSRVLTGPGQSPGVG 62

Db 180 G-----VGVPVGVPGVG 192

RESULT 13

B71559

probable metalloproteinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: B71559

R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A:Reference number: A71570; MUID:9900809

A:Accession: B71559

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-619 <ARN>

A:Cross-references: GB:AE001282; GB:AE001273; NID:93328466; PID:AMC67663.1; PID:9332 A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: yael

Query Match 17.5%; Score 63; DB 2; Length 619;

Best Local Similarity 28.4%; Pred. No. 33;

Matches 21; Conservative 19; Mismatches 18; Indels 16; Gaps 5;

OY 1 QIREDEK-----EGSEQALSRDAPVQHPLALPSGYEDPQTILDDHLSRVLT 53

Db 458 KFRDEQERRYTLERLEAKRISL--GIPLK-DLAV-----QYNDPWTLMESVSDSLKT 510

OY 54 PGQSPGVGRYSR 67

Db 511 --VKALGMGRVSPQ 522

RESULT 14

T31113

mucin-like glycoprotein 900 - Cryptosporidium parvum

C:Species: Cryptosporidium parvum

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T31113

R:Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dub Mol. Biochem. Parasitol. 96, 93-110, 1998

A:Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum media A:Reference number: 220989; MUID:99066935

A:Accession: T31113

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1832 <BAR>

A:Cross-references: EMBL:AF068065; NID:g4063041; PID:g4063042; PIDN:AMC98153.1

Query Match 17.4%; Score 62.5; DB 2; Length 1832;

Best Local Similarity 29.2%; Pred. No. 1.3e+02;

Matches 21; Conservative 8; Mismatches 26; Indels 17; Gaps 3;

OY 8 KEGSEQALSRDAPVQHPLALPSGYEDPQT-----ILDDHLSRVLT--PGC 56

Db 1647 KAGSQSKSSDSEGNPID-----PSTNMPYDPKTKLIDPESGLAIDNSGVGATVPGT 1700

OY 57 QSPGVGRYSRPS 68

Db 1701 AAPKKGVTIPES 1712

RESULT 15

I49262

cyclin cdk inhibitor p57 - mouse

N:Alternate names: CDI p57; cyclin-cyclin-dependent kinase inhibitor p57; p57-kip2 C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999

C:Accession: I49262

R:Lee, M.H.; Reynolds, T.; Massague, J. Genes Dev. 9, 639-649, 1995

A:Title: Cloning of p57KIP2, a cyclin-dependent kinase inhibitor with unique domain s

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:10:31; Search time 39.03 Seconds
(Without alignments)
60.559 Million cell updates/sec

Title: US-09-587-574-4
Perfect score: 360

Sequence: 1 QIREDEKRCGSEGLASSRDC.....VLKTPCGQSGVGRVSPRSR 69

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	100.0	838	1 AXN2_RAT	O70240 rattus norv
2	360	100.0	840	1 AXN2_MOUSE	O08566 mus musculu
3	332	92.2	843	1 AXN2_HUMAN	O99211 homo sapien
4	217.5	60.4	812	1 AXN2_BRARE	P57095 brachydanto
5	158	43.9	842	1 AXN_XENLA	O99490 xenopus lae
6	149	41.4	835	1 AXN1_BRARE	P57094 brachydanto
7	146	40.6	841	1 AXN1_CHICK	O42400 gallus galli
8	139.5	38.8	893	1 AXN1_RAT	O70239 rattus norv
9	139.5	38.8	992	1 AXN1_MOUSE	O35625 mus musculu
10	113.5	31.5	900	1 AXN1_HUMAN	O13169 homo sapien
11	72	20.0	409	1 EF1G_SCHPO	P40921 schizosach
12	71	19.7	793	1 FURI_MOUSE	P23188 mus musculu
13	68.5	19.0	441	1 PPAS_HUMAN	O03181 homo sapien
14	68	18.9	206	1 Y688_METJA	O58298 methanococ
15	65	18.1	793	1 FURI_RAT	P23377 rattus norv
16	62.5	17.4	134	1 CLX2_MAKRA	O94105 natke japon
17	62.5	17.4	708	1 ABB1_MOUSE	O49xj1 mus musculu
18	62	17.2	348	1 CDNC_MOUSE	P49919 mus musculu
19	62	17.2	471	1 MM13_BOVIN	O77656 bos taurus
20	61.5	17.1	745	1 AXN1_DROME	O99407 drosophila
21	61	16.9	1490	1 CRK7_HUMAN	O99404 homo sapien
22	60.5	16.8	593	1 DR11_HUMAN	O99856 homo sapien
23	59	16.4	1267	1 DHR1_YEAST	O04217 saccharomyc
24	59	16.4	1581	1 ACC8_CRICR	O09427 cricetus cr
25	58.5	16.2	379	1 PATA_ANASP	P11210 murine cyto
26	58.5	16.2	595	1 VIE1_MCMVS	P30117 epstein-bar
27	58	16.1	217	1 YKR4_EBV	P10264 homo sapien
28	58	16.1	413	1 GAG2_HUMAN	P45452 homo sapien
29	58	16.1	471	1 MM13_HUMAN	O62806 oryctolagus
30	58	16.1	471	1 MM13_RABIT	P31796 avian spleen
31	58	16.1	1320	1 PURL_NEIMA	O91WCS neisseria m
32	58	16.1	1320	1 PURL_NEIMA	O91WCS neisseria m
33	58	16.1	1320	1 PURL_NEIMA	O91WCS neisseria m

34	58	16.1	1580	1 ACC8_RAT	O09429 rattus norv
35	58	16.1	3924	1 ANK2_HUMAN	O01484 homo sapien
36	57.5	16.0	730	1 MM02_MOUSE	P41245 mus musculu
37	57	15.8	237	1 CAS1_MACEU	P28549 macropus eu
38	57	15.8	449	1 CMGA_BOVIN	P05059 bos taurus
39	57	15.8	472	1 MM13_HORSE	O18927 equus caball
40	57	15.8	913	1 UBPK_HUMAN	O992K6 homo sapien
41	56.5	15.7	243	1 AX28_SOYAN	P13089 glycine max
42	56.5	15.7	330	1 NDPM_CHICK	P79766 gallus galli
43	56.5	15.7	348	1 P2C2_CAEEL	P49596 caenorhabdi
44	56.5	15.7	423	1 TIG_BACSU	P80698 bacillus su
45	56.5	15.7	457	1 CMGA_HUMAN	P10645 homo sapien

ALIGNMENTS

RESULT 1	ID	AXN2_RAT	STANDARD:	PRT:	838 AA.
AC	O70240:				
DR	01-OCT-2000 (Rel. 40, Last sequence update)				
DR	01-OCT-2000 (Rel. 40, Last sequence update)				
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)				
DE	(AXIL).				
GN	AXIN2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=9826558; PubMed=9566905;				
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.;				
RT	"Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of xenopus embryos."				
RT	Mol. Cell. Biol. 18:2867-2875(1998).				
RL	-1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).				
CC	-1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX.				
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.				
CC	-1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY P2A.				
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.				
CC	-----				
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CC	-----				
CC	EMBL: AF017757; AAC40089.1; -				
DR	HSSP: P49799; IACR.				
DR	InterPro: IPR000342; -				
DR	InterPro: IPR001158; -				
DR	Pfam: PR00615; RGS. 1.				
DR	Pfam: PR00778; DIX. 1.				
DR	PROSITE: P550132; RGS. 1.				
KW	Developmental protein; Phosphorylation.				
FT	DOMAIN 81 200				
FT	DOMAIN 327 413				
FT	GSK-3B BINDING SITE (BY SIMILARITY).				

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FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 SIMILARITY).
FT DOMAIN 756 838 POLY-HIS.
SQ SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;

Query Match 100.0%; Score 360; DB 1; Length 838;
Best Local Similarity 100.0%; Pred. No. 8.3e-32;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIREDEKEGSEQALSSHDGAPVOHPHLLPSGSYEEDPOTILDDHLSRVLTGCGSPG 60
DB 397 QIREDEKEGSEQALSSHDGAPVOHPHLLPSGSYEEDPOTILDDHLSRVLTGCGSPG 456
OY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465

RESULT 2
AXN2_MOUSE STANDARD; PRT; 840 AA.
ID AXN2_MOUSE
AC 088566; 090XJ6;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.-A., Muerlele M., Grimm J., Asbrand C.,
RA Wirtz R., Kuehl M., Wedlich D., Birchmeier W.,
RT "Functional interaction of an axin homolog, conductin, with beta-
RT catenin, APC, and GSK3beta."
RL Science 280:596-599(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATEININ. THE INTERACTION BETWEEN AXIN AND BETA-CATEININ
CC OCCURS VIA THE ARMD/DILLO REPEATS CONTAINED IN BETA-CATEININ.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL; AF073788; AAC26047.1; -
CC EMBL; AF205889; AAF22800.1; -

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DR MGD: 1270862; Axin2.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001156; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR PROSITE: PS01332; RGS; 1.
KW Anti-oncogene; Phosphorylation.
FT DOMAIN 81 200 RGS.
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 469 476 POLY-HIS.
FT DOMAIN 758 840 DIX.
FT CONFLICT 101 101 R -> K (IN REF. 2).
FT CONFLICT 474 474 H -> Y (IN REF. 2).
FT CONFLICT 484 484 S -> P (IN REF. 2).
FT CONFLICT 503 503 F -> S (IN REF. 2).
FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA; 92934 MW; A07D5EFP25DE/277 CRC64;

Query Match 100.0%; Score 360; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 8.3e-32;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIREDEKEGSEQALSSHDGAPVOHPHLLPSGSYEEDPOTILDDHLSRVLTGCGSPG 60
DB 397 QIREDEKEGSEQALSSHDGAPVOHPHLLPSGSYEEDPOTILDDHLSRVLTGCGSPG 456
OY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465

RESULT 3
AXN2_HUMAN STANDARD; PRT; 843 AA.
ID AXN2_HUMAN
AC Q9Y2T1; Q9UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24."
RL Genomics 55:341-344(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATEININ. THE INTERACTION BETWEEN AXIN AND BETA-CATEININ
CC OCCURS VIA THE ARMD/DILLO REPEATS CONTAINED IN BETA-CATEININ.
CC TERNARY COMPLEX (BY SIMILARITY).
CC -----

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CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC -1- PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF078165; AAD20976.1; -.
CC EMBL: AF205888; AAF22799.1; -.
CC MIM: 604025; -.
CC InterPro: IPR000342; -.
CC InterPro: IPR001158; -.
CC Pfam: PF00615; RGS; 1.
CC Pfam: PF00778; DIX; 1.
CC PRINTS: PR01301; RGS/PROTEIN.
CC PROSITE: PS50132; RGS; 1.
CC KW Developmental protein; Phosphorylation.
CC FT DOMAIN 81 200 RGS.
CC FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
CC FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
CC FT SIMILARITY).
CC FT DOMAIN 469 474 DIX.
CC FT DOMAIN 761 843 POLY-HIS.
CC FT CONFLICT 37 62 OPGVKGQVTKPMYSVSNTRRREDGL -> HHGGGQPGHQI
CC FT CONFLICT 346 346 Q -> R (IN REF. 2).
CC FT CONFLICT 572 636 MISSING (IN REF. 2).
CC FT CONFLICT 687 687 P -> S (IN REF. 2).
CC FT CONFLICT 696 696 Q -> H (IN REF. 2).
CC FT SEQUENCE 843 AA: 93557 MW: 17862BED6A84664D CRC64;
SQ
Query Match 92.2%; Score 332; DB 1; Length 843;
Best Local Similarity 89.9%; Pred. No. 9.7e-29;
Matches 62; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 QIREDKEKSGEQALSSRGAPVQHPLALPSGSEYEDPQTIIIDHLRYLKTGCGSPG 60
DB 397 QIREDKEKSGEQALSSRGAPVQHPLALPSGSEYEDPQTIIIDHLRYLKTGCGSPG 456
QY 61 VGRYSPRSR 69
DB 457 VGRYSPRSR 465
RESULT 4
AXN2_BRAE STANDARD: PRT: 812 AA.
ID AXN2_BRAE
AC P37093;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2).
GN AXIN2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; PubMed=10704853;
RX Shintzu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
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RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000)
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC EMBL: AB032263; BAA92440.1; -.
CC HSP: P49799; IAGR.
CC InterPro: IPR000342; -.
CC InterPro: IPR001158; -.
CC Pfam: PF00615; RGS; 1.
CC Pfam: PF00778; DIX; 1.
CC PROSITE: PS50132; RGS; 1.
CC KW Developmental protein; Phosphorylation.
CC FT DOMAIN 84 203 RGS.
CC FT DOMAIN 329 415 GSK-3B BINDING SITE (BY SIMILARITY).
CC FT DOMAIN 415 467 BETA-CATENIN BINDING SITE (BY
CC FT SIMILARITY).
CC FT DOMAIN 412 419 POLY-SER.
CC FT DOMAIN 730 812 DIX.
CC FT SEQUENCE 812 AA: 91496 MW: 46550A6DE2240CC CRC64;
SQ
Query Match 60.4%; Score 217.5; DB 1; Length 812;
Best Local Similarity 63.8%; Pred. No. 3.1e-16;
Matches 44; Conservative 9; Mismatches 11; Indels 5; Gaps 1;
QY 1 QIREDKEKSGEQALSSRGAPVQHPLALPSGSEYEDPQTIIIDHLRYLKTGCGSPG 60
DB 399 QIREDKEKSGEQALSSRGAPVQHPLALPSGSEYEDPQTIIIDHLRYLKTGCGSPG 453
QY 61 VGRYSPRSR 69
DB 454 LTRHSPRSR 462
RESULT 5
AXN2_XENLA STANDARD: PRT: 842 AA.
ID AXN2_XENLA
AC Q9YGY0;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE AXIN OR AXIN.
GN AXIN OR AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae.
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; PubMed=10072781;
RX Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RT expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
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CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC (BY SIMILARITY).
CC CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
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CC OR SEND AN EMAIL TO license@isb-sib.ch.
CC -----
CC CCBML; AF097313; AAC71036.1; -.
CC DR HSSB; P49799; IAGR.
CC DR InterPro; IPRO00342; -.
CC DR InterPro; IPRO01158; -.
CC DR Pfam; PF00615; RGS: 1.
CC DR Pfam; PF00778; DIX: 1.
CC DR PROSITE; PS50132; RGS: 1.
CC KW DEVELOPMENTAL PROTEIN; Phosphorylation.
CC FT DOMAIN 88 211 RGS.
CC FT DOMAIN 438 433 GSK-3B BINDING SITE (BY SIMILARITY).
CC FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY SIMILARITY).
CC FT DOMAIN 438 508
CC FT SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64; DIX.
CO QUERY MATCH 43.9%; SCORE 158; DB 1; LENGTH 842;
BEST LOCAL SIMILARITY 40.0%; Pred. No. 1.le-09;
MATCHES 34; Conservative 14; Mismatches 11; Indels 26; Gaps 3.
QY 7 EEKGEQALNSDGAAPVOPRLALPLPSG-----SYEDPQTILD 44
DB 419 EEGEGDGVDSGPSV-ISKK---LFSGPPMHFNSTRYSLETGCVMQIRAHENPEISLD 474
QY 45 DHLSRYLKTPGCOSPVGGRYSRSPRS 69
DB 475 EHVRVMTKPTGCOSPCTGRHSFKSR 499
RESULT 6
AXNI_BRAKE STANDARD; PRT; 835 AA.
AC P57094;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE AXIN1 (AXIS INHIBITION PROTEIN 1).
GN AXIN1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP MEDLINE=20171051; PubMed=10704853;
RA Shimizu T., Yamanaoka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
BA Bae Y.-K., Hibb M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish.";
RT Mech. Dev. 91:293-303(2000).
RT -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
RT BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA
RT CATENIN AND APC BY GSK-3B (BY SIMILARITY).
RT -1- SUBCELLULAR LOCATION: CYTOSOLASMIC (BY SIMILARITY).
RT -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
```

[illegible]

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DR EMBL: AF09012; AAC60245.1; -
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PSS0132; RGS; 1.
DR Developmental protein: Phosphorylation.
FT DOMAIN 88 211 RGS.
FT 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DIX.
SQ DOMAIN 759 841
SEQUENCE 841 AA; 94931 MW; 400D0C90E72506FE CRC64;

Query Match 40.6%; Score 146; DB 1; Length 841;
Best Local Similarity 34.7%; Pred. No. 2.2e-08;
Matches 35; Conservative 14; Mismatches 14; Indels 38; Gaps 4;

OY 3 REDEER-----EGSEQALSSRDGAPVQHPALLPSC----- 33
DB 403 REAELEERLKRVAEEGEDADISSGFSV-ISHK---MPSAQPHHFAPRYSEMGACG 458
OY 34 -----SYEDPOTILDDHLSRYLKTGCGSPGVGRYSPRS 69
DB 459 MQRDAHEHPESILDEHVQRVWKTGCGSPGGRHSPKR 499

RESULT 8
AXIN1_RAT
ID AXIN1_RAT STANDARD: PRT; 893 AA.
AC 070239;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
GN AXIN1 OR AXIN
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-98151361; PubMed-9482734;
RA Ikeda S., Kishida S., Yamamoto H., Murali H., Koyama S., Kikuchi A.;
RT Axin1, a negative regulator of the Wnt signaling pathway, forms a
RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
RT dependent phosphorylation of beta-catenin.;
RL EMBL J.171371-1384(1998).
RL
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARADILLO REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
CC FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
CC SPLEEN AND LIVER.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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DR EMBL: AF017756; AAC40066.1; ALT_INIT.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -
DR InterPro: IPR001158; -
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PSS0132; RGS; 1.
DR Developmental protein: Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 154 277 RGS.
FT 414 498 GSK-3B BINDING SITE.
FT DOMAIN 499 567 BETA-CATENIN BINDING SITE.
FT 811 893 DIX.
SQ SEQUENCE 893 AA; 99188 MW; 3CCBD2224EDD384C CRC64;

Query Match 38.8%; Score 139.5; DB 1; Length 893;
Best Local Similarity 35.3%; Pred. No. 1.2e-07;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIREDEEREGSEQALSSRDGAPVQHPALLPSC-----GSYEDPOTIL 43
DB 481 RVMEEGEGEGEMP---SCPMSHKLPSVPAWHFPPRYVDMCGSLRDHAHEHPESIL 536
OY 44 DDHLSRYLKTGCGSPGVGRYSPRS 68
DB 537 DEHVQRVWKTGCGSPGGRHSPDS 561

RESULT 9
AXIN1_MOUSE
ID AXIN1_MOUSE STANDARD: PRT; 992 AA.
AC 035625;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
GN AXIN1 OR AXIN OR FU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE-97373830; PubMed-9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vassilek T.J., Perry W.L. III,
RA Lee J.J., Tilgman S.M., Gunhiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
RL
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARADILLO REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF009011; AAC53285.1; -
CC DR HSSP: P49799; IAGR.
CC MGD: MGI:1096327; Axin.
CC DR InterPro: IPR000342; -
CC DR InterPro: IPR001158; -
CC DR Pfam: PF00615; RGS; 1.
CC DR Pfam: PF00778; DIX; 1.
CC DR PROSITE: PS50132; RGS; 1.
CC KW Developmental protein; Phosphorylation; Alternative splicing.
CC FT NON_TER 1 18 POLY-ALA.
FT DOMAIN 10 18
FT DOMAIN 217 340 RGS-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 477 561 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 562 630 SIMILARITY).
FT DOMAIN 910 992 DIX.
FT VARSPLIC 860 895 MISSING (IN ISOPFORM 2).
FT SEQUENCE 992 AA; 109917 MW; 70EBB53D387BD26F CRC64;
SO
Query Match 38.8%; Score 139.5; DB 1; Length 992;
Best Local Similarity 35.3%; Pred. No. 1.3e-07;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;
QY 1 QIREDEKESGSEALSSRDGAPVOHPALPLPS-----GSYEEDPQTILL 43
DB 544 RVRMEEGEDGEMP-----SGPMASHKLPSPVAMHHPRYVDMGCSGLRDAAHENPESIL 599
DB 44 DDHLSRYLKTPTGCCSPGVGRYSPRS 68
DB 600 DEHYORVMKTPGCCSPGPHRSPDS 624
RESULT 10
AXIN1_HUMAN STANDARD; PRT; 900 AA.
ID AXIN1_HUMAN
AC 015169;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN1 (AXIN INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eultheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
RA Lee J.D., Tildgman S.M., Gumbiner B.M., Costantini F.,
RA "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RA pathway that regulates embryonic axis formation.";
RT Cell 90:181-192(1997).
RL
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B.
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX MAY ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN),
CC APC, DVL AND PP2A.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.

CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC
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CC
CC EMBL: AF009674; AAC51624.1; -
CC DR HSSP: P49799; IAGR.
CC DR MIM: 603816; -
CC DR InterPro: IPR000342; -
CC DR InterPro: IPR001158; -
CC DR Pfam: PF00615; RGS; 1.
CC DR Pfam: PF00778; DIX; 1.
CC DR PROSITE: PS50132; RGS; 1.
CC KW Developmental protein; Phosphorylation.
CC FT NON_TER 1 1
FT DOMAIN 125 248 RGS.
FT DOMAIN 385 470 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
FT DOMAIN SIMILARITY).
FT SEQUENCE 900 AA; 99803 MW; EE5F90B11FC7B3B CRC64;
SO
Query Match 31.5%; Score 113.5; DB 1; Length 900;
Best Local Similarity 34.4%; Pred. No. 8.4e-05;
Matches 33; Conservative 10; Mismatches 22; Indels 31; Gaps 3;
QY 3 REDEK-----EGSEALSSRDGAPVOHPALPLPS-----GSYEEDPQTILL 32
DB 440 REAEKLEERLKRVRMEEGEDGDPSSGPRPC-HKLPAPAMHHPRLCWTACAGLR 498
QY 33 GSYEEDPQTILLDHLRYLKTPTGCCSPGVGRYSPRS 68
DB 499 DAHENPESITIDEHYORVLRFTTGROSPGPHRSPDS 534
RESULT 11
EPLG_SCHPO STANDARD; PRT; 409 AA.
ID EPLG_SCHPO
AC P40921; O14005;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA).
GN TEF3 OR SPAC29A4.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 226-244.
RA STRAIN=972;
RA MEDLINE=94063505; PubMed=8244022;
RA Momoi H., Yamada H., Ueguchi C., Mizuno T.;
RA "Sequence of a fission yeast gene encoding a protein with extensive
RA homology to eukaryotic elongation factor-1 gamma.";
RT gene 134:119-122(1993).
RL
CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN ANCHORING THE COMPLEX TO OTHER
CC CELLULAR COMPONENTS.

CC -1 SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,
CC DELTA, AND GAMMA.
CC -1 SIMILARITY: TO OTHER SPECIES; GAMMA SUBUNIT AS WELL AS TO THE
CC N-TERMINAL OF SOME EUKARYOTIC AMINO ACID-TRNA SYNTHETASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D14606; BAA03456.1; -
DR EMBL: Z97210; CAB10129.1; -
DR PIR: J70764; J70764.
DR InterPro: IPR000521; -
DR InterPro: IPR001662; -
DR Pfam: PF00647; EF1G_domain.1.
DR Pfam: PF00043; GST.1.
DR PROSITE: PS50040; EF1G.1.
DR Elongation factor; Protein biosynthesis.
DR CONFLICT 246 R->A (IN REF. 2).
FT SEQUENCE 409 AA; 45786 MW; A49CB947A9F66DF0 CRC64;
SQ

Query Match 20.0%; Score 72; DB 1; Length 409;
Best Local Similarity 35.3%; Pred. No. 1.2;
Matches 12; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

3 REDEKESQALSRDQAPVQHPLALPSCSYE 36
DB 231 KDKKKKNAKPKPAERKPRKHPPLASPNGSFD 264

RESULT 12
ID FUR1_MOUSE STANDARD: PRT: 793 AA.
AC P23188;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FURIN PRECURSOR (EC 3.4.21.75) (PAIRED BASIC AMINO ACID RESIDUE
DE CLEAVING ENZYME) (PACE) (DIBASIC PROCESSING ENZYME).
GN FUR OR PCSK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91093035; PubMed=2266110;
RA Hatazawa K., Hosaka M., Nakagawa T., Nagase M., Shoda A.,
RA Murakami K., Nakayama K.;
RT "Structure and expression of mouse furin, a yeast Kex2-related
RT protease. Lack of processing of coexpressed prorenin in GH4C1
RT cells.";
RT J. Biol. Chem. 265:22075-22078(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Creemers J.W.M., Roebroek A.J.M., van den Ouweland A.M.W.,
RA van Duijnhoven H.L.P., van de Ven W.J.M.;
RT "Cloning and functional expression of a 4.3 kbp mouse fur cDNA:
RT evidence for differential expression.";
RT Life Sci. Adv. (Mol. Biol.) 11:127-138(1992).
CC -1 FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(R/R)R CONSENSUS MOTIF.
CC -1 CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTIC ACTIVITY: RELEASE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS. RELEASES ALBUMIN,
CC COMPLEMENT COMPONENT C3 AND VON WILLEBRAND FACTOR FROM THEIR

CC RESPECTIVE PRECURSORS.
CC -1 COFACTOR: CALCIUM-DEPENDENT (BY SIMILARITY).
CC -1 ENZYME REGULATION: COULD BE INHIBITED BY THE NOT SECONDLY CLEAVED
CC PROPEPTIDE.
CC -1 SUBCELLULAR LOCATION: SEEMS TO BE LOCALIZED INTRACELLULARLY TO THE
CC TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR
CC EXIT OF FURIN MOLECULES OUT OF THE ENDOPLASMIC RETICULUM (ER).
CC SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK
CC (TGN), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO
CC FURIN AND THE ACTIVATION OF FURIN.
CC -1 TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED UBIQUITOUSLY.
CC -1 DOMAIN: CONTAINS A HOMO B DOMAIN, ALSO KNOWN AS P OR MIDDLE DOMAIN
CC AND A SUBTILISIN-LIKE CATALYTIC DOMAIN. ESSENTIAL DOMAINS FOR
CC CATALYTIC ACTIVITY.
CC -1 DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN
CC LOCALIZATION AND RECYCLING FROM THE CELL SURFACE.
CC -1 PTM: THE PROPEPTIDE IS AUTOCATALYTICALLY REMOVED THROUGH AN
CC INTRAMOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULUM
CC (ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULD LEAD
CC TO THE ACTIVATION OF FURIN.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8, ALSO KNOWN AS THE
CC SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURIN-LIKE ENZYMES.
CC -----
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CC -----
DR EMBL: X54056; CAA37988.1; -
DR EMBL: U26489; AAA37643.1; -
DR PIR: A23679; KXMF.
DR HSP: O99405; IMPF.
DR MEROPS: S08_071; -
DR MGD: MGI:97513; PCSK3.
DR InterPro: IPR002029; -
DR InterPro: IPR002884; -
DR InterPro: IPR01483; P; 1.
DR Pfam: PF01483; P; 1.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
DR PROSITE: PS00139; SUBTILASE_TYR; 1.
KW Hydrolyase; Serine protease; Transmembrane; Glycoprotein; Signal;
KW Zymogen; Calcium.
FT SIGNAL 1 24
FT PROPEP 25 107
FT CHAIN 108 793
FT DOMAIN 356 705
FT TRANSMEM 715 735
FT ACT_SITE 153 153
FT ACT_SITE 194 194
FT ACT_SITE 368 368
FT DISULFID 211 360
FT DISULFID 303 333
FT CARBOHYD 387 387
FT CARBOHYD 440 440
FT CARBOHYD 553 553
FT SITE 70 75
FT SITE 104 107
FT SITE 758 761
FT SITE 772 778
FT SITE 498 500
FT SITE 746 746
FT CONFLICT 746 746
FT SEQUENCE 793 AA; 86804 MW; 5F121C3DE2E1A42D CRC64;
SQ

Query Match 19.7%; Score 71; DB 1; Length 793;
Best Local Similarity 40.0%; Pred. No. 3.2;
Matches 20; Conservative 3; Mismatches 27; Indels 0; Gaps 0;

OY 7 EKEGSEALSSRDGAPVQHPLALPPSGSYEEEDPQTLLDHLRLVLTGPG 56
 DB 672 EQGCSROSOSRESRPOQOPPALPEVEMERLQGLASHLEPVLAGLSC 721

RESULT 13
 PPAS_HUMAN STANDARD: PRT: 441 AA.

AC 003181;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA)
 DE (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NRC1) (NRC1)
 GN PPARB OR NR1C2 OR PPARB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93078797; PubMed=1333051;
 RA Schmidt A., Endo N., Rutledge S.J., Vogel R., Shinar D.,
 RA Rodan G.A.;
 RT "Identification of a new member of the steroid hormone receptor
 RT superfamily that is activated by a peroxisome proliferator and fatty
 RT acids."
 RL Mol. Endocrinol. 6:1634-1641(1992).
 CC -1- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
 CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
 CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
 CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE
 CC PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
 CC -1- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.

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 CC EMBL: L07592; AAA36469.1; -
 DR PIR: A45360; A45360.
 DR HSSP: P03372; IHCO.
 DR MIM: 600409; -
 DR InterPro: IPR0000536; -
 DR InterPro: IPR001628; -
 DR InterPro: IPR001723; -
 DR InterPro: IPR003074; -
 DR InterPro: IPR003075; -
 DR Pfam: PF00104; hormone_rec.1.
 DR Pfam: PF00105; zf-C4.1
 DR PRINTS: PR00047; STROIPDINGER.
 DR PRINTS: PR00398; STRDHOMONER.
 DR PRINTS: PR01288; PROXISOMPAR.
 DR PRINTS: PR01290; PROXISOMPAR.
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
 KW Receptor; Transcription regulation; Activator; DNA-binding;
 KW Nuclear protein; Zinc-finger; Multigene family
 FT DNA_BIND 74 138 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 74 94 C4-TYPE.
 FT ZN_FING 111 133 C4-TYPE.
 FT DOMAIN 254 441 LIGAND-BINDING (BY SIMILARITY).
 SO SEQUENCE 441 AA; 49903 MW; 94FBB2A4B46521E8 CRC64;

Query Match 19.0%; Score 68.5; DB 1; Length 441;
 Best Local Similarity 30.3%; Pred. No. 3.1;

Matches 23; Conservative 10; Mismatches 26; Indels 17; Gaps 4;
 OY 1 OIREDEKESGSEALSSRDGAPVQH--PLALLPPSGSYEE-----DPQTLLDHLRLVLTGPG 53
 DB 10 EVREDEKEEVAER-----EGAPELNGCPQHALLPSSSYTDLSSRSPSLDQ-----IQ 59

OY 54 PGCQSPGVGRYSPRSR 69
 DB 60 MCGDGCAGCSGLNMECR 75

RESULT 14
 Y888_METJA STANDARD: PRT: 206 AA.
 ID Y888_METJA
 AC 058298;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ0888.
 GN MJ0888.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SFRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervaege A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.J.,
 RA Kierulff R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RA jannaschii."
 RT Science 273:1058-1073(1996).
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: WEAK, TO B.SUBTILIS Y0GX AND TO M.JANNASCHII MJ0296.

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 CC EMBL: U67532; AAB98892.1; -
 DR TIGR: MJ0888; -
 DR InterPro: IPR001279; -
 DR Pfam: PF00753; lactamase_B.1.
 KW Hypothetical protein.
 SO SEQUENCE 206 AA; 23229 MW; AC2C59F1E80840E CRC64;

Query Match 18.9%; Score 68; DB 1; Length 206;
 Best Local Similarity 32.8%; Pred. No. 1.4;
 Matches 19; Conservative 10; Mismatches 21; Indels 8; Gaps 2;

OY 2 IREDEE---KEGSEALSSRDGAPVQHPLALPPSGSYEEEDPQTLLDHLRLVLTGPG 55
 DB 76 IIEDEKVEHLKNGDEVTVSSLGAKLNPKPKETIPLSEIEE---LKSIGLEITRTPG 129

RESULT 15
 FURL_RAT STANDARD: PRT: 793 AA.
 ID FURL_RAT
 AC P23377;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

Db 457 VGRYSPRSR 465

RESULT 2

ID 088566 PRELIMINARY; PRT: 840 AA.

AC 088566;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE CONDUCTIN.

GN AXIN2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98221239; PubMed=9554852;

RA Behrens J., Jerchow B.A., Wurtzle M., Grimm J., Asbrand C., Wirtz R.,
Kuhl M., Wedlich D., Birchmeier W.;

RT "Functional interaction of an axin homolog, conductin, with beta-

catenin, APC, and GSK3beta.";

RL Science 280:596-599(1998).

DR EMBL; AF073378; AAC26047.1; -

DR HSSP; P49799; IAGR.

DR MGD; MG1:1270862; Axin2.

DR INTERPRO; IPR000342; -

DR INTERPRO; IPR001158; -

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRODOM; PD001580; -; 1.

DR PRODOM; PD003639; -; 1.

SQ SEQUENCE 840 AA; 92934 MW; A07D5EB25DE7277 CRC64;

Query Match 100.0%; Score 360; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 5,5e-34;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIREDEKESQALSSRDGAPVQHPALILPSGSYEEDPQTILDDHLSRVLTPTGCSFG 60

DB 397 QIREDEKESQALSSRDGAPVQHPALILPSGSYEEDPQTILDDHLSRVLTPTGCSFG 456

QY 61 VGRYSPRSR 69

DB 457 VGRYSPRSR 465

RESULT 3

ID 090XJ6 PRELIMINARY; PRT: 840 AA.

AC 090XJ6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE AXIN2.

GN AXIN2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation.";

RL Submitted (NOV-1999) to the EMBL/genbank/DBJ databases.

DR EMBL; AF205889; AAF22800.1; -

DR HSSP; P49799; IAGR.

DR INTERPRO; IPR000342; -

DR INTERPRO; IPR001158; -
DR PFAM; PF00615; RGS; 1.
DR PFAM; PF00778; DIX; 1.
DR PRINTS; PRO1301; RGSPTROTIN.
DR SEQUENCE 840 AA; 92896 MW; 767D546B43C921C5 CRC64;

Query Match 100.0%; Score 360; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 5,5e-34;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIREDEKESQALSSRDGAPVQHPALILPSGSYEEDPQTILDDHLSRVLTPTGCSFG 60

DB 397 QIREDEKESQALSSRDGAPVQHPALILPSGSYEEDPQTILDDHLSRVLTPTGCSFG 456

QY 61 VGRYSPRSR 69

DB 457 VGRYSPRSR 465

RESULT 4

ID 090UH4 PRELIMINARY; PRT: 777 AA.

AC 090UH4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE AXIN2.

GN AXIN2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE-BRAIN; LYMPHOBLAST;

RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation.";

RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF205888; AAF22799.1; -

DR HSSP; P49799; IAGR.

DR INTERPRO; IPR000342; -

DR INTERPRO; IPR001158; -

DR PFAM; PF00615; RGS; 1.

DR PFAM; PF00778; DIX; 1.

DR PRINTS; PRO1301; RGSPTROTIN.

SQ SEQUENCE 777 AA; 86857 MW; 3A4943ABF430BBD3 CRC64;

Query Match 92.2%; Score 332; DB 4; Length 777;

Best Local Similarity 89.9%; Pred. No. 9,8e-31;

Matches 62; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QIREDEKESQALSSRDGAPVQHPALILPSGSYEEDPQTILDDHLSRVLTPTGCSFG 60

DB 396 QIREDEKESQALSSRDGAPVQHPALILPSGSYEEDPQTILDDHLSRVLTPTGCSFG 455

QY 61 VGRYSPRSR 69

DB 456 VGRYSPRSR 464

RESULT 5

ID 09Y2T1 PRELIMINARY; PRT: 843 AA.

AC 09Y2T1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE CONDUCTIN.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99168905; PubMed=10049590;
 RX Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
 RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
 RT chromosome 17q23-q24."
 RL Genomics 55:341-344(1999).
 DR EMBL: AF078165; AAD20976.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -
 DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 SO SEQUENCE 843 AA; 93557 MW; F7B62BBD6A84664D CRC64;

Query Match 92.2%; Score 332; DB 4; Length 843;
 Best Local Similarity 89.9%; Pred. No. 1,1e-30;

Matches 62; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 QREDEKESGQALSSRDGAPVQHPLALPSSGYEDPQTILDDHLSRVLTGCGSPG 60
 DB 397 QREDEKESGQALSSRDGAPVQHPLALPSSGYEDPQTILDDHLSRVLTGCGSPG 456
 OY 61 VGRYSPRSR 69
 DB 457 VGRYSPRSR 465

RESULT 6
 OYGYO PRELIMINARY; PRT; 842 AA.

AC OYGYO;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE AXIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99173782; PubMed=10072781;
 RX Hedgepeth C.M., Deardorff M.A., Klein P.S.;
 RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
 RT expressed in the anterior midbrain."
 RL Mech. Dev. 80:147-151(1999).
 DR EMBL: AF097313; AAC71036.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -
 DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoae; Pipidae;
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRODOM: PD001580; -; 1.
 DR PRODOM: PD003639; -; 1.
 SO SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 43.9%; Score 158; DB 13; Length 842;
 Best Local Similarity 40.0%; Pred. No. 3e-10;

Matches 34; Conservative 14; Mismatches 11; Indels 26; Gaps 3;

OY 7 EKSGSQAALSSRDGAPVQHPLALPSSGYEDPQTILDDHLSRVLTGCGSPG 44
 DB 419 EKSGSQAALSSRDGAPVQHPLALPSSGYEDPQTILDDHLSRVLTGCGSPG 474
 OY 45 DHSRLVLTGCGSPGVRSPRSR 69

DB 475 EHYQVRVMTKTPGCGSPGVRSPRSR 499

RESULT 7
 ID 042400 PRELIMINARY; PRT; 841 AA.

AC 042400;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE AXIN.
 GN AXIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Fogotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,
 RA Ili Lee J., Tilghman S.M., Gumbiner B.M., Constantini F.;
 RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation."
 RL Cell 90:181-192(1997).
 DR EMBL: AF009012; AAC60245.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -
 DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRODOM: PD001580; -; 1.
 DR PRODOM: PD003639; -; 1.
 SO SEQUENCE 841 AA; 94931 MW; 40DDC90E72506FE CRC64;

Query Match 40.6%; Score 146; DB 13; Length 841;
 Best Local Similarity 34.7%; Pred. No. 7.7e-09;

Matches 35; Conservative 14; Mismatches 14; Indels 38; Gaps 4;

OY 3 REDEKESGQALSSRDGAPVQHPLALPSSGYEDPQTILDDHLSRVLTGCGSPG 33
 DB 403 REDEKESGQALSSRDGAPVQHPLALPSSGYEDPQTILDDHLSRVLTGCGSPG 458
 OY 34 -----SYEDPQTILDDHLSRVLTGCGSPGVRSPRSR 69
 DB 459 MQRDAHEENPESILDEHYQVRVMTKTPGCGSPGVRSPRSR 499

RESULT 8
 ID 070239 PRELIMINARY; PRT; 832 AA.

AC 070239;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE RAXIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98151361; PubMed=9482734;
 RX Ikeda S., Yamamoto H., Murali H., Kishida S., Kikuchi A.;
 RT "Axin, a negative regulator of the Wnt signaling pathway, forms a
 RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
 RT dependent phosphorylation of beta-catenin."
 RL EMBL: JF.17:1371-1384(1998).
 DR EMBL: AF017756; AAC40066.1; -
 DR HSSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -

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DR INTERPRO: IPR001158;
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001360; -. 1.
DR PRODOM: PD003639; -. 1.
SQ SEQUENCE 832 AA; 92856 MW; B489504C7E594347 CRC64;

Query Match
Best Local Similarity 35.3%; Pred. No. 4,4e-08;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIRDEKEGSEQALSSRDGAPVOHPALPLPS-----GSYEDPOTIL 43
DB 420 RVRMEEGEDDEMP-----SGPMASHKLPSPVAMNHPPRYVMGCGSLRDHAHEENPESIL 475
OY 44 DDHLSRYLKTGCGSPGVGRYSPRS 68
DB 476 DEHVORVMRTGCGSPGVGRYSPRS 500

RESULT 9
ID 035625 PRELIMINARY; PRT: 992 AA.
AC 035625;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RX Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009011; AAC53285.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1096327; Axin.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PRO1301; RGSPROTEIN.
DR NON_TER 1
FT SEQUENCE 992 AA; 109917 MW; 70EEB53D387BD26F CRC64;
SQ

Query Match
Best Local Similarity 38.8%; Score 139.5; DB 11; Length 992;
Matches 30; Conservative 14; Mismatches 20; Indels 21; Gaps 2;

OY 1 QIRDEKEGSEQALSSRDGAPVOHPALPLPS-----GSYEDPOTIL 43
DB 544 RVRMEEGEDDEMP-----SGPMASHKLPSPVAMNHPPRYVMGCGSLRDHAHEENPESIL 599
OY 44 DDHLSRYLKTGCGSPGVGRYSPRS 68
DB 600 DEHVORVMRTGCGSPGVGRYSPRS 624

RESULT 10
ID 015169 PRELIMINARY; PRT: 900 AA.
AC 015169;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

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DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RX Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
DR EMBL: AF009674; AAC51624.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PRO1301; RGSPROTEIN.
DR NON_TER 1
FT SEQUENCE 900 AA; 99803 MW; EE5F90B11FC7B3B CRC64;
SQ

Query Match
Best Local Similarity 31.5%; Score 113.5; DB 4; Length 900;
Matches 33; Conservative 10; Mismatches 22; Indels 31; Gaps 3;

OY 3 REDEEK-----EGSEQALSSRDGAPVOHPALPLPS----- 32
DB 440 REAEKLEERLKRVRMEEGEDGDPSSGPPGPGC-HKLRPRAMHPPRLCWTACAGLR 498
OY 33 GSYEDPOTILDDHLSRYLKTGCGSPGVGRYSPRS 68
DB 499 DAHEENPESILDEHVORVRLRTGCGSPGVGRYSPRS 534

RESULT 11
ID 09PTP2 PRELIMINARY; PRT: 706 AA.
AC 09PTP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AXIN-RELATED PROTEIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=OVARY;
RX Itoh K., Antipova A., Ratcliffe M., Sokol S.;
RT "Dishevelled transduces a signal by displacing GSK3 from axin-GSK3
RT complex.";
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF140243; AA022574.1; -.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PRO1301; RGSPROTEIN.
DR NON_TER 1
FT SEQUENCE 706 AA; 79196 MW; C3D0AF0D9540F162 CRC64;
SQ

Query Match
Best Local Similarity 31.2%; Score 112.5; DB 13; Length 706;
Matches 28; Conservative 13; Mismatches 16; Indels 17; Gaps 3;

OY 1 QIRDEKEGSEQALSSRDGAPVOHPALPLPSGSYEDPOTILDDHLSRYLKTG----- 55

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DB 357 RUKKEEELADVDIPSSHE-----TVPQALEDDPQSLDDHVSRLKTPANLSPR 407
 OY 56 COSPGV---GRYSP 66
 DB 408 SOSPFVORKKFP 421

RESULT 12

0918W3 PRELIMINARY: PRT: 443 AA.

AC 0918W3: PRELIMINARY: PRT: 443 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR BETA.
 GN PPARBETA.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20267232; PubMed=10809235;
 RA Takada I., Yu R.T., Xu H.E., Lambert M.H., Montana V.G., Klierer S.A.,
 RA Evans R.M., Umesono K.;
 RT "Alteration of a single amino acid in peroxisome proliferator-
 activated receptor-alpha (PPAR alpha) generates a PPAR delta
 phenotype.";
 RT Mol. Endocrinol. 14:733-740(2000).
 DR EMBL: AF163810; AAF80480.1;
 KW Receptor.
 SQ SEQUENCE 443 AA; 50108 MW; EB6E0C39554C76CD CRC64;

Query Match 19.4%; Score 70; DB 13; Length 443;
 Best Local Similarity 32.4%; Pred. No. 3.2;
 Matches 24; Conservative 12; Mismatches 26; Indels 12; Gaps 4;

OY 1 QIREDEKESQALSSRDG--PVQHPALALPSGSYEEDPQT---LDDHLSRVLKTPG 55
 DB 10 EYREEEEEE--EEAVTVSGASDPSPSSSLPSSSYTDLSSQSSPSLSLQIQM-----G 62
 OY 56 COSPGVGRYSPRSR 69
 DB 63 CEETASGALNVECR 76

RESULT 13

09JUL71 PRELIMINARY: PRT: 1098 AA.

AC 09JUL71: PRELIMINARY: PRT: 1098 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TEASHIRT 2 (FRAGMENT).
 GN TSH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Caudit X., Core N., Boned A., Kerridge S., Djabali M., Fasano L.;
 RT "vertebrate orthologues of the Drosophila region-specific patterning
 gene teashirt.";
 RT Mech. Dev. 91:445-448(2000).
 DR EMBL: AF207880; AAF64095.1;
 FT NON_TER 1
 FT NON_TER 1098
 SQ SEQUENCE 1098 AA; 121367 MW; 42BA01C7DB2BAFEB CRC64;

Query Match 18.8%; Score 67.5; DB 11; Length 1098;
 Best Local Similarity 35.0%; Pred. No. 17;
 Matches 21; Conservative 11; Mismatches 23; Indels 5; Gaps 3;

OY 4 EDEKEGSEQALSSRDG-APVQHPALALPSGSYEEDPQTILDDHLSRV---LKTPEGCOSP 59
 DB 726 OKEKEPELEPVSLTNGCAPANHTPA-LPSINPLSALQSVLNNHILGKATEPLRSPSCSSP 784

RESULT 14

029576 PRELIMINARY: PRT: 563 AA.

AC 029576: PRELIMINARY: PRT: 563 AA.
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE SUCCINATE DEHYDROGENASE, FLAVOPROTEIN SUBUNIT A (SDHA).
 GN AF0681.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 NC NCB1_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrtides N.C.,
 RA Fleischmann D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirschner S., Rench C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RT Nature 390:364-370(1997).
 RL EMBL: AE001057; AAB90557.1;
 DR HSSP: P00363; 1FUM.
 DR TIGR: AF0681;
 DR INTERPRO: IPR000464;
 DR INTERPRO: IPR001005;
 DR PFAM: PF00890; FAD_Binding_2; 1.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 563 AA; 63189 MW; 7F2B932DFD242311 CRC64;

Query Match 18.3%; Score 66; DB 1; Length 563;
 Best Local Similarity 25.3%; Pred. No. 12;
 Matches 19; Conservative 10; Mismatches 12; Indels 34; Gaps 3;

OY 10 GSEQALSSRDGAPVQ-----HPLALPLPSGSYEEDPQTILDDHLSRVLKTCGQSPG--- 60
 DB 208 GGLAIAYRNGIPLKDMFEQFHPGLVPSG-----ILMTSCRGEGGY 251
 OY 61 -----VGRYSP 66
 DB 252 LUNKGERFMKRYAP 266

RESULT 15

09JUL71 PRELIMINARY: PRT: 679 AA.

AC 09JUL71: PRELIMINARY: PRT: 679 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 73.8 KDA PROTEIN.
 GN L7836.04.

OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Oliver K., Harris D., Ivens A.C., Lawson D., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.E.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-143(1998).
DR EMBL; AL117263; CAB55379.1; -.
KM Hypothetical protein.
SQ SEQUENCE 679 AA; 73834 MW; 1FCDF361BD81243E CRC64;

Query Match 18.28; Score 65.5; DB 5; Length 679;
Best Local Similarity 39.38; Pred. No. 18;
Matches 17; Conservative 6; Mismatches 13; Indels 7; Gaps 2;
QY 11 SEQALSRDGA-PVOHPLAL-----PSGSYEEDPQTIIDH 46
DB 129 SEPAPAAATGAQPRRRGLAMLNIAIRKHPEGSTIEQGVVTEKH 171

Search completed: June 7, 2001, 02:09:43
Job time: 446 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:01:18 ; Search time 80.96 Seconds
(without alignments)
36.009 Million cell updates/sec

Title: US-09-587-574-5

Perfect score: 276
Sequence: 1 LTLGHFKKQLSKGNRYRF.....VFEELMDETVLPMEGRIL 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : A_Geneseq_0401.*
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
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18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.*
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20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	276	100.0	840	20	W93570 Human conductin pr
2	276	100.0	840	20	W93569 Human conductin pr
3	191	69.2	900	20	W96264 Human axin. Homo
4	190	68.8	992	20	W96265 Murine axin. Mus
5	61	22.1	601	21	Y90851 Castor bean casden
6	56.5	20.5	1018	21	B01769 Simian immunodef
7	55.5	20.1	301	21	G13112 Arabidopsis thalia
8	55.5	20.1	391	21	G13111 Arabidopsis thalia
9	55.5	20.1	394	21	G13110 Arabidopsis thalia
10	55.5	20.1	975	21	G45799 Arabidopsis thalia
11	54.5	19.7	566	17	W04271 B.L. neutral prote

12	54.5	19.7	594	21	G43722 Arabidopsis thalia
13	54.5	19.7	615	21	G43721 Arabidopsis thalia
14	54.5	19.7	699	21	G43720 Arabidopsis thalia
15	54	19.6	1036	13	R20599 ROD HIV-2 polymera
16	54	19.6	1055	18	W13055 HIV-2 provirus-enc
17	53.5	19.4	314	10	P93143 Sequence encoded b
18	53.5	19.4	594	21	G47035 Arabidopsis thalia
19	53.5	19.4	594	21	G47041 Arabidopsis thalia
20	53.5	19.4	615	21	G47034 Arabidopsis thalia
21	53.5	19.4	615	21	G47040 Arabidopsis thalia
22	53.5	19.4	699	21	G47033 Arabidopsis thalia
23	53.5	19.4	699	21	G47039 Arabidopsis thalia
24	53	19.2	309	16	R70909 Human melanoma ant
25	53	19.2	309	20	W81548 Tumour rejection a
26	53	19.2	445	20	Y06592 CLTFA-MAGE-1-HIS f
27	53	19.2	446	20	Y06590 Lipoprotein D-MAGE
28	52.5	19.2	1332	20	Y01084 Human IKAP protein
29	52.5	19.0	158	21	B01778 Simian immunodef
30	52.5	19.0	329	18	W11328 Bacillus subtilis
31	52.5	19.0	616	21	G39767 Arabidopsis thalia
32	52.5	19.0	700	21	G39766 Arabidopsis thalia
33	52.5	19.0	704	21	Y77930 A. thaliana enviro
34	52.5	19.0	705	21	G39765 Arabidopsis thalia
35	52	18.8	995	20	Y04658 L.lactis HsdR subu
36	52	18.8	1337	16	R85203 huDHP-1. Homo sep
37	52	18.8	3080	10	P93285 Sequence of clone
38	52	18.8	3210	9	P81771 Deduced sequence e
39	51.5	18.7	151	19	W70219 Leishmania antigen
40	51.5	18.7	501	12	R14372 Tomato endo-1,4-B-
41	51.5	18.7	501	17	R89278 CM-cellulase. Lyc
42	51.5	18.7	620	14	R32548 Tomato hsp80. Lyc
43	51.5	18.7	659	14	R32549 Pol gene of simian
44	51.5	18.7	1061	11	R04192 Pinosylvine syntha
45	51	18.5	190	14	R33698

ALIGNMENTS

RESULT 1	
W93570	W93570 standard; Protein: 840 AA.
XX	
AC	W93570;
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human conductin protein.
XX	
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polyposis Coll.; APC;
KW	tumour suppressor.
XX	
OS	Homo sapiens.
XX	
PN	W09911780-A2.
XX	
PD	11-MAR-1999.
XX	
PF	01-SEP-1998; 98WO-DE02621.
XX	
PR	02-SEP-1997; 97DE-1038205.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Behrens J, Birchmeier W;
XX	
DR	WPI; 1999-214706/18.
XX	
DR	N-PDB; X23370.
XX	
PT	Tumor-suppressing protein conductin - used for treatment and
	diagnosis of tumors

XX Claim 11: Fig 3: 22pp; German.

CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 XX
 XX Sequence 840 AA:

Query Match 100.0%; Score 276; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2.7e-29;
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OY 1 LTLGHFKQLSKNGNYRYFFKKASDFACGAVFEIIMDETVLPMEGRIL 51
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 DB 783 ltlghfkqlskngnyryffkkasdefacgavfeiwdeivlpmyegrll 833

RESULT 2
 ID W93569 standard; Protein; 840 AA.

XX W93569;

DT 17-JUN-1999 (first entry)

DE Human conductin protein.

XX Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
 KW therapy; cytoplasmic degradation; blockade; wnt signalling pathway;
 KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
 KW tumour suppressor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 78..200 /note= "Regulator of G protein signalling domain as

FT Binding-site 343..396 described in claim 12"

FT /note= "GSK 3-beta binding region as described in

FT Binding-site 397..465 claim 13"

FT /note= "Beta-catenin binding domain as described in

FT Region 783..833 claim 14"

FT /note= "Dishevelled homology region as described in

FT Claim 15"

XX WO9911780-A2.

XX 11-MAR-1999.

XX 01-SEP-1998; 98WO-DE02621.

XX 02-SEP-1997; 97DE-1038205.

XX (DEIB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Behrens J, Birchmeier W;

XX WPI: 1999-214706/18.

XX N-PSDB; X23369.

XX Tumor-suppressing protein conductin - used for treatment and

XX diagnosis of tumors

PS Claim 11: Fig 1: 22pp; German.

CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 XX
 XX Sequence 840 AA:

Query Match 100.0%; Score 276; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2.7e-29;
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OY 1 LTLGHFKQLSKNGNYRYFFKKASDFACGAVFEIIMDETVLPMEGRIL 51
 |||||
 DB 783 ltlghfkqlskngnyryffkkasdefacgavfeiwdeivlpmyegrll 833

RESULT 3
 ID W96264 standard; Protein; 900 AA.

XX W96264;

DT 14-JUN-1999 (first entry)

DE Human axlin.

XX Axlin; cancer; breast cancer; colorectal cancer;
 KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin.

XX Homo sapiens.

XX WO9902179-A1.

XX 21-JAN-1999.

XX 09-JUL-1998; 98WO-US14414.

XX 10-JUL-1997; 97US-0890865.

XX (UNCO) UNIV COLUMBIA NEW YORK.

XX Constantini F, Zeng L;

XX WPI: 1999-120510/10.

XX N-PSDB; X09012.

XX Newly isolated nucleic acid encoding "axis inhibition" protein

XX (Axlin) - useful for detecting, diagnosing and treating cancer

XX Disclosure: Figure 11; 95pp; English.

XX Nucleic acids encoding mutant and wild type Axlin and

XX oligonucleotides derived from them are useful for detecting

XX mutations in the Axlin gene and for determining whether a subject is

XX likely to develop cancer (including breast, colorectal). The wild

XX type Axlin and homologues of Axlin are useful for treating subjects

XX who are likely to develop cancer (thyroid carcinomas). The nucleic

XX acids are also useful for diagnosing cancer and for detecting

XX mutations in cancerous cells. Wild type Axlin, its antisense

XX molecule and identified compounds form pharmaceutical compositions

XX in the treatment of cancer. The compositions are also useful for

XX treating cancer by inhibiting tumorigenesis (by inducing degradation

XX of beta-catenin). The nucleic acid encoding Axlin acts through

Query Match 22.1%; Score: 61; DB 21; Length 601;
Best Local Similarity 29.2%; Pred. No. 5.4;
Matches 14; Conservative 12; Mismatches 20; Indels 2; Gaps 2;

OY 2 TLGHRKQLSKKG-NYR-YFKRASDEPACGAFEEIMDETVLPMYE 47
DB 399 ttfetektlaegksyvkvgreatqelrvyyleavwvdegkipsfd 446

RESULT 6
B01769
ID B01769 standard; Protein: 1018 AA.
XX B01769;
AC B01769;
DE 03-JAN-2001 (first entry)
XX
XX Simian immunodeficiency virus SIVrcm Pol protein #1.
DE
XX Red capped monkey; simian immunodeficiency virus; SIV; SIVrcm;
KW vaccination; Pol protein.
XX
OS Simian immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 569 /note="encoded by GACTMA"
FT
XX WO200034529-A1.
XX
XX 15-JUN-2000.
XX
XX 03-DEC-1999; 99WO-US28638.
XX
XX 07-DEC-1998; 98US-0206551.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Hahn BH, Shaw GM, Gao F, Marx PA, Smith SM, Georges-Courbot MC;
PI Lu CY;
XX
XX WPI: 2000-423454/36.
XX
XX N-PSDB: A51008.
XX
XX B01775, B01776.
XX
XX New polypeptide, useful for producing antibodies and for diagnosis of
PT simian viral infection in humans comprises complete genome of new
PT simian immunodeficiency virus isolate -
XX
PS Disclosure: Page 152-156; 173pp; English.
XX
XX The present sequence is the Pol protein from the simian immunodeficiency
CC virus found in the red capped mangabey and designated SIVrcm. This virus
CC is related to the HIV viruses that cause AIDS in humans. Knowing the
CC sequence of the Pol protein and its gene is useful as it enables
CC screening of the Pol protein to take place in humans and animals (there is a
CC possibility that this virus undergoes cross-species transmission), allows
CC vaccines to be produced and aids research into the origin of these
CC viruses. This latter is important if an AIDS vaccine is to be found.
XX
SQ Sequence 1018 AA;

Query Match 20.5%; Score 56.5; DB 21; Length 1018;
Best Local Similarity 24.2%; Pred. No. 43;
Matches 15; Conservative 12; Mismatches 24; Indels 11; Gaps 1;

OY 1 LTLGHRKQLSKKG-NYR-YFKRASDEPACG-----AFEEIMDETVLPMYEGR 49
DB 936 latnklqgisklqifrvyregtdqlwrpakiikwkgavvigeetgdlkvvprtkak 995

OY 50 IL 51
DB 996 IL 997

RESULT 7
G13112
ID G13112 standard; Protein: 301 AA.
XX
XX G13112;
AC
XX
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SpQ ID NO: 12483.
XX
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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XX 05-MAR-1999; 99US-0123180.
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XX 09-MAR-1999; 99US-0123548.
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XX 23-MAR-1999; 99US-0125788.
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XX 25-MAR-1999; 99US-0126264.
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XX 29-MAR-1999; 99US-0126785.
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PR 18-JUN-1999; 99US-0139463.
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PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
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PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
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PR 14-JUL-1999; 99US-0143624.
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PR 16-JUL-1999; 99US-0144085.
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PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
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PR 23-JUL-1999; 99US-0145192.
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PR 23-JUL-1999; 99US-0145224.
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PR 27-JUL-1999; 99US-0145913.
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PR 09-AUG-1999; 99US-0147493.
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PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 20.1%; Score 55.5; DB 21; Length 301;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 13; Conservative 8; Mismatches 11; Indels 7; Gaps 1;

QY 1 LTLGHFEOLSKKGNRYXFKKASDEFACGAVFEIWD 39
Db 37 ltmgnhelnmiedgdiryvtkgleef-----qlvad 68
RESULT 8
G13111

ID G3111 standard; Protein; 391 AA.
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AC
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XX Arabidopsis thaliana.
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XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SRO ID NO: 54681.

XX Protein identification: signal transduction pathway; metabolic pathway;

KM hybridisation assay; genetic mapping; gene expression control; promoter;

KM termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

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XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 54680.
XX KM Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PE 25-FEB-2000; 2000EP-0301439.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143342.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161921.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161923.
 PR 29-OCT-1999; 99US-0162142.

Query Match 19.7%; Score 54.5; DB 21; Length 699;
 Best Local Similarity 34.8%; Pred. No. 51;

Matches 16; Conservative 5; Mismatches 14; Indels 11; Gaps 1;

Oy 6 PKEQLSKKGNRYFFKKASDEFACGAVFEIWDDETVLPMYEGRL 51
 Db 478 fleklkkkyevlymwdaldehyagqlke-----fegkkl 512

RESULT 15

R20599
 ID R20599 standard; Protein; 1036 AA.

XX AC R20599;

DT 19-MAY-1992 (first entry)

DE ROD HIV-2 polymerase.

XX KW Human Immunodeficiency virus; AIDS.

OS Human Immunodeficiency virus-2 ROD isolate.

XX PN US50793342-A.

XX PD 07-JAN-1992.

XX PE 11-FEB-1987; 87US-0013477.

XX PR 11-FEB-1987; 87US-0013477.

XX PA (INSP) INST PASTEUR.

XX PI Allison M, Montagnier L, Gautard D, Clavel F, Sonigo P, Guyader M;

XX DR WPI: 1992-041067/05.

XX DR N-PSDB: Q20616.

XX PT Peptide(s) corresp. to HIV-2 amino acid sequences - used in

XX PT diagnosis in vaccines and in prodn. of antibodies for diagnosis

XX PS Disclosure: Page 13; 30pp; English.

XX CC The amino acid sequence is that of a polymerase from the ROD HIV-2

XX CC isolate, it is encoded by nucleotides 1829-4936. See also R20596-

XX CC R20596-R20608 and R22745-R22749.

XX SQ Sequence 1036 AA;

Query Match 19.6%; Score 54; DB 13; Length 1036;
 Best Local Similarity 25.5%; Pred. No. 96;
 Matches 13; Conservative 12; Mismatches 16; Indels 10; Gaps 1;
 Oy 11 SKKGNRYFFKKASDEF-----ACGAVFEIWDDETVLPMYEGRL 51
 Db 961 sklkdfryfregtdqlwkpgsllwkggavlvkvgtdiklilprkakll 1011

Search completed: June 7, 2001, 02:01:19
 Job time: 5661 sec

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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:02:11 ; Search time 40.76 Seconds

(without alignments)
24.037 Million cell updates/sec

Title: US-09-587-574-5

Perfect score: 276

Sequence: 1 LRLGHKEQLSKGNRYRYF.....VFEEIMDERVLPWYEGRL 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 1921087 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA:*

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- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCRU.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	19.9	1055	2	US-08-659-251-5
2	55	19.9	1055	5	PCR-US96-11445-5
3	54.5	19.7	566	1	US-08-415-823-4
4	54.5	19.7	566	2	US-09-086-662-4
5	53	19.2	309	1	US-08-465-167A-24
6	53	19.2	309	2	US-08-993-118-10
7	53	19.2	309	3	US-08-845-528C-10
8	53	19.2	1332	2	US-08-971-244-2
9	53	19.2	1332	4	US-09-286-891-2
10	52.5	19.0	477	2	US-08-432-016-3
11	52.5	19.0	477	2	US-08-684-594-3
12	52	18.8	1337	4	US-08-854-585-2
13	52	18.8	1337	5	PCR-US95-05512-2
14	52	18.8	3080	6	523423-4
15	51.5	18.7	501	1	US-07-687-466B-2
16	51.5	18.7	501	1	US-08-434-702-2
17	51.5	18.7	501	6	5168064-4
18	51.5	18.7	501	6	5168064-4
19	50.5	18.3	328	3	US-08-826-611-6
20	50	18.1	236	1	US-08-307-499-28
21	50	18.1	314	2	US-08-928-615-2
22	49.5	17.9	3174	2	US-08-477-451-3
23	48.5	17.6	166	3	US-08-765-381-4
24	48.5	17.6	1069	1	US-07-777-715-9
25	48.5	17.6	1069	1	US-08-170-126-4
26	48.5	17.6	1069	3	US-08-954-418-4
27	48	17.4	250	1	US-08-144-121-7

28	48	17.4	250	2	US-08-460-309-7	Sequence 7, Appl
29	48	17.4	250	2	US-08-125-077-7	Sequence 7, Appl
30	48	17.4	250	2	US-08-735-893-7	Sequence 19, Appl
31	47.5	17.2	187	1	US-08-644-664B-19	Sequence 19, Appl
32	47.5	17.2	187	2	US-08-761-277A-19	Sequence 19, Appl
33	47.5	17.2	187	5	PCR-US94-00658-3	Sequence 2, Appl
34	47.5	17.2	193	1	US-08-192-479-2	Sequence 2, Appl
35	47.5	17.2	193	1	US-08-637-508-2	Sequence 2, Appl
36	47.5	17.2	193	1	US-08-417-791-2	Sequence 2, Appl
37	47.5	17.2	193	5	PCR-US96-04546-2	Sequence 2, Appl
38	47.5	17.2	368	4	US-09-433-428D-58	Sequence 58, Appl
39	47.5	17.2	439	4	US-09-433-428D-57	Sequence 57, Appl
40	47.5	17.2	471	1	US-08-257-341-9	Sequence 9, Appl
41	47.5	17.2	524	4	US-08-557-210A-3	Sequence 3, Appl
42	47.5	17.2	539	4	US-08-557-210A-4	Sequence 4, Appl
43	47.5	17.2	539	4	US-08-557-210A-5	Sequence 5, Appl
44	47	17.0	518	4	US-09-113-309-19	Sequence 19, Appl
45	47	17.0	914	1	US-08-484-105-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-659-251-5

Sequence 5, Application US/08659251

Patent No. 5883081

GENERAL INFORMATION:

APPLICANT: Kraus, Guenter

APPLICANT: Wong-Staal, Flossie

APPLICANT: Talbot, Randy

APPLICANT: Poeschla, Eric

TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Provirus

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659,251

FILING DATE: No. 5883081 yet assigned

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 60/001,441

FILING DATE: 26-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Wackowski, Eugenia

REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 02307E-0564100S

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1055 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1055

OTHER INFORMATION: /note="pol protein encoded by HIV-2KR"

US-08-659-251-5

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-662-4

Query Match 19.7%; Score 54.5; DB 2; Length 566;
Best Local Similarity 38.5%; Pred. No. 11;
Matches 15; Conservative 5; Mismatches 16; Indels 3; Gaps 1;

OY 13 KGNRYRFRKASDEFACGAVEEIMDETLPV---YEG 48
DB 72 KGDYKIGKSAQDSFKVKQKADVTSTVYRQGVYEG 110

RESULT 5

US-08-465-167A-24
Sequence 24, Application US/08465167A
Patent No. 5750395

GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-24

Query Match 19.2%; Score 53; DB 1; Length 309;
Best Local Similarity 50.0%; Pred. No. 8.9;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 34 EIMDETLPVMEGR 49
DB 212 EIMWELSVMEYDGR 227

RESULT 6

US-08-993-118-10

Sequence 10, Application US/08993118
Patent No. 5997872

GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMET, Charles;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528
FILING DATE: April 25, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 309
TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-993-118-10

Query Match 19.2%; Score 53; DB 2; Length 309;
Best Local Similarity 50.0%; Pred. No. 8.9;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 34 EIMDETLPVMEGR 49
DB 212 EIMWELSVMEYDGR 227

RESULT 7

US-08-845-528C-10
Sequence 10, Application US/08845528C
Patent No. 6027924

GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMET, Charles;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-854-585-2

Query Match 18.8%; Score 52; DB 4; Length 1337;
Best Local Similarity 36.4%; Pred. No. 74;
Matches 12; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

OY 7 KEOLSKKGNRYRYFFKKASDFACGAVFEIIMDD 39
DB 1017 KSKLIRVENFEAFYFKKQADSNCG--FAFEYED 1047

RESULT 13
PCT-US95-05512-2
; Sequence 2, Application PC/TUS9505512

; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K. and Stman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine
; TITLE OF INVENTION: Phosphatase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 233 South Wacker Drive, Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05512
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27866/31954
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-05512-2

Query Match 18.8%; Score 52; DB 5; Length 1337;
Best Local Similarity 36.4%; Pred. No. 74;
Matches 12; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

OY 7 KEOLSKKGNRYRYFFKKASDFACGAVFEIIMDD 39
DB 1017 KSKLIRVENFEAFYFKKQADSNCG--FAFEYED 1047

RESULT 14
523423-4
; Patent No. 523423
; APPLICANT: FRANCHINI, GENOVEFRA;WONG-STAL, FLOSSIE;
; GALLO, ROBERT

TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/15
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/331,212
; FILING DATE: 03-31-1989
; SEQ ID NO:4
; LENGTH: 3080
523423-4

Query Match 18.8%; Score 52; DB 6; Length 3080;
Best Local Similarity 25.5%; Pred. No. 2e+02;
Matches 13; Conservative 11; Mismatches 17; Indels 10; Gaps 1;

OY 11 SKKGNRYRYFFKKASDFE-----ACGAVFEIIMDETLYPMYEGRI 51
DB 1543 SKLKNFRYFREGRNQWOGGELMKDGAIVYVGIDIVIPRKAKTI 1593

RESULT 15
US-07-687-466B-2
; Sequence 2, Application US/07687466B

; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: Endo-1,4-Beta-Glucanase Genes and
; TITLE OF INVENTION: Their Use in Plants
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin L. Bastian
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/687,466B
; FILING DATE: 19910418
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 2307-304-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-687-466B-2

Query Match 18.7%; Score 51.5; DB 1; Length 501;
Best Local Similarity 46.4%; Pred. No. 26;
Matches 13; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

OY 7 KEOLSKKGNRYRYFFKKASDFACGAVFE 34
DB 282 KEYLNGKSNLE-KFKKADSFICGLMPE 308

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Job time: 5406 sec

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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:03:24 ; Search time 56.43 seconds
(without alignments)
62.110 Million cell updates/sec

Title: US-09-587-574-5

Perfect score: 276
Sequence: 1 LTLGHFKKQSKKGNRYRFF.....VFEEIMDETVLPMTYEGRTL 51

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Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.67.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	838	2 T08423	Axin homolog Ax1
2	190	68.8	832	2 T08422	negative regulator
3	109.5	39.7	623	2 A49840	segment polarity p
4	95.5	34.6	716	2 JCS763	dishevelled protei
5	78.5	28.4	736	2 T51691	dishevelled homolo
6	65.5	23.7	186	1 RDBOD	dihydrofolate redu
7	65	23.6	863	2 S74447	ferrichrome-iron r
8	61.5	22.3	336	2 T19802	hypothetical prote
9	58	21.0	1616	2 T16600	vitellogenin vit-1
10	57.5	20.8	666	2 T43171	cytoplasmic signal
11	57.5	20.8	672	2 T24507	hypothetical prote
12	57	20.7	357	2 E64233	membrane transport
13	57	20.7	1238	2 S68700	Hsp70 Delta-like tyr
14	56.5	20.5	430	1 KGRRT1	T-kininogen I prec
15	56	20.3	1034	1 GNLJCA	pol polyprotein -
16	55.5	20.1	433	2 A28055	K-kininogen, LMW I
17	55.5	20.1	499	2 S18865	heat shock protein
18	55.5	20.1	639	2 A25486	kininogen, HMW I p
19	55.5	20.1	895	2 T23191	hypothetical prote
20	55	19.9	186	2 S17984	dihydrofolate redu
21	55	19.9	273	2 T48175	transcription regu
22	55	19.9	682	2 T48175	receptor like prot
23	55	19.9	1055	1 GNLJST	pol polyprotein -
24	55	19.9	1055	2 S53092	DNA-directed RNA p
25	55	19.9	1174	2 S28976	hypothetical prote
26	55	19.9	1265	2 T21782	hypothetical prote
27	55	19.9	1465	2 T23056	vitellogenin vit-2
28	55	19.9	1613	2 A43081	calcium channel al
29	55	19.9	1851	2 T13980	

30	54.5	19.7	186	1 RDHY75	dihydrofolate redu
31	54.5	19.7	566	1 HYBSU	bacillolysin (EC 3
32	54.5	19.7	699	2 S25541	heat shock protein
33	54	19.6	509	2 S73348	glucose-6-phosphat
34	54	19.6	680	2 T42923	infected cell prot
35	53.5	19.4	303	1 OOVZFI	F1 protein - vacci
36	53.5	19.4	314	2 B35390	replication protei
37	53.5	19.4	340	1 OOVZPI	F1 protein - vacci
38	53.5	19.4	340	2 T23159	I10R protein - var
39	53.5	19.4	340	2 S33086	G9R protein - vari
40	53.5	19.4	340	2 T28510	hypothetical prote
41	53.5	19.4	447	2 B73355	37K myristicliprotei
42	53.5	19.4	447	2 B75212	amidophosphoribosy
43	53.5	19.4	650	2 D71021	hypothetical prote
44	53.5	19.4	888	2 T51593	GTP-binding regula
45	53.5	19.4	901	2 T01135	hypothetical prote

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax1 - rat
N:Alternate names: Ax1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence,revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A>Title: Ax1, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: Z16414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A>Note: Interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match 100.0%; Score 276; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 1.9e+26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LTLGHFKKQSKKGNRYRFFKASDEFACGAVFEIIMDETVLPMTYEGRTL 51
Db 781 LTLGHFKKQSKKGNRYRFFKASDEFACGAVFEIIMDETVLPMTYEGRTL 831

RESULT 2
T08422
negative regulator axin [imported] - rat
N:Alternate names: Axin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Nov-1999 #sequence,revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08422
R:Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A>Title: Axin, a negative regulator of the Wnt signaling pathway, forms a complex wit
A:Reference number: Z16413; MUID:98151961
A:Accession: T08422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-832 <IKE>
A:Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A>Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction

Query Match 68.8%; Score 190; DB 2; Length 832;
Best Local Similarity 64.7%; Pred. No. 1e+15;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

```
Oy      1    LTTGHHFEOLSKKNRYRFFYFKKASDFEAGVAFEEIMQDEVLPMYEGRIL 51
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      775 VTLGGFHELLTKKGSRYRFKKAVSDPEFGVGVEEVREDAILLVFEEKII 825

RESULT      3
A:Accession A49840
segment polarity protein dishevelled - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1998
C:Accession: A49840
R:Klingensmith, J.; Nusse, R.; Perrimon, N.
Genes Dev. 8, 118-130, 1994
A:title: The Drosophila segment polarity gene dishevelled encodes a novel protein regulator
A:Reference number: A49840; MUID:9411685
A:Accession: A49840
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-623 <KLID>
A:Cross-references: GB:L26974; MID:g435043; PID:g458866
C:Genetics:
A:Gene: dsh
A:Cross-references: FlyBase:FBgn0000499
C:Superfamily: GLGF domain homology
F:258-333/Domain: GLGF domain homology <GLIG2>
```

A:Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BA16599.1; PID:g165167
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: fruA_1
A:Start codon: GTG
C:Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
C:Keywords: iron transport
F:240-375/Domain: tonB-dependent receptor amino-terminal homology <TNB>
F:581-863/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>

Query Match 23.6%; Score 65; DB 2; Length 863;
Best Local Similarity 28.0%; Pred. No. 4.1;
Matches 14; Conservative 14; Mismatches 14; Indels 8; Gaps 2;

Oy 6 FKEQLSKGNRYRYFKKASDEFACGAFEEI-----WDETVLPMEYEG 48
Db 495 FADQDCQGSYSFY-TNAVGFSTGSVKHLLAGIDYMNSEISILTFGC 543

RESULT 8
T19802
hypothetical protein C37A5.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T19802
R:White, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19180
A:Accession: T19802
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <MIL>
A:Cross-references: EMBL:292828; PIDN:CAB07332.1; GSPDB:GN00019; CESP:C37A5.9
A:Experimental source: clone C37A5
C:Genetics:
A:Gene: CESP:C37A5.9

A:Map position: 1
A:introns: 33/3; 124/1; 265/1; 298/2; 328/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C37A5.9

Query Match 22.3%; Score 61.5; DB 2; Length 336;
Best Local Similarity 29.4%; Pred. No. 4.1;
Matches 15; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

Oy 1 LTGFHEQLS-KKGNRYRYFKKASDEFACGAFEEIWDDETVLPMEYEGRI 50
Db 281 WTAEKRRHRLPNGAHQLPFTCECEGSGAPQLLIKDHHLIPVEGRH 331

RESULT 9
T16600
vitellogenin vit-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16600
R:Bentley, D.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence of C. elegans cosmid K09F5.
A:Reference number: Z18544
A:Accession: T16600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1616 <BEN>
A:Cross-references: EMBL:U37430; NID:g1019963; PID:g1945496; PIDN:AAB52675.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone K09F5
C:Genetics:
A:Gene: CESP:vit-1
A:Map position: X
A:introns: 291/3; 386/3; 1448/3; 1531/1
C:Superfamily: vitellogenin

Query Match 21.0%; Score 58; DB 2; Length 1616;
Best Local Similarity 44.4%; Pred. No. 60;
Matches 16; Conservative 7; Mismatches 7; Indels 6; Gaps 2;

Oy 7 KEQLSKGNRYRY--FKKASDEFACGAFEEIWDDE 40
Db 1482 EERLSEKKNRKRYDERKYESEYS---PEETDYDE 1513

RESULT 10
T43171
cytoplasmic signaling transducer - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43171
R:Guo, C.
submitted to the EMBL Data Library, May 1998
A:Description: Mig-5, a gene that controls cell fate determination and cell migration
A:Reference number: Z22326
A:Accession: T43171
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-666 <GUO>
A:Cross-references: EMBL:AF063244; PIDN:AAC16434.1
C:Genetics:
A:Gene: mig-5

Query Match 20.8%; Score 57.5; DB 2; Length 666;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Oy 2 TLGFHEQLSKKGNRYRYFKK 22
Db 37 TLGNFKNSFTKRG-YKYAKE 56

RESULT 11
T24507
hypothetical protein T05C12.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24507
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19901
A:Accession: T24507
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-672 <MIL>
A:Cross-references: EMBL:266500; PIDN:CAA91307.1; GSPDB:GN00020; CESP:T05C12.6
A:Experimental source: clone T05C12
C:Genetics:
A:Gene: CESP:T05C12.6
A:Map position: 2
A:introns: 13/3; 63/2; 114/3; 140/1; 299/2; 340/2; 449/1; 624/1

Query Match 20.8%; Score 57.5; DB 2; Length 672;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Oy 2 TLGFHEQLSKKGNRYRYFKK 22
Db 37 TLGNFKNSFTKRG-YKYAKE 56

RESULT 12
E64233
membrane transport protein (glnQ) homolog MG303 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999

[illegible]

A:Accession: A01286; D25486; A28526; PLO193; J00027; B25488; A28525; S68036
 R:Funuro-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 12054-12059, 1985
 A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin a
 inhibitor.
 A:Reference number: A92496; MUID:86008264
 A:Accession: A01286
 A:Molecule type: mRNA
 A:Residues: 1-430 <EUR>
 A:Cross-references: GB:M11883; NID:g205084; PIDN:AAA4149.1; PID:g205085
 R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 262, 2190-2198, 1987
 A:Title: Differing expression patterns and evolution of the rat kininogen gene family
 A:Reference number: A92825; MUID:87137443
 A:Accession: D25486
 A:Molecule type: DNA
 A:Residues: 375-430 <KIT>
 R:Enjiyoji, K.; Kato, H.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 973-979, 1988
 A:Title: Purification and characterization of rat T-kininogens isolated from plasma o
 A:Reference number: A92729; MUID:88087226
 A:Accession: A28526
 A:Molecule type: Protein
 A:Residues: 'E', 20-48; 376-430 <ENJ>
 R:Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiyu, S.; Tomino, S.; Nagase, S.
 Jpn. J. Cancer Res. 81, 63-68, 1990
 A:Title: Identification of a protein increasing in serum of Nagase analbuminemic rats
 A:Reference number: PLO193; MUID:90216390
 A:Accession: PLO193
 A:Molecule type: mRNA
 A:Residues: 330-420, 'R', 422-429, 'P' <KAN>
 R:Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
 Gene 81, 119-128, 1989
 A:Title: Primary structure of a gene encoding rat T-kininogen.
 A:Reference number: J00027; MUID:90034172
 A:Accession: J00027
 A:Molecule type: DNA
 A:Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258
 A:Experimental source: Strain Sprague-Dawley
 R:Kageyama, R.; Kitamura, N.; Okubo, H.; Nakanishi, S.
 J. Biol. Chem. 262, 2345-2351, 1987
 A:Title: Differing utilization of homologous transcription initiation sites of rat K
 A:Reference number: A25488; MUID:87137465
 A:Accession: B25488
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-48 <KAC>
 A:Cross-references: GB:M14356; NID:g205090; PIDN:AAA41492.1; PID:g205091
 R:Enjiyoji, K.; Kato, H.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 965-972, 1988
 A:Title: Purification and characterization of two kinds of low molecular weight kinin
 A:Reference number: A28525; MUID:88087225
 A:Accession: A28525
 A:Molecule type: Protein
 A:Residues: 376-430 <ENJ>
 R:Sierra, F.; Walter, R.; Vautravers, P.; Gulgoz, Y.
 Arch. Biochem. Biophys. 322, 333-338, 1995
 A:Title: Identification of several isoforms of T-kininogen expressed in the liver of
 A:Reference number: S68034; MUID:96032652
 A:Accession: S68036
 A:Molecule type: mRNA
 A:Residues: 340-430 <SID>
 A:Experimental source: clone pSG17
 A:Comment: At least three types of LMW kininogen precursors are present in rat plasma
 ceding bradykinin.
 C:Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after
 d of an Arg or Lys, it is probably not released from its precursor by either tissue o
 C:Comment: The T-kininogens are produced in response to an inflammatory stimulant.
 C:Genetics:
 A:Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
 C:Superfamily: kininogen, cystatin homology
 C:Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glyc
 F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-430/Product: T-kininogen I #status experimental <MAT>
 F:19-130/Domain: cystatin homology <CY1>
 F:141-252/Domain: cystatin homology <CY2>
 F:263-374/Domain: cystatin homology <CY3>
 F:378-386/Product: bradykinin #status predicted <BDY>
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
 F:82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/disulfide bonds: #status

Query Match 20.5%; Score 56.5; DB 1; Length 430;
 Best Local Similarity 33.3%; Pred. No. 22;
 Matches 12; Conservative 8; Mismatches 11; Indels 5; Gaps 1;

OY 3 LGHFKQLSKGNRYF-----KASDEFACGAVF 33
 DB 281 LGHSIAOLNAOHNIIFYFKIDPVKATSOVAVGVY 316

RESULT 15

GNLJCA
 pol polyprotein - human immunodeficiency virus type 2 (isolate CAN2/Guinea-Bissau)
 N:Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
 C:Species: human immunodeficiency virus type 2, HIV-2
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-1997
 C:Accession: B38475; J00974
 R:Ristlem, M.; Hill, F.; Karpas, A.
 J. Gen. Virol. 72, 721-724, 1991
 A:Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus ty
 A:Reference number: A38475; MUID:91170959
 A:Accession: B38475
 A:Molecule type: DNA
 A:Residues: 1-1034 <TRI>
 A:Note: readthrough of the terminator TGA may occur between codons ATT for 564-Ile and G
 C:Comment: The cleavage sites of this polyprotein have not been determined.
 C:Genetics:
 A:Gene: pol
 C:Superfamily: pol polyprotein
 C:Keywords: AIDS; aspartic protease; endonuclease; hydrolase; immunodeficiency; nucleoc
 F:85-183/Product: retropepsin #status predicted <RTP>
 F:109/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 20.3%; Score 56; DB 1; Length 1034;
 Best Local Similarity 25.5%; Pred. No. 66;
 Matches 13; Conservative 11; Mismatches 17; Indels 10; Gaps 1;

OY 11 SKKGNRYFYFKKASDEF-----ACGAVFEELMDDETIVLPMYEGRTL 51
 DB 959 SKLKNRYFYFREGDQLMKPGELMKGDGAVIVKGTDIKIIIPRKAKIT 1009

Search completed: June 7, 2001, 02:03:25
 Job time: 5038 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:10:32 ; Search time 39.03 seconds

(without alignments)
44.761 Million cell updates/sec

Title: US-09-587-574-5

Sequence: 1 LTCHKEQLSKKGNRYTF.....VFEEIMDETVLPMEGRIL 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	838	1	AXN2_RAT
2	276	100.0	840	1	AXN2_MOUSE
3	272	98.6	843	1	AXN2_HUMAN
4	246	89.1	812	1	AXN2_BRARE
5	197	71.4	841	1	AXN_CHICK
6	195	70.7	842	1	AXN_XENLA
7	191	69.2	900	1	AXN1_HUMAN
8	190	68.8	893	1	AXN1_RAT
9	190	68.8	992	1	AXN1_MOUSE
10	175	63.4	835	1	AXN1_BRARE
11	109.5	33.7	623	1	DSH_PROME
12	102	37.0	736	1	DVL2_HUMAN
13	102	37.0	736	1	DVL2_MOUSE
14	95.5	34.6	716	1	DVL3_HUMAN
15	95.5	34.6	716	1	DVL3_MOUSE
16	95	34.4	670	1	DVL1_HUMAN
17	95	34.4	670	1	DVL1_MOUSE
18	95	34.4	695	1	DVL1_RAT
19	95	34.4	695	1	DVL1_MOUSE
20	85	30.8	745	1	AXN1_MOUSE
21	78.5	28.4	736	1	DVL2_XENLA
22	65.5	23.7	186	1	DYR_BOVIN
23	62.5	22.6	417	1	MTE8_ECOLI
24	58	21.0	1616	1	VIRL_CAEL
25	57	20.7	357	1	P3PJ_MOUSE
26	57	20.7	1238	1	P3PJ_MOUSE
27	56.5	20.5	430	1	TDM_BP186
28	56	20.3	146	1	TDM_BP186
29	56	20.3	1034	1	POL_HVZCA
30	55.5	20.1	499	1	HS82_TOBAC
31	55.5	20.1	639	1	KNG_RAT
32	55	19.9	186	1	DYR_AEDAL
33	55	19.9	273	1	BLTR_BACSU

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	838 AA.
AXN2_RAT				
AC	070240;			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)			
DE	(AXIL).			
GN	AXIN2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;			
OX	NCBI_Taxid-10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98226558; PubMed=9566905;			
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,			
RA	Kikuchi A.,			
RT	"Axil, a member of the Axin family, interacts with both glycogen			
RT	synthase kinase beta and beta-catenin and inhibits axis formation of			
RT	Xenopus embryos."			
RL	Mol. Cell. Biol. 18:2867-2875(1998).			
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES			
CC	BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-			
CC	CATENIN AND APC BY GSK-3B (BY SIMILARITY).			
CC	- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)			
CC	AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN			
CC	OCCURS VIA THE ARMA/ITIL REPEATS CONTAINED IN BETA-CATENIN.			
CC	TERNARY COMPLEX.			
CC	- SUBCELLULAR LOCATION: CYTOSOL; PLASMA MEM.			
CC	- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.			
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY			
CC	PP2A.			
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	-----			
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CC	or send an email to license@sdb.ch).			
CC	-----			
CC	EMBL: AF017757; AAC40089.1; -			
CC	HSSP: P49799; IAGR.			
CC	InterPro: IPR000342; -			
CC	InterPro: IPR001158; -			
CC	Pfam: PF00615; RGS; 1.			
CC	Pfam: PF00778; DIX; 1.			
CC	PROSITE: PS50132; RGS; 1.			
CC	Developmental protein; Phosphorylation.			
CC	DOMAIN 81 200 RGS.			
CC	DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).			

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FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
FT DOMAIN 469 474 SIMILARITY).
FT DOMAIN 756 838 POLY-HIS.
SQ SEQUENCE 838 AA; 92947 MW; 45B825C13BA07E37 CRC64;
DIX.
Query Match 100.0%; Score 276; DB 1; Length 838;
Best Local Similarity 100.0%; Pzed. No. 3..3e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTGHEKQSLKNGNRYRYFKKASDFACGAFVEIMDDETVLPWYGRIL 51
DB 781 LTGHEKQSLKNGNRYRYFKKASDFACGAFVEIMDDETVLPWYGRIL 831

RESULT 2
AXIN2_MOUSE STANDARD: PRT; 840 AA.
ID AXIN2_MOUSE
088566; Q9QXJ6;
AC 01-OCF-2000 (Rel. 40, Created)
DT 01-OCF-2000 (Rel. 40, Last sequence update)
DT 01-OCF-2000 (Rel. 40, Last annotation update)
DT 01-OCF-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIN INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.-A., Muertele M., Grimm J., Asbrand C.,
RA Wirtz R., Knehl M., Wedlich D., Birchmeier W.;
RT "Functional interaction of an axin homolog, conductin, with beta-
RT catenin, APC, and GSK3beta.";
RL Science 280:596-599(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TENARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL; AF073788; AAC26047.1; -
DR EMBL; AF205889; AAF22800.1; -
DR MGD; MGI:1270862; Axin2.
DR HSSP; P49799; IAGR.
DR InterPro; IPR000342; -
DR InterPro; IPR001158; -

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DR Pfam: PF00615; RGS: 1.
DR Pfam: PF00778; DIX: 1.
DR PRINTS; PRO1301; RGS-PROTEIN.
DR PROSITE; PS50132; RGS: 1.
KW Anti-oncogene; Phosphorylation.
FT DOMAIN 81 200 RGS-
FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 469 476 POLY-HIS.
FT DOMAIN 758 840 DIX.
FT CONFLICT 101 101 R -> K (IN REF. 2).
FT CONFLICT 474 474 H -> Y (IN REF. 2).
FT CONFLICT 484 484 S -> P (IN REF. 2).
FT CONFLICT 503 503 F -> S (IN REF. 2).
FT CONFLICT 603 603 G -> A (IN REF. 2).
SQ SEQUENCE 840 AA; 92934 MW; A07D5EFB25DE7277 CRC64;

Query Match 100.0%; Score 276; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 3,3e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTIGHEKQSLKSGKGYRYYFKKASDEPACGAVFEIMDETFLVLMYEGRI 51
Db 783 LTLGHEKQSLKSGKGYRYYFKKASDEPACGAVFEIMDETFLVLMYEGRI 833

RESULT 3
AXN2_HUMAN STANDARD; PRI; 843 AA.
ID AXN2_HUMAN
AC Q9Y2T1; Q9UH84;
DT 01-OCT-2000 (Ref. 40, Created)
DT 01-OCT-2000 (Ref. 40, Last sequence update)
DT 01-OCT-2000 (Ref. 40, Last annotation update)
DE AXIN 2 (AXIN INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99168905; PubMed=10049590;
RX Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.;
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RL Genomics 55:341-344(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain, and Lymphoblast;
RC Zhang T., Pasotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Constanti F.;
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation."
RT submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY)
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC -1- TERNARY COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL;SMC.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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DR EMBL: AF078165; AAD20976.1; -
 DR EMBL: AF205888; AAF22799.1; -
 DR MIM: 604025; -
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS01301; RGS-PROTEIN.
 DR PROSITE: PS50132; RGS; 1.
 KW Developmental protein. Phosphorylation.
 FT DOMAIN 81 200 RGS.
 FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 413 476 BETA-CATENIN BINDING SITE (BY
 FT DOMAIN 469 474 SIMILARITY).
 FT DOMAIN 761 843 POLY-HIS.
 FT CONFLICT 37 62 DIX.
 FT CONFLICT 346 346 O -> R (IN REF. 2).
 FT CONFLICT 572 636 MISSING (IN REF. 2).
 FT CONFLICT 687 687 P -> S (IN REF. 2).
 FT CONFLICT 696 696 Q -> H (IN REF. 2).
 SQ SEQUENCE 843 AA; 93557 MW; F7B62BED6A84664D CRC64;

Query Match 98.6%; Score 272; DB 1; Length 843;
 Best Local Similarity 98.0%; Pred. No. 1; Le-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 51
 Db 786 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 836

RESULT 4
 AXN2_BRARE STANDARD; PRT; 812 AA.
 AC P57095;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN 2 (AXIS INHIBITION PROTEIN 2).
 GN AXIN2.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 NCBI_TaxID=7955.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20171051; Pubmed=10704853;
 RA Shimizu T., Yamane Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
 RA Bae Y.-K., Hibi M., Hirano T.;
 RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
 RT formation of the dorsal organizer in zebrafish.";
 RT Mech. Dev. 91:293-303(2000).
 RL - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
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DR EMBL: AB032263; BAA92440.1; -
 DR HSSP: P49799; IAGR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 KW Developmental protein. Phosphorylation.
 FT DOMAIN 84 203 RGS.
 FT DOMAIN 329 415 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 415 467 BETA-CATENIN BINDING SITE (BY
 FT DOMAIN 412 419 SIMILARITY).
 FT DOMAIN 730 812 POLY-SER.
 SQ SEQUENCE 812 AA; 91496 MW; 465DA6DE2240CC CRC64;

Query Match 89.1%; Score 246; DB 1; Length 812;
 Best Local Similarity 86.3%; Pred. No. 2e-23;
 Matches 44; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 51
 Db 755 LTLGHFEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRL 805

RESULT 5
 AXN2_CHICK STANDARD; PRT; 841 AA.
 AC O42400;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN (AXIS INHIBITION PROTEIN).
 GN AXIN OR AXN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=97373830; Pubmed=9230313;
 RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
 RA Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
 RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation.";
 RT Cell 90:181-192(1997).
 RL - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
 CC - PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
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CC -----
DR EMBL: AF009012: AAC60245.1;
DR HSP: P49799: IAGR.
DR InterPro: IPR000342;
DR InterPro: IPR001158;
DR Pfam: PF00615: RGS; 1.
DR Pfam: PF00778: DIX; 1.
DR PROSITE: PS50132: RGS; 1.
DR Developmental protein: Phosphorylation.
KM DOMAIN 88 211 RGS
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
SQ DOMAIN 759 841 DIX.
SEQUENCE 841 AA; 94931 MW; 400D0C90E72506FE CRC64;

Query Match 71.4%; Score 197; DB 1; Length 841;
Best Local Similarity 66.7%; Pred. No. 3.2e-17;
Matches 34; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 LTLGHFKQLSKKGNRYRYFKKASDFACGAFVEEIMDEVLPYEGRIIL 51
Db 784 VTLAGQFKLLTRKGNRYRYFKKVSDFDCGVFEEVREDMDILPYEKII 834

RESULT 6
AXN1_XENLA STANDARD: PRT: 842 AA.
AC 01-0CT-2000 (Rel. 40, Created)
DT 01-0CT-2000 (Rel. 40, Last sequence update)
DT 01-0CT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (AXIN).
GN AXIN OR AXN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99173782; PubMed=10072781;
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
RT expressed in the anterior midbrain."
RL Mech. Dev. 80:147-151(1999).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: WEAKLY AND UBQUITOUSLY EXPRESSED THROUGHOUT
CC EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR
CC MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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CC -----
CC EMBL: AF097313: AAC71036.1;
CC HSP: P49799: IAGR.
CC InterPro: IPR000342;
CC InterPro: IPR001158;
CC Pfam: PF00615: RGS; 1.
CC Pfam: PF00778: DIX; 1.
CC PROSITE: PS50132: RGS; 1.
CC Developmental protein: Phosphorylation.
CC NON_TER 1

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DR PROSITE: PS50132: RGS; 1.
DR Developmental protein: Phosphorylation.
KM DOMAIN 88 211 RGS.
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
SQ DOMAIN 760 842 DIX.
SEQUENCE 842 AA; 94459 MW; BDAL52734C97191E CRC64;

Query Match 70.7%; Score 195; DB 1; Length 842;
Best Local Similarity 66.7%; Pred. No. 5.7e-17;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTLGHFKQLSKKGNRYRYFKKASDFACGAFVEEIMDEVLPYEGRIIL 51
Db 785 VTLAGQFKLLTRKGNRYRYFKKVSDFDCGVFEEVREDMDILPYEKII 835

RESULT 7
AXN1_HUMAN STANDARD: PRT: 900 AA.
AC 015169;
DT 01-0CT-2000 (Rel. 40, Created)
DT 01-0CT-2000 (Rel. 40, Last sequence update)
DT 01-0CT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (AXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
RA Lee J.-J., Tilghman S.M., Gambiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B.
CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLOBIN (GAMA-CATENIN),
CC APC, DVL AND PP2A.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
CC EMBL: AF009674: AAC51624.1;
CC HSP: P49799: IAGR.
CC MIM: 603816;
CC InterPro: IPR000342;
CC InterPro: IPR001158;
CC Pfam: PF00615: RGS; 1.
CC Pfam: PF00778: DIX; 1.
CC PROSITE: PS50132: RGS; 1.
CC Developmental protein: Phosphorylation.
CC NON_TER 1

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FT DOMAIN 125 248 RGS.
FT DOMAIN 365 470 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY
SIMILARITY).
FT DOMAIN 818 900 DIX.
SQ SEQUENCE 900 AA; 99803 MW; EESF990B11FC7B3B CRC64;

Query Match 69.2%; Score 191; DB 1; Length 900;
Best Local Similarity 66.7%; Pred. No. 2e-16;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTIGHFKEQLSKGNRYFYFKKASDEFACGAVEEIMDETVLPMEGRIL 51
Db 843 VTIGOFKELLTKKGSYRYFYFKKASDEFDCGVEEVEEVEDEALVPFEKII 893

RESULT 8
AXNL_MOUSE
ID AXNL_MOUSE STANDARD; PRT; 992 AA.
AC 070239;
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=97373830; PubMed=923013;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L. III,
Lee J.J., Tligman S.M., Gumbiner B.W., Costantini F.;
RT The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.*;
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAOGLOBIN (GAMMA-CATENIN). APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL: AF017756; AAC40066.1; ALT_INIT.
CC HSSP: P49799; IAGR.
CC MGD: MGI:1096327; Axin.
CC InterPro: IPR000342;
CC InterPro: IPR001158;
CC Pfam: PF00615; RGS; 1.
CC Pfam: PF00778; DIX; 1.
CC PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 10 18 POLY-ALA.
FT DOMAIN 217 340 RGS.

FT DOMAIN 414 498 GSK-3B BINDING SITE.
FT DOMAIN 499 567 BETA-CATENIN BINDING SITE.
FT DOMAIN 811 893 DIX.
SQ SEQUENCE 893 AA; 99188 MW; 3CCBD2242EDD384C CRC64;

Query Match 68.8%; Score 190; DB 1; Length 893;
Best Local Similarity 64.7%; Pred. No. 2.6e-16;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTIGHFKEQLSKGNRYFYFKKASDEFACGAVEEIMDETVLPMEGRIL 51
Db 836 VTIGOFKELLTKKGSYRYFYFKKASDEFDCGVEEVEEVEDEALVPFEKII 886

RESULT 9
AXNL_MOUSE
ID AXNL_MOUSE STANDARD; PRT; 992 AA.
AC 035625;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
GN AXIN1 OR AXIN OR FU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=97373830; PubMed=923013;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L. III,
Lee J.J., Tligman S.M., Gumbiner B.W., Costantini F.;
RT The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.*;
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAOGLOBIN (GAMMA-CATENIN). APC, DVL AND PP2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
PP2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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or send an email to license@isb-sib.ch).
CC EMBL: AF009011; AAC53285.1; -.
CC HSSP: P49799; IAGR.
CC MGD: MGI:1096327; Axin.
CC InterPro: IPR000342;
CC InterPro: IPR001158;
CC Pfam: PF00615; RGS; 1.
CC Pfam: PF00778; DIX; 1.
CC PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 10 18 POLY-ALA.
FT DOMAIN 217 340 RGS.

DR InterPro: IPR001158; -
 DR InterPro: IPR001478; -
 DR Pfam: PF00610; DEP: 1.
 DR PROSITE: PS50186; DEP: 1.
 DR Pfam: PF00778; DIX: 1.
 DR PROSITE: PS50186; PDZ: 1.
 DR PROSITE: PS50106; PDZ: 1.
 DR PROSITE: PS50106; PDZ: 1.
 DR Developmental protein; Phosphorylation; Segmentation polarity protein.
 FT DOMAIN 252 324 PDZ.
 FT DOMAIN 404 478 DEP.
 FT DOMAIN 119 146 POLY-GLN.
 FT DOMAIN 154 159 POLY-GLN.
 FT DOMAIN 551 557 POLY-SER.
 FT DOMAIN 599 608 POLY-GLY.
 FT CONFLICT 276 276 D -> N (IN REF. 2).
 FT CONFLICT 565 565 T -> I (IN REF. 2).
 FT CONFLICT 619 619 S -> F (IN REF. 2).
 SQ SEQUENCE 623 AA: 68845 MW: 0BA253CEAC0B71F5 CRC64;

Query Match 39.7%; Score 109.5; DB 1; Length 623;
 Best Local Similarity 46.2%; Pred. No. 2,6e-06;
 Matches 24; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

OY 1 LTLGHEKQLSKK-GNYRYFKKASDFACGAVFEETMDDETVLPMEGRIL 51
 DB 35 VTLRDFKVLNKNNNKTKFFKSMADF--GVYKEIADSTILPCFNGRV 84

RESULT 12
 ID DVL2_HUMAN STANDARD; PRT: 736 AA.

AC 014641;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-2 (DISHEVELLED-2)
 DE (DSH HOMOLOG 2).
 GN DVL2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
 RA Semenov M.V., Snyder M.;
 RA MEDLINE-97336056; PubMed-9192851;
 RT "Human dishevelled genes constitute a DHR-containing multigene family.";
 RT Genomics 42:302-310(1997).

CC - FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC - PTM: PHOSPHORYLATED.
 CC - SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC - SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC - SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

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 CC -----
 CC EMBL: AF006012; AAB5243.1; -
 CC HSP: P31016; 1BFE.
 CC MIM: 602151; -
 CC InterPro: IPR000591; -
 CC InterPro: IPR001158; -
 CC InterPro: IPR001478; -
 CC Pfam: PF00610; DEP: 1.
 CC Pfam: PF00778; DIX: 1.

DR Pfam: PF00778; DIX: 1.
 DR Pfam: PF00595; PDZ: 1.
 DR PROSITE: PS50186; DEP: 1.
 DR PROSITE: PS50106; PDZ: 1.
 DR PROSITE: PS50106; PDZ: 1.
 DR Developmental protein; Phosphorylation.
 FT DOMAIN 7 12 POLY-GLY.
 FT DOMAIN 235 240 POLY-ARG.
 FT DOMAIN 267 339 PDZ.
 FT DOMAIN 433 507 DEP.
 FT DOMAIN 686 694 POLY-PRO.
 SQ SEQUENCE 736 AA: 78947 MW: 4BAD95B6C3FE531B CRC64;

Query Match 37.0%; Score 102; DB 1; Length 736;
 Best Local Similarity 41.2%; Pred. No. 2,8e-05;
 Matches 21; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

OY 1 LTLGHEKQLSKKGNRYRYFKKASDFACGAVFEETMDDETVLPMEGRIL 51
 DB 38 ITLGDFKSVLGRPAKAKYFFKSMADF--GVYKEISDNNRLPCFNGRV 86

RESULT 13
 ID DVL2_MOUSE STANDARD; PRT: 736 AA.

AC 060838;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-2 (DISHEVELLED-2)
 DE (DSH HOMOLOG 2).
 GN DVL2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BALB/C; TISSUE-Brain;
 RA MEDLINE-97042042; PubMed-8887313;
 RA Klingensmith J., Yang Y., Axelrod J.D., Beler D.R., Perrimon N.,
 RA Sussman D.J.;
 RT "Conservation of dishevelled structure and function between flies and mice: isolation and characterization of Dvl2.";
 RT Mech. Dev. 58:15-26(1996).

CC - FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - TISSUE SPECIFICITY: UBIQUITOUS.
 CC - SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC - SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC - SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

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 CC or send an email to license@isb-stb.ch).
 CC -----

CC EMBL: U24160; AAC52827.1; -
 CC HSP: P31016; 1BFE.
 CC MGD: MGI:106613; DVL2.
 CC InterPro: IPR000591; -
 CC InterPro: IPR001158; -
 CC InterPro: IPR001478; -
 CC Pfam: PF00610; DEP: 1.
 CC Pfam: PF00778; DIX: 1.
 CC Pfam: PF00595; PDZ: 1.
 CC Pfam: PF00778; DIX: 1.
 CC PROSITE: PS50186; DEP: 1.
 CC PROSITE: PS50106; PDZ: 1.
 CC Developmental protein.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=97081279; PubMed=8922524;
 RA Tsang M., Lijam N., Yang Y., Belter D.R., Wynshaw-Boris A.,
 RA Susman D.J.;
 RT Isolation and characterization of mouse dishevelled-3";
 RL Dev. Dyn. 207:253-262(1996).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
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 CC -----
 CC EMBL: 041285; AAB01761.1; -
 DR HSSP: P31016; 1BFE.
 DR MGD: MGI:108100; DV13.
 DR InterPro: IPR000591; -
 DR InterPro: IPR001158; -
 DR InterPro: IPR001478; -
 DR Pfam: PF00610; DEP; 1.
 DR Pfam: PF00778; DIX; 1.
 DR Pfam: PF00595; PDZ; 1.
 DR PROSITE: PS50186; DEP; 1.
 DR PROSITE: PS50106; PDZ; 1.
 DR Developmental protein.
 KM DOMAIN 249 321 PDZ.
 FT DOMAIN 422 496 DEP.
 SO SEQUENCE 716 AA; 78122 MW; 55412C03202301F0 CRC64;

Query Match 34.6%; Score 95.5; DB 1; Length 716;
 Best Local Similarity 41.2%; Pred. No. 0.00018;
 Matches 21; Conservative 11; Mismatches 16; Indels 3; Gaps 2;
 OY 1 LTLGHEKELSKRGNYRYFKKASDEFACGAVFEETWDETVLPMYEGRTL 51
 Db 28 VTLADKGYL-QNPSTKFFKSMDDF--GVVKEETSDNAKLPCFNGRYV 75

Search completed: June 7, 2001, 02:10:34
 Job time: 422 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 02:09:43 ; Search time 81.06 Seconds
(without alignments)
73.743 Million cell updates/sec

Title: US-09-587-574-5
Predicted score: 276
Sequence: 1 LTGHEFKQSLSKGNRYRFF.....VFEEIMDETVLPMYEGRIL 51

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP. Archaea:*
2: SP. Bacteria:*
3: SP. Fungi:*
4: SP. Human:*
5: SP. Invertebrate:*
6: SP. Mammal:*
7: SP. Mhc:*
8: SP. Organelle:*
9: SP. Phage:*
10: SP. Plant:*
11: SP. Rodent:*
12: SP. Unclassified:*
13: SP. Vertebrate:*
14: SP. Virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	838	11 070240	070240 ratu
2	276	100.0	840	11 088566	088566 mus musculu
3	276	100.0	840	11 090X06	090X06 mus musculu
4	272	98.6	777	4 090H84	090H84 homo sapien
5	272	98.6	843	4 09Y2T1	09Y2T1 homo sapien
6	197	71.4	841	13 042400	042400 gallu
7	195	70.7	842	13 09YGY0	09YGY0 xenopus lae
8	191	69.2	900	4 015169	015169 homo sapien
9	190	68.8	832	11 070239	070239 ratu
10	190	68.8	992	11 035625	035625 mus musculu
11	159	57.6	706	13 09PTP2	09PTP2 xenopus lae
12	109.5	39.7	623	5 09VYZ9	09VYZ9 drosophila
13	102.5	37.1	685	5 09NL46	09NL46 clon
14	95	34.4	695	11 090UG5	090UG5 ratu
15	85	30.8	743	5 09XYC1	09XYC1 drosophila
16	85	30.8	745	5 09V407	09V407 drosophila
17	66	23.6	863	10 081634	081634 elaeis olei
18	65	23.6	863	2 P72599	P72599 synechocyst
19	61.5	22.3	336	5 062090	062090 caenorhabd

20	59	21.4	511	10 09MB73	09MB73 citru
21	57.5	20.8	666	5 061720	061720 caenorhabd
22	57.5	20.8	672	5 022227	022227 caenorhabd
23	57	20.7	361	11 061373	061373 mus musculu
24	57	20.7	1216	11 062884	062884 ratu
25	56.5	20.5	430	11 063581	063581 ratu
26	56	20.3	1035	14 073194	073194 human immun
27	55.5	20.1	205	14 073955	073955 human immun
28	55.5	20.1	895	5 045631	045631 caenorhabd
29	55.5	20.1	930	10 09LG18	09LG18 arabidopsi
30	55.5	20.1	1702	10 09LEP3	09LEP3 arabidopsi
31	55	19.9	212	10 09LLY3	09LLY3 nicotiana t
32	55	19.9	381	6 09MZ21	09MZ21 sus scrofa
33	55	19.9	682	10 09M021	09M021 arabidopsi
34	55	19.9	827	10 09ZS85	09ZS85 arabidopsi
35	55	19.9	1019	5 09VDC9	09VDC9 drosophila
36	55	19.9	1059	14 076630	076630 human immun
37	55	19.9	1265	5 062231	062231 caenorhabd
38	55	19.9	1347	4 015050	015050 homo sapien
39	55	19.9	1465	5 017909	017909 caenorhabd
40	55	19.9	1848	5 09YTR8	09YTR8 drosophila
41	54.5	19.7	260	11 064742	064742 cricetus
42	54.5	19.7	316	5 018516	018516 aplysia cal
43	54.5	19.7	566	2 032309	032309 bacillus th
44	54.5	19.7	699	10 003986	003986 arabidopsi
45	54.5	19.7	700	10 09XGFI	09XGFI triticum ae

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	838 AA.
070240	070240			
1	070240			
RT	01-AUG-1998 (TREMblrel. 07, Created)			
DT	01-AUG-1998 (TREMblrel. 07, Last sequence update)			
DT	01-OCT-2000 (TREMblrel. 15, Last annotation update)			
DE	AXIL.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98226558; Pubmed=9566905;			
RA	Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,			
RA	Kikuchi A.;			
RT	"Axil, a member of the Axin family, interacts with both glycogen			
RT	synthase kinase 3beta and beta-catenin and inhibits axis formation of			
RT	Xenopus embryos."			
RL	MOL. Cell. Biol. 18:2867-2875(1998).			
DR	EMBL: AF017757; AAC40089.1; -			
DR	HSSP: P49799; IAGR.			
DR	INTERPRO: IPR000342; -			
DR	INTERPRO: IPR001158; -			
DR	PRAM: PF00615; KGS; 1.			
DR	PRAM: PF00778; DIX; 1.			
DR	PRODOM: PD001580; -; 1.			
DR	PRODOM: PD003639; -; 1.			
SQ	SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;			

Query Match 100.0%; Score 276; DB 11; Length 838;
Best Local Similarity 100.0%; Pred. No. 4.7e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTGHEFKQSLSKGNRYRFFPKASDEPACGAVFEEIMDETVLPMYEGRIL 51
DB 781 LTGHEFKQSLSKGNRYRFFPKASDEPACGAVFEEIMDETVLPMYEGRIL 831

RESULT 2

088566 ID 088566 PRELIMINARY; PRT: 840 AA.
AC 088566:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CONDUCTIN.
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX NCB1 [1]
SEQUENCE FROM N.A.
RP MEDLINE=98221239; PubMed=9554852;
RA Behrens J., Jerchow B.-A., Murtels M., Grimm J., Asbrand C., Wirtz R.,
Kuhl M., Wedlich D., Birchmeier W.,
RT "Functional interaction of an axin homolog, conductin, with beta-
catenin, APC, and GSK3beta."
RL Science 280:596-599(1998).
DR EMBL: AF073788; AAC26047.1; -
DR HSSP: P49799; IAGR.
DR MGD: MGI:1270862; Axin2.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -; 1.
DR PRODOM: PD003639; -; 1.
SO SEQUENCE 840 AA; 92896 MW; A07D5F8B25DE7277 CRC64;

Query Match 100.0%; Score 276; DB 11; Length 840;
Best Local Similarity 100.0%; Pred. No. 4,7e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLGHFKQLSKKNGYRYFFKASDFACGAVFEIWDDETVLPMYEGRI 51
Db 783 LTLGHFKQLSKKNGYRYFFKASDFACGAVFEIWDDETVLPMYEGRI 833
|||||
RESULT 3
ID 090XJ6 PRELIMINARY; PRT: 840 AA.
AC 090XJ6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN2.
GN AXIN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX NCB1 [1]
SEQUENCE FROM N.A.
RP Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF205889; AAF22800.1; -
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPPROTEIN.
SO SEQUENCE 840 AA; 92896 MW; 767D546B43C921C5 CRC64;

Query Match 100.0%; Score 276; DB 11; Length 840;

Best Local Similarity 100.0%; Pred. No. 4,7e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLGHFKQLSKKNGYRYFFKASDFACGAVFEIWDDETVLPMYEGRI 51
Db 783 LTLGHFKQLSKKNGYRYFFKASDFACGAVFEIWDDETVLPMYEGRI 833
|||||

RESULT 4
ID 090H84 PRELIMINARY; PRT: 777 AA.
AC 090H84:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN2.
GN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX NCB1 [1]
SEQUENCE FROM N.A.
RP TISSUE=BRAIN, LYMPHOBLAST;
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Costantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF205888; AAF22799.1; -
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPPROTEIN.
SO SEQUENCE 777 AA; 86857 MW; 3A4943ABF430BBD3 CRC64;

Query Match 98.6%; Score 272; DB 4; Length 777;
Best Local Similarity 98.0%; Pred. No. 1,4e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLGHFKQLSKKNGYRYFFKASDFACGAVFEIWDDETVLPMYEGRI 51
Db 720 LTLGHFKQLSKKNGYRYFFKASDFACGAVFEIWDDETVLPMYEGRI 770
|||||

RESULT 5
ID 09Y2T1 PRELIMINARY; PRT: 843 AA.
AC 09Y2T1:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CONDUCTIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX NCB1 [1]
SEQUENCE FROM N.A.
RP MEDLINE=99168905; PubMed=10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.,
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
chromosome 55:341-344(1999)."
RL Genomics 55:341-344(1999).
DR EMBL: AF078165; AAD20976.1; -
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -
DR INTERPRO: IPR001158; -
DR PFAM: PF00615; RGS; 1.

DR PFAM: PF00778; DIX: 1.
SQ SEQUENCE 843 AA; 93557 MW; F7B62BBD6AB4664D CRC64;

Query Match 98.6%; Score 272; DB 4; Length 843;
Best Local Similarity 98.0%; Pred. No. 1.5e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 51
DB 786 VTIGQFRELTKKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 836

RESULT 6
042400 PRELIMINARY; PRT; 841 AA.

AC 042400;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Constantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
DR EMBL: AF009012; AAC60245.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -. 1.
DR PRODOM: PD003639; -. 1.
SQ SEQUENCE 841 AA; 94931 MW; 400D0C90E72506FE CRC64;

Query Match 71.4%; Score 197; DB 13; Length 841;
Best Local Similarity 66.7%; Pred. No. 3.1e-16;
Matches 34; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 LTIGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 51
DB 784 VTIGQFRELTKKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 834

RESULT 7
09YGYO PRELIMINARY; PRT; 842 AA.

AC 09YGYO;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; PubMed=10072781;
RA Hedgespeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is

RT expressed in the anterior midbrain.";
RL Mech. Dev. 80:147-151(1999).
DR EMBL: AF097313; AAC71036.1; -.
DR HSSP: P49799; IAGR.

DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRODOM: PD001580; -. 1.
DR PRODOM: PD003639; -. 1.
SQ SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;

Query Match 70.7%; Score 195; DB 13; Length 842;
Best Local Similarity 66.7%; Pred. No. 5.6e-16;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTIGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 51
DB 785 VTIGQFRELTKKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 835

RESULT 8
015169 PRELIMINARY; PRT; 900 AA.

AC 015169;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN (FRAGMENT).
GN AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Constantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
DR EMBL: AF009674; AAC51624.1; -.
DR HSSP: P49799; IAGR.
DR INTERPRO: IPR000342; -.
DR INTERPRO: IPR001158; -.
DR PFAM: PF00615; RGS; 1.
DR PFAM: PF00778; DIX; 1.
DR PRINTS: PR01301; RGSPROTEIN.
DR NON_TER
SQ SEQUENCE 900 AA; 99803 MW; EEF5F90B11FC7B3B CRC64;

Query Match 69.2%; Score 191; DB 4; Length 900;
Best Local Similarity 66.7%; Pred. No. 1.9e-15;
Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTIGHFEQLSKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 51
DB 843 VTIGQFRELTKKGNRYFFKASDEFACGAVEEIMDETVLPMEGRIL 893

RESULT 9
070239 PRELIMINARY; PRT; 832 AA.

AC 070239;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98151361; PubMed=9482734;
 RA Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
 RT Axin, a negative regulator of the Wnt signaling pathway, forms a
 RT complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
 RT dependent phosphorylation of beta-catenin.";
 RL EMBL J. 17:1371-1384(1998).
 DR EMBL: AF017756; AAC40066.1; -.
 DR HSP: P49799; IAGR.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRODOM: PD001580; -; 1.
 DR PRODOM: PD003639; -; 1.
 SQ SEQUENCE 832 AA; 92856 MW; B489504C7E594347 CRC64;

Query Match 68.8%; Score 190; DB 11; Length 832;
 Best Local Similarity 64.7%; Pred. No. 2.3e-15;
 Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
 OY 1 LTLGHFKQLSKKGNRYFFKASDEFACGAVFEETIMDETVLPMYEGRII 51
 DB 775 VTLGQFKELTKKSGYRYFFKASDEFACGAVFEETIMDETVLPMYEGRII 825

RESULT 10
 ID 035625 PRELIMINARY; PRT; 992 AA.
 AC 035625;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE AXIN (FRAGMENT).
 GN AXIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasilek T.J., Perry W.L.,
 RA Ili Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
 RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 DR EMBL: AF009011; AAC53285.1; -.
 DR HSP: P49799; IAGR.
 DR MGD: MGI:1096327; Axin.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM: PF00615; RGS; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGSPTROTEIN.
 FT NON_TER
 SQ SEQUENCE 992 AA; 109917 MW; 70EBE53D387BD26F CRC64;

Query Match 68.8%; Score 190; DB 11; Length 992;
 Best Local Similarity 66.7%; Pred. No. 2.8e-15;
 Matches 34; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 LTLGHFKQLSKKGNRYFFKASDEFACGAVFEETIMDETVLPMYEGRII 51
 DB 935 VTLGQFKELTKKSGYRYFFKASDEFACGAVFEETIMDETVLPMYEGRII 985

RESULT 11

Q9PRP2
 ID Q9PRP2 PRELIMINARY; PRT; 706 AA.
 AC Q9PRP2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE AXIN-RELATED PROTEIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RA Itoh K., Antipova A., Ratcliffe M., Sokol S.;
 RT "Dishevelled transduces a signal by displacing GSK3 from axin-GSK3
 RT complex.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF140243; AAF22574.1; -.
 DR INTERPRO: IPR000342; -.
 DR INTERPRO: IPR001158; -.
 DR PFAM: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGSPTROTEIN.
 SQ SEQUENCE 706 AA; 79196 MW; C3D0AF0D9540F162 CRC64;

Query Match 57.6%; Score 159; DB 13; Length 706;
 Best Local Similarity 56.9%; Pred. No. 1.4e-11;
 Matches 29; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 1 LTLGHFKQLSKKGNRYFFKASDEFACGAVFEETIMDETVLPMYEGRII 51
 DB 649 VTLGQFKELTKKSGNRYFFKASDEFACGAVFEETIMDETVLPMYEGRII 699

RESULT 12
 ID Q9VYZ9 PRELIMINARY; PRT; 623 AA.
 AC Q9VYZ9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE DSH PROTEIN.
 GN DSH.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Adayani A., An H.-J., Andrews-Plamkoc C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke G., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasero P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Mishina N.V., Modyarty C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wesserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong X., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003485; AAF48033.1; -
 DR HSSP: Q12959; 1PBR.
 DR FLVBASE: FBgn0000499; dash.
 DR INTERPRO: IPR000591; -
 DR INTERPRO: IPR001158; -
 DR INTERPRO: IPR001478; -
 DR PFAM: PF00595; PDZ; 1.
 DR PFAM: PF00610; DEP; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PFAM: PF00778; DIX; 1.
 SQ SEQUENCE 623 AA; 68917 MW; 0BA24ED350666CFS CRC64;

Query Match 39.7%; Score 109.5; DB 5; Length 623;
 Best Local Similarity 46.2%; Pred. No. 1.7e-05;
 Matches 24; Conservative 10; Mismatches 15; Indels 3; Gaps 2;
 QY 1 LTLGHKEQLSKK-GNYRYFFKASDEFACGAVFEIIMDETVLPMYEGRI 51
 DB 35 VTLRDEKVLNQNNNYKFFKSMADF--GVYKEIADSTILPCFNRRV 84

RESULT 13
 O9NLA6 PRELIMINARY; PRT; 685 AA.
 ID O9NLA6
 AC O9NLA6
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE DISHEVELLED HOMOLOG.
 GN CDSH.
 OS Clona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
 OC Clonidae; Clona.
 OX NCBI_TaxID-7719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imai K., Takada N., Satoh N., Satou Y.;
 RT "An essential role of beta-catenin in the endoderm specification of
 RT ascidian embryo."
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB031541; BAA92183.1; -
 DR EMBL: AB031541; BAA92183.1; -
 SQ SEQUENCE 685 AA; 75759 MW; B7E211C6D48BC95 CRC64;

Query Match 37.1%; Score 102.5; DB 5; Length 685;
 Best Local Similarity 41.2%; Pred. No. 0.00014;
 Matches 21; Conservative 14; Mismatches 13; Indels 3; Gaps 2;

OY 1 LTLGHKEQLSKKGNRYFFKASDEFACGAVFEIIMDETVLPMYEGRI 51
 DB 29 IYLGFKAH-KRINYKFFKSTADF--GVYKEEVTNDRKSTILPCFNRRV 76
 RESULT 14

O9UG5 PRELIMINARY; PRT; 695 AA.
 ID O9UG5
 AC O9UG5
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE DISHEVELLED-1.
 GN DVL-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SHRSP, AND WKY.
 RA De Lange R.P.D., Burr K., Clark J.S., Negri C.D., Brosnan M.J.,
 RA St Clair D.M., Shaw D.J., Dominiczak A.F.;
 RT "Does Dishevelled-1 determine sensitivity to cerebral ischaemic insult
 RT in a rat model of stroke?"
 RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF143546; AAD33897.2; -
 DR EMBL: AF143545; AAD33896.2; -
 DR HSSP: P31016; 1BE9.
 DR INTERPRO: IPR000591; -
 DR INTERPRO: IPR001158; -
 DR INTERPRO: IPR001478; -
 DR PFAM: PF00595; PDZ; 1.
 DR PFAM: PF00610; DEP; 1.
 DR PFAM: PF00778; DIX; 1.
 DR PFAM: PF00778; DIX; 1.
 SQ SEQUENCE 695 AA; 75446 MW; EEC4AA99A117D22A CRC64;

Query Match 34.4%; Score 95; DB 11; Length 695;
 Best Local Similarity 39.6%; Pred. No. 0.0012;
 Matches 21; Conservative 10; Mismatches 18; Indels 4; Gaps 2;
 QY 1 LTLGHKEQLSKK-GNYRYFFKASDEFACGAVFEIIMDETVLPMYEGRI 51
 DB 28 VTLADKRVNLNRPVHAKFFKSMQDF--GVYKEIADSTILPCFNRRV 78

RESULT 15
 O9XYC1 PRELIMINARY; PRT; 743 AA.
 ID O9XYC1
 AC O9XYC1
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE D-AXIN.
 GN D-AXIN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID-7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamada F., Tomoyasu Y., Takatsu Y., Nakamura M., Nagai S., Suzuki A.,
 RA Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T.;
 RT "Negative regulation of wingless signaling by D-axin, a *Drosophila*
 RT homolog of axin."
 RL Science 283:1739-1742(1999).
 DR EMBL: AF086811; AAD24886.1; -
 DR INTERPRO: IPR000342; -
 DR INTERPRO: IPR001158; -
 DR PFAM: PF00778; DIX; 1.
 DR PFAM: PF00778; DIX; 1.
 SQ SEQUENCE 743 AA; 81515 MW; 840B91BCE6618FA CRC64;

Query Match 30.8%; Score 85; DB 5; Length 743;
 Best Local Similarity 33.3%; Pred. No. 0.023;
 Matches 15; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 18:46:26 ; Search time 4956.99 Seconds
(without alignments)
8404.839 Million cell updates/sec

Title: US-09-587-574-6

Perfect score: 2825
Sequence: 1 cagcgcgtcgcgatgatatt.....accctgtctcagcctaagc 2825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pi1:*
13: gb_pi2:*
14: gb_pi3:*
15: gb_pi4:*
16: gb_pi5:*
17: gb_pi6:*
18: gb_pi7:*
19: gb_pi8:*
20: gb_pi9:*
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95: em_pi49:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2825	100.0	2825	9 AF073788	AF073788 Mus muscu
3	2645.2	93.6	3016	94 AF205889	AF205889 Mus muscu
4	2389.2	84.6	3216	94 AF017757	AF017757 Ratus no
5	1944.4	68.8	3072	88 AF078165	AF078165 Homo sapi
6	1571.2	55.6	2538	88 AF205888	AF205888 Homo sapi
7	1359.2	48.1	2104	89 AK025718	AK025718 Homo sapi
8	955	33.8	191041	69 AC024114	AC024114 Mus muscu
9	850.2	30.1	3485	8 AB032263	AB032263 Danio rer
10	698.2	24.7	184263	85 AC004805	AC004805 Homo sapi
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12	401.8	14.2	3411	88	AF009674
13	378.6	13.4	1863	85	AB052751
14	369	13.1	369	9	A98522
15	337.6	12.0	3761	94	AF009011
16	316	11.2	3156	8	AF009012
17	312.2	11.1	3460	94	AF017756
18	265	9.4	2529	8	AF097313
19	256.6	9.1	3066	8	AB032262
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21	209.4	7.4	35054	91	HS333B10
22	209.4	7.4	39170	85	AC005202
23	209.4	7.4	133069	70	AC026836
24	209.4	7.4	187272	74	AC069076
25	207	7.3	207	9	A98524
26	165.8	5.9	2121	8	AF140243
27	162	5.7	162	9	A98523
28	153	5.4	153	9	A98525
29	79.2	2.8	31557	91	HS31464
30	79.2	2.8	133069	70	AC026836
31	79.2	2.8	187272	74	AC069076
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36	59.4	2.1	278229	76	AC074322
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38	58.8	2.1	2132	93	HS094829
39	58.8	2.1	2383	10	I65400
40	58.8	2.1	2383	93	HSU70426
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ALIGNMENTS

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DEFINITION	Sequence 6 from Patent WO911780.				
ACCESSION	A98521				
VERSION	A98521.1	GI:6781607			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 2825)				
AUTHORS	Blitchmeier, W. and Behrens, J.				
TITLE	CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TUMOR ILLNESSES				
JOURNAL	Patent: WO 9911780-A 6 11-MAR-1999;				
FEATURES	BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)				
Source	Location/Qualifiers				
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Matches 2825; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS	AF073788 2825 bp mRNA
DEFINITION	Mus musculus conductin mRNA, complete cds.
ACCESSION	AF073788
VERSION	AF073788.1 GI:3309246
KEYWORDS	
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus
AUTHORS	Behrens,J., Jerchow,B.-A., Wurttele,M., Grimm,J., Asbrand,C., Wirtz,R., Kuhl,M., Wedlich,D. and Birnmeier,W.
TITLE	Functional interaction of an axlin homolog, conductin, with beta-catenin, APC, and GSK3beta
JOURNAL	Science 280 (5363), 596-599 (1998)
MEDLINE	9821239
REFERENCE	2 (bases 1 to 2825)
AUTHORS	Behrens,J., Jerchow,B.-A. and Birnmeier,W.
TITLE	Direct Submmission
JOURNAL	Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for Molecular Medicine, Robert-Koessle 10, Berlin 13122, Germany
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BASE COUNT 703 a 815 c 813 g 494 t

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Matches 2825; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS	AF205889	3016 bp	mRNA	ROD	03-JAN-2000
DEFINITION	Mus musculus Axin2 (Axin2) mRNA, complete cds.				
ACCESSION	AF205889				
VERSION	AF205889.1	GI:653585			
KEYWORDS					
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 3016)				
TITLE	Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G., Jenkins,N.A., Warburton,D. and Costantini,F.				
JOURNAL	Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic axis formation				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 3016)				
TITLE	Zhang,T. and Costantini,F.				
JOURNAL	Direct Submission				
FEATURES	Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 M16th St. HSC 1416, New York, NY 10032, USA				
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gene	RYVKKKASDEPACCAVFEEIWDDETVPMYEGRLGKVERID"				
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REFERENCE	1 (bases 1 to 3072)		
AUTHORS	Ma1,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.		
TITLE	Cloning of the human homolog of conductin (AXIN2), a gene mapping		
JOURNAL	to chromosome 17q23-q24		
MEDLINE	Genomics 55 (3), 341-344 (1999)		
REFERENCE	2 (bases 1 to 3072)		
AUTHORS	Ma1,M., Qian,C., Smith,D.I. and Liu,W.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,		
FEATURES	200 First Street SW, Rochester, MN 55905, USA		
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ORIGIN

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 REFERENCE 1 (bases 1 to 2538)
 Zhan, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
 Jenkins, N.A., Warburton, D. and Costantini, F.,
 TITLE Properties of mouse Axin2 and human AXIN2: Chromosomal location,
 expression pattern, interaction with Axin and effects on embryonic

axis formation
 unpublished
 2 (bases 1 to 2538)
 Zhan, T. and Costantini, F.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
 University, 701 Wictheth St. HMSC 1416, New York, NY 10032, USA
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LOCUS Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT
DEFINITION
SEQUENCE, 30 unordered pieces.
AC024114
AC024114.8 GI:11094615
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191041)
Worley, K.C.,
Dedert, D., Thomas, S., Okun, G., Carlock, C., Garner, T.,
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Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
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Fernandez, C., Ferraruto, D., Fortum-Tansey, J., Gail, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogue, M.,
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Kovach, C., Liu, J., Liu, W., Louie, H., Lozano, R., Martin, R.,
Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogun, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Wallington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstein, G.,
Worley, K. and Gibbs, R.
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 191041)

AUTHORS
TITLE
JOURNAL

COMMENT

Worley, K.C.
Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 4, 2000 this sequence version replaced gi:9929587.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MACA
Center clone name: RP23-278J12
----- Summary Statistics
Sequencing vector: M13, L08821
Chemistry: Dye-primer, Big Dye 3, 95% of reads
Chemistry: Dye-terminator, Big Dye 3, 5% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; average-tp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 30 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 19344: contig of 19344 bp in length
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DEFINITION Danio rerio mRNA for axin2, complete cds.
ACCESSION AB032263
VERSION AB032263.1 GI:7229079
KEYWORDS
SOURCE
ORGANISM
Danio rerio
Danio rerio cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.

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REFERENCE
1 (sites)
Shimizu, T., Yamana, Y., Ryu, S.L., Hashimoto, H., Yabe, T.,
Hirata, T., Bae, Y.K., Hibi, M. and Hirano, T.
Cooperative roles of Bozozok/Dharma and Nodal-related proteins in
the formation of the dorsal organizer in zebrafish
Mech. Dev. 91 (1-2), 293-303 (2000)
2 (bases 1 to 3485)
Hirano, T., Hibi, M. and Shimizu, T.
Direct Submission
Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Hirano, Biomedical Research Center, Osaka Univ. Med. School,
Department of Molecular Research Center, 2-2, Yamadaoka, Suita, Osaka
565-0871, Japan (E-mail: hirano@molonc.med.osaka-u.ac.jp,
URL: http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html,
Tel: 81-6-879-3880, Fax: 81-6-879-3889)

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ACCESSION	AC024114		
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SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
AUTHORS	1 (bases 1 to 191041) Metzger M.L., Lewis L.R., Hume J., Edwards C., Harris C., Dederich D., Thomas S., Okunoue G., Carlack C., Garner T., Addison S., Pece A., Williams G., Bonnin D., Brooks A., Brown J., Buhay C., Bunac C., Burkett C., Chacko J., Chen G., Chen Z., Cox C., Davis C., Delgado O., Ding Y., Dugan-Rocha S., Fernandez C., Ferraguto D., Forcun-Tansley J., Gill R., Gorell J.H.R., Gunaratne P., Haller G., Hernandez J., Hoques M., Hosak H., Hou X., Huber J., Jackson L., Jia Y., Kelly J., Kelly S., Kovar C., Liu J., Liu W., Louisseged S., Lozano R.J., Martin R., Massey E., McLeod M.P., Mel G., Moore S., Morgan M., Morris S., Neal D., Nelson A., Nguyen R., Nguyen N., Ogulu M., Parrish B., Perez L., Reiter D., Say J., Shen H., Vasquez L., Watlington S., Williamson A., Wrensford G., Zhou X., Bouck J., Hodgson A., Muzny D.M., Rives M., Scherer S., Sodergren E., Weinstock G., Morley K. and Gibbs R.		
TITLE	Direct Submission		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 191041)		
AUTHORS	Morley K.C.		
JOURNAL	Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
COMMENT	On Nov 4, 2000 this sequence version replaced gi:1929587.		

Chemistry: Dye-terminator Big Dye: 5% of reads	
Assembly program: Phrap: version 0.990329	
Consensus quality: 158769 bases at least Q40	
Consensus quality: 172780 bases at least Q30	
Consensus quality: 179030 bases at least Q20	
Estimated insert size: 180377; sum-of- <i>contigs</i> estimation	
Quality coverage: 0x in Q20 bases; agscore- <i>fp</i> estimation	
Quality coverage: 3.2x in Q20 bases; sum-of- <i>contigs</i> estimation	

* NOTE: Estimated insert size may differ from sequence length	
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).	
* NOTE: This is a 'working draft' sequence. It currently	
* consists of 30 <i>contigs</i> . The true order of the pieces	
* is not known and their order in this sequence record is	
* arbitrary. Gaps between the <i>contigs</i> are represented as	
* runs of N, but the exact sizes of the gaps are unknown.	
* This record will be updated with the finished sequence	
* as soon as it is available and the accession number will	
* be preserved.	
1	19344: <i>contig</i> of 19344 bp in length
19345	19444: gap of unknown length
19445	33763: <i>contig</i> of 14319 bp in length
33764	33863: gap of unknown length
33864	47738: <i>contig</i> of 13875 bp in length
47739	47838: gap of unknown length
47839	59611: <i>contig</i> of 11773 bp in length
59612	59711: gap of unknown length
59712	67897: <i>contig</i> of 8186 bp in length
67898	67997: gap of unknown length
67998	77929: <i>contig</i> of 9932 bp in length
77930	78029: gap of unknown length
78030	86605: <i>contig</i> of 8576 bp in length
86606	86705: gap of unknown length
86706	93904: <i>contig</i> of 7199 bp in length
93905	94004: gap of unknown length
94005	104236: <i>contig</i> of 10232 bp in length
104237	104336: gap of unknown length
104337	113241: <i>contig</i> of 8905 bp in length
113242	113341: gap of unknown length
113342	120171: <i>contig</i> of 6830 bp in length
120172	120271: gap of unknown length
120272	125989: <i>contig</i> of 5718 bp in length
125990	126089: gap of unknown length
126090	131869: <i>contig</i> of 5780 bp in length
131870	131969: gap of unknown length
131970	139294: <i>contig</i> of 7325 bp in length
139295	139394: gap of unknown length
139395	146006: <i>contig</i> of 6612 bp in length
146007	146106: gap of unknown length
146107	150788: <i>contig</i> of 4682 bp in length
150789	150888: gap of unknown length
150889	156925: <i>contig</i> of 6037 bp in length
156926	157025: gap of unknown length
157026	161170: <i>contig</i> of 4145 bp in length
161171	161270: gap of unknown length
161271	164311: <i>contig</i> of 3041 bp in length
164312	164411: gap of unknown length
164412	167354: <i>contig</i> of 2943 bp in length
167355	167454: gap of unknown length
167455	171291: <i>contig</i> of 3837 bp in length
171292	171391: gap of unknown length
171392	174233: <i>contig</i> of 2842 bp in length
174234	174333: gap of unknown length
174334	177744: <i>contig</i> of 3411 bp in length
177745	177844: gap of unknown length
177845	179402: <i>contig</i> of 1558 bp in length
179403	179502: gap of unknown length
179503	182420: <i>contig</i> of 2918 bp in length
182421	182520: gap of unknown length
182521	184923: <i>contig</i> of 2403 bp in length
184924	185023: gap of unknown length
185024	187054: <i>contig</i> of 2031 bp in length
187055	187154: gap of unknown length

Db 2690 GAGAAAGTGGAGTATGAGCTGTGGCTGGCCGCTGTGGCAAGCAGGCCCTTGGCGG 2749
QY 2783 cac 2485
Db 2750 CAC 2752

RESULT 13
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LOCUS Homo sapiens Axln2 mRNA for conductin, partial cds and 3' UTR.
DEFINITION AB052751
ACCESSION AB052751
VERSION AB052751.1 GI:11967903
KEYWORDS
SOURCE Homo sapiens CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Takahashi, M. and Furukawa, Y.
TITLE Identification of 3' UTR of Axln2
JOURNAL Published Only in Database (2000) In press
REFERENCE 2 (bases 1 to 1863)
AUTHORS Nakamura, Y., Furukawa, Y. and Takahashi, M.
TITLE Direct Submision
JOURNAL Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yotchi
Furukawa, Institute of Medical Science, Human Genome Center, 4-6-1-
Shirokanebashi, Minato-Ku, Tokyo 108-1639, Japan
(E-mail: furukawa@ims.u-tokyo.ac.jp, Tel: 81-35449-5373,
Fax: 81-35449-5406)

FEATURES
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Matches 408; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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Db 1 AGCTGAGGAGGCGCTGCTGCCAGGCTAGCTGAGGTGTGGAAGCCCCCAAAGCAGCGGTGCT 60

QY 2352 ggcgtgcacagtcagcaggaaggaagaaacacacgcgtcgtcgtcagcaggaagcctcac 2411
Db 61 GGTGTGGCCAGTGCAGAGAGGAGAGAAATCATTCGGCCACTGTTCAGACGGAGCCACAC 120

QY 2412 ccttcgcaaaccccaagcctgcgtccagaagatcacaaagagcgaagaagaaactgcgaagt 2471
Db 121 CCTTTCCTCAATTCACACCTGCTGCCAAGATACAAAGAGCCAAAGAACTGCGAGGTG 180

QY 2472 tccacagcgtccacagcagtcgaagtcgtgtgtcaccactcttctgtgtgagaagaatlc 2531
Db 181 TCCACGCGCTCCAGGCGCAGTGTGTGTCTTACTTCTTGTGTGGGGAAGAAATTC 240

QY 2532 catacagaggaatgctcgaaggtctcaaaagcttgacccttggtgcaactcaagagagcagctca 2591

Db 241 CATACCGAGAGATGCTGAGAGGCTCAGACGTTGACCTGGGCCACTTAAGACACTCA 300
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Db 301 GCAAAAAGGAAATATAGTATTACTTCAAAAAACAAGCAGTGTGCTGTGGAG 360

QY 2652 cagttttgagagatcttgcgcagcagcagatgtctcccatgtacgaagagagatcc 2711
Db 361 CGGTGTTTGGAGATCTGGAGAGATGAGACGGTGTCTCCGATGTGAAGCGCGGATTC 420

QY 2712 tggcgaagtggagagatcagatcagcttgcctc 2748
Db 421 TGGCAAAAGTGGAGCGGATCGATTGAGCCCTGGGGTC 457

RESULT 14
A98522 369 bp DNA PAT 26-JAN-2000
LOCUS A98522
DEFINITION Sequence 7 from Patent WO9111780.
ACCESSION A98522
VERSION A98522.1 GI:6781608
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 369)
AUTHORS Birnmeier, W. and Behrens, J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
JOURNAL TUMOR ILLNESSES
PATENT: WO 9111780-A 7 11-MAR-1999;
BIRNMEIER WALTER (DE); BEHRENS JURGEN (DE)

FEATURES
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Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 506 ttccctggagaggaagaatgtgtgatacgtcgtgacttcctggttctgttaatgtgttc 565
Db 61 TTCTGTGAGAGGAGGAAGAAATGTGTGATACGCTGACTCTGTGTTCTGTAAATGGGTTT 120

QY 566 aggcagatgacacttgaagatlaccaaaacttgcgagtcgagcgaagcaatcctaagag 625
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QY 626 tacattgaaacaacagcgtgtgtcctcaagcagctgaagccgcaccacaagacctacata 665
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QY 806 gaatalcgtg 814
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QY 2730	tcgaactagccttgacctcctc 2751	
Db 2974	TGGACTGAGCACTGGCAGCAC 2995	

Search completed: June 7, 2001, 00:34:09
Job time: 20863 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 22:08:02 ; Search time 276.75 Seconds
(without alignments)
5959.105 Million cell updates/sec

Title: US-09-587-574-6

Perfect score: 2825
Sequence: 1 cagccgttcgcgatgatatt.....accctgtctcagcctaagc 2825

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 22: /SID52/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2825	100.0	2825	20	X23369 Human conductin DN
2	2523	89.3	2523	20	X23370 Human conductin CD
3	401.8	14.2	3411	20	X09012 Murine axin gene.
4	337.6	12.0	3761	20	X09013 CDNA encoding huma
5	322.2	11.4	1205	21	A77843 p53 response prote
6	317.8	11.2	401	21	A77754 Human cyclin res
7	58.8	2.1	2383	17	T11418 Human CRI CDNA. H
8	58.8	2.1	2406	21	A39660 Cytokine response
9	58.8	2.0	606	21	A39678 Human RATH1.1 DNA.
10	57.2	2.0	746	19	V34780
11	57.2	2.0	746	19	V34780

12	50.8	1.8	2272	19	V34779	Mouse RATH1.1 DNA.
13	49.2	1.7	7720	21	A53800	Genomic DNA encodi
14	48.2	1.7	1505	15	O55750	Genomic clone G1FF
15	42.6	1.5	2006	22	A89195	Wheat phytochelati
16	42.2	1.5	10732	21	A10594	Gene encoding a su
17	40.6	1.4	18660	21	A58472	Nucleotide sequenc
18	40.6	1.4	2172	19	V02996	Mammalian Ena (Men
19	39.8	1.4	1848	18	T97129	Human netrin-1 cDN
20	39.6	1.4	2356	21	A87736	Human secreted pro
21	39.4	1.4	1000	21	A02484	Human colon cancer
22	39.4	1.4	745	19	V38084	Human regulator of
23	39	1.4	1691	21	Z36910	CDNA encoding a re
24	39	1.4	1721	17	T39752	Macaque mucosal ad
25	39	1.4	1923	20	X51745	DNA encoding a hum
26	38.6	1.4	1357	20	Z1263	Human gene expres
27	38.4	1.4	4839	18	T85642	Ras-binding protei
28	38.2	1.4	5059	20	X84332	Stealth virus nucl
29	38	1.3	756	12	O15508	Modified Fl-spectif
30	38	1.3	1164	21	A52090	Murine RGS protein
31	37.8	1.3	799	21	A31144	Plant microsatellit
32	37.4	1.3	1933	21	F14882	Trichoderma reesei
33	37.4	1.3	2898	19	V02998	Mouse neural Wena+
34	37	1.3	2457	22	A89216	Moraxella catarrha
35	37	1.3	5868	21	A28019	Quelling deficient
36	37	1.3	6916	21	A28018	Genomic DNA sequen
37	36.8	1.3	1704	17	T11413	Sequence encoding
38	36.8	1.3	114955	20	X35491	Human adenostine A1
39	36.6	1.3	795	19	V55830	FLG Insert Stabli
40	36.6	1.3	799	19	V55831	Nucleotide sequenc
41	36.6	1.3	1218	21	A02488	Human colon cancer
42	36.6	1.3	1976	21	A50254	Epstein Barr virus
43	36.6	1.3	2560	21	A75454	Nucleotide sequenc
44	36.6	1.3	5452	20	X90923	Anti-sense strand
45	36.6	1.3	8705	20	Z23778	Vector pShuttle DN

ALIGNMENTS

RESULT 1	
ID X23369	standard; cDNA; 2825 BP.
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XX 17-JUN-1999	(first entry)
XX	
DE Human conductin DNA.	
XX	
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW Wntless signalling pathway; Adenomatous Polyposis Coli; APC;	
KW tumour suppressor; ss.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
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FT	/tag- a
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FT	446..814
FT	/tag- b
FT	/note= "regulator of G-protein signalling region as described in Claim 19"
FT	1241..1402
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FT	/note= "as described in Claim 20"
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FT	2561..2713
FT	misc_feature

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Db	2761	cttgagcagaacacctgcgcgtgcacccatgagccgaagcccaagacctgtctccaagcc	2820
QY	2821	tacgc 2825	
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RESULT	2		
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XX	AC	X23370;	
XX	DT	17-JUN-1999 (first entry)	
XX	DE	Human conductin cDNA.	
XX	KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW	KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW	KW	Wingless signalling pathway; Adenomatous Polyposis Coli; APC;	
XX	OS	tumour suppressor; ss.	
XX	OS	Homo sapiens.	
XX	PN	W09911780-A2.	
XX	PD	11-MAR-1999.	
XX	PF	01-SEP-1998; 98WO-DE02621.	
XX	PR	02-SEP-1997; 97DE-1038205.	
XX	PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX	PI	Behrens J, Birchmeier W;	
XX	DR	WPI: 1999-214706/18.	
XX	DR	P-PSDB: W93570.	
XX	PT	Tumour-suppressing protein conductin - used for treatment and	
XX	PT	diagnosis of tumors	
XX	PS	Claim 18; Fig 3; 22pp; German.	
XX	XX	This invention describes a novel human conductin protein which has	
CC	CC	anti-tumour activity. Detecting the presence or amount of conductin,	
CC	CC	at protein or nucleic acid levels, is used to diagnose tumours, while	
CC	CC	agents that (re)activate conductin are used for tumour therapy.	
CC	CC	Conductin binds to beta-catenin and induces its cytoplasmic degradation,	
CC	CC	resulting in blockade of the Wnt/Wingless signalling pathway in	
CC	CC	vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)	
CC	CC	fragments and, in conjunction with APC, acts as a tumour suppressor.	
XX	XX	Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;	
QY	Query Match	89.3%; Score 2523; DB 20; Length 2523;	
Db	Best Local Similarity	100.0%; Pred. NO. 0; Mismatches 0; Indels 0; Gaps 0;	
Db	Matches 2523; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	215	atgagtagcgccggttgtagtgcactctccatgccagacgagcgtcttcgagagat	274
Db	1	atgagtagcgccggttgtagtgcactctccatgccagacgagcgtcttcgagagat	60
QY	275	gtccgcgagcccggttcgcggagagaagggagacccacggtgcagcctagtgtg	334

[illegible]

QY	1415	ga7gaaagaaagaaagaggtctctgaagcaagccctgaagctcaacgagatctgaagacacgcgtccag	1474
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QY	1475	caaccccttgagcctctctacacctctccgagcaactctgaagagagaccccaaacacatttgagac	1534
Db	1261	caaccccttgagcctctctacacccctccgagcaactctgaagagagaccccaaacacatttgagac	1320
QY	1535	gaccacactctccagaggtgctcccaagaaaccccgagctctgaattcccccgtgtgtgtctgctaac	1594
Db	1321	gaccacactctccagaggtgctcccaagaaaccccgagctctgaattcccccgtgtgtgtctgctaac	1380
QY	1595	agcccaacgctccgcgtctcccccagaccacacacacagacacacacacacacacacacacacacac	1654
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QY	1715	aagagctctctcgacacaaacagacgagaaagacagttctcaacacacacacacacacacacacac	1774
Db	1501	aagagctctctctcgacacaaacagacgagaaagacagttctcaacacacacacacacacacacacac	1560
QY	1775	gcacgtccccaagaaagaaagagagatcgagacacagacacacacagagagctccgtctgtccctc	1834
Db	1561	gcacgtccccaagaaagaaagagagatcgagacacagacacacacacagagagctccgtctgtccctc	1620
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QY	2015	gcagagagagcccccaagctctctcttgagagaaagagagagacaggtctcaacagagatgtctctgagaggt	2074
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QY	2135	agctaacacatctgagatctgtccacgtctgtcgccccacagagaaacgagatcaagcccgagacacatctg	2194
Db	1921	agctaacacatctgagatctgtccacgtctgtcgccccacagagaaacgagatcaagcccgagacacatctg	1980
QY	2195	cttgagagagcagagagacacatcccgatctgaatctgtgccccgagctccacacacatttacccaaagacaccc	2254
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QY	2255	gacatagctcccccctctaaccccaacacacacatttgagacacagctctgaagagaaagctgtcccgacag	2314
Db	2041	gacatagctcccccctctaaccccaacacacacatttgagacacagctctgaagagaaagctgtcccgacag	2100
QY	2315	cttgagagagaggtgtctgaagagcccaagagacagctgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2374
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QY	2375	aggaacacactctgtgctgtctgtctcaagagagagcctctcaacccctctgtccaaacccaaagcctgtgct	2434
Db	2161	aggaacacactctgtgctgtctgtctcaagagagagcctctcaacccctctgtccaaacccaaagcctgtgct	2220
QY	2435	ccagagagatctcaaaagagcccaagaaactctgtgacaaagtgtctcaacgctctccaaagccagctgtgag	2494
Db	2221	ccagagagatctcaaaagagcccaagaaactctgtgacaaagtgtctcaacgctctccaaagccagctgtgag	2280

ID	Sequence	Location/Qualifiers
Oy	2495 ctgtgtctacccactctttctctgtgagaagaattccctacagaagatctgtgaagct	2534
Db	2281 ctgtgtctccaccactcttctctgtgagaagaattccctacagaagatctgtgaagct	2340
Oy	2555 caaagcttgacccttgaggccactcaaggagcagctcagcaaaaaggaaattacagtat	2614
Db	2341 caaagcttgacccttgaggccactcaaggagcagctcagcaaaaaggaaattacagtat	2400
Oy	2615 tatttcaagaagagcagtgacgaattgtccctgcgagcagatttttgagagatctggagc	2674
Db	2401 tatttcaagaagagcagtgacgaattgtccctgcgagcagatttttgagagatctggagc	2460
Oy	2675 gacgagacagatgtctccccaatcagaagcagatctctggcacaagtctgagagatcgac	2733
Db	2461 gacgagacagatgtctccccaatcagaagcagatctctggcacaagtctgagagatcgac	2520
Oy	2735 tga 2737	
Db	2521 tga 2523	
RESULT	3	
OS	X09012	
ID	X09012	standard; DNA; 3411 BP.
XX	XX	
AC	X09012;	
XX	XX	
DT	14-JUN-1999	(first entry)
XX	XX	
DE	Human axin gene.	
XX	XX	
KW	Axin; cancer; breast cancer; colorectal cancer;	
KW	gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;	
KW	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;	
KW	beta-catenin; ss.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	2..2704
FT		/*tag- a
FT		/product= Axin
XX	XX	
PN	W09902179-A1.	
PD	21-JAN-1999.	
XX	XX	
PE	09-JUL-1998; 98MO-US14414.	
XX	XX	
PR	10-JUL-1997; 97US-0890865.	
XX	XX	
PA	(UYCO) UNIV COLUMBIA NEW YORK.	
XX	XX	
PI	Constantini F, Zeng L;	
XX	XX	
DR	WPI: 1999-120510/10.	
DR	P-PSDB: W96264.	
XX	XX	
PT	Newly isolated nucleic acid encoding "axis inhibition" protein	
PT	(Axin) - useful for detecting, diagnosing and treating cancer	
XX	XX	
PS	Disclosure: Figure 10A-10B; 95pp; English.	
XX	XX	
CC	Nucleic acids encoding mutant and wild type Axin and	
CC	oligonucleotides derived from them are useful for detecting	
CC	mutations in the Axin gene and for determining whether a subject is	
CC	likely to develop cancer (including breast, colorectal,	
CC	gastrointestinal, esophageal, carcinomas or melanomas). The wild	
CC	type Axin and homologues of Axin are useful for treating subjects	
CC	who are likely to develop cancer (thyroid carcinomas). The nucleic	
CC	acids are also useful for diagnosing cancer and for detecting	
CC	mutations in cancerous cells. Wild type Axin, its antisense	
CC	molecule and identified compounds form pharmaceutical compositions	

CC In the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
SQ Sequence 3411 BP, 752 A, 1010 C, 1066 G, 582 T, 1 other;

Query Match	14.2%;	Score 401.8;	DB 20;	Length 3411;
Best Local Similarity	52.7%;	Pred. No. 1.6e-97;		
Matches 1297;	Conservative	0;	Mismatches 1052;	Indels 114;
				Gaps 15;

QY	404	gagccgagggcgggcggtcccccgcgattccctcttgacccaaggctggaaccaagctttaaac	463
Db	323	gagcctctggaggcagctgctcccccaccccaaccacatactgaaagggcgctgagacatctgcat	382
QY	464	tcctctgttgggttgacacagatactgtgtacatacctctcccgagacttccctgtgagagagaa	523
Db	383	tcctctgtctggatgacccaagatgtgataagcgtcttcaagacttctcgaagagaaagggc	442
QY	544	tgtgtgtgatacgtctgagactctcgtctgtctgtctgtaatgggttccagcagatg- -----	574
Db	443	tgtgcgcagctgtgcgactctctgtgttgcctgcgacatgcgtctcagagagctgagaccgtc	502
QY	575	aaactcgaaaggtataccaaaactcttgcgagatggtgccaaagcatctataaagggtaca- ---	631
Db	503	gacttcgaaacgagagaaagagcgtctaaagctctggcgagagacatacttaaccgaaagtatactct	562
QY	632	gagaaacaacagcgtctgtctccaaagcagctgaaagcccgccacaagacatacagaagat	691
Db	563	gataacaaatgcatcgtgtctccggcagagccaagcgcagccacaagagctctcaataaaggcc	622
QY	692	ggacatacaagaaagcaacagatctgcgtctgatactgtgacaaaggtacagacgagatacag	751
Db	623	tgcatacatgaagagcagctgtgatactctgtcagatcttcttgacaagggccagacgaatacag	682
QY	752	gcaagtgtatggagagaaatagctctacacagtgcttcttgaactctgcacatttactctgaaat	811
Db	683	gccaactaaggagagaaacacactctccctctccataagctctgatacttattttgtgaaat	742
QY	812	gttgaaaggatgtggggggagaaacaacagctctatacagatgaacggg- -----	865
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QY	1262	ctatactttccgagaaacacacgcgctctcccaagagaaatgacgctgtgtgaaactgtctgc	1321

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Db      1217 cctccacatcccccagatcccggtccgaaagagt-----ccgctggtgagcctccaaag 1273
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      2750 cac 2752

Db      2750 cac 2752

RESULT 4
X09013
ID      X09013 standard; DNA: 3761 BP.
XX
AC      X09013;
XX
DT      14-JUN-1999 (first entry)
XX
DE      Murine axin gene.
XX
KW      Axin; cancer; breast cancer; colorectal cancer;
      gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
      diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
      beta-catenin; ss.
XX
OS      Mus musculus.
XX
FH      Key Location/Qualifiers
FT      CDS 1..2981
FT      /tag=a
FT      /product= Axin
XX
PN      W09902179-A1.
XX
PD      21-JAN-1999.
XX
PF      09-JUL-1998; 98MO-US14414.
XX
PR      10-JUL-1997; 97US-0890865.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Constantini F, Zeng L;
XX
XX      WPI; 1999-120510/10.
XX      P-PSDB; W96265.
XX
PT      Newly isolated nucleic acid encoding "axin inhibition" protein

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```

OY 2157 gtgcggcccaagagagatcagccgacacatctgttgaggcgagacatccc 2216
DB 2374 ggccttgcatacagcgtctcgtggcgctgcacccctcgtgtaagcgtacgttggga 2433
OY 2217 gctcagtcggccggcgctaccacattacccagagacccctgcagtcctcccttaacccac 2276
DB 2434 attctgtccagcctctctatcttctatccaaagatccacacatgcacacacacacagcc 2493
OY 2277 ccaacacttggcagcagtagaagaagccttcgcagcgttcgacagagtgtcga----- 2331
DB 2494 ctatccctctaccacagctggaagagcccgacgctgttggaaagaagaagagag 2553
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DB 2794 gggcgctgctgtccacccctggcgacgtcgaagagcgtgtaacagagagggagactaca 2853
OY 2610 ggtatatttcaagaagcagatgtacgaattgtcgtgcgagcagtttttgaggagatct 2669
DB 2854 gatactacttcaagaagtgatgtgattgtgactgtgtgtgtgacttggagagatgc 2913
OY 2670 gggagacagacagatgcctcccatgtacagagcagagatcctgtggcgaagtgcagagga 2729
DB 2914 gggagagatgagagccgtcttgcctgtcttgaagaaagatcatcgcaagtgagaaag 2973
OY 2730 tgcactgagccttggtcctc 2751
DB 2974 tggactgagcactgggacagcac 2995

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RESULT 5

A77843 standard; CDNA; 1205 BP.

AC A77843:

14-NOV-2000 (first entry)

CDNA encoding human colon tumour polypeptide. SEQ ID NO:123.

Human colon tumour polypeptide; tumour antigen; cancer; vaccine;

immunotherapy; diagnosis; progression; ss.

Homo sapiens.

WO200037643-A2.

29-JUN-2000.

23-DEC-1999; 99MO-US30909.

23-DEC-1998; 98US-0221298.

22-SEP-1999; 99US-0347496.

19-NOV-1999; 99US-0444242.

02-DEC-1999; 99US-0454150.

(CORI-) CORIXA CORP.

```

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yugu J;
DR WPI: 2000-442671/38.
XX New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer -
PS Claim 1; Page 125-126; 229pp; English.
XX
CC Sequences A77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumors.
CC The invention also specifically discloses 8 human colon tumour proteins
CC (B1897-B1904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs), preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be
CC cloned and then administered back to the patient to inhibit cancer
CC development. Nucleic acids encoding the polypeptides and antibodies
CC against the polypeptides may be used to determine the expression level
CC of a tumour protein of the invention, and therefore to determine whether
CC cancer cells are present. Such diagnostic methods may also be used to
CC monitor the progression of a cancer by repeating the processes at time
CC intervals, and comparing the current result to previous results. The
CC present sequence represents a cDNA encoding a human colon tumour
CC polypeptide.
SQ Sequence 1205 BP; 316 A; 248 C; 324 G; 317 T; 0 other:

```

Query Match 11.4%; Score 322.2; DB 21; Length 1205;
Best Local Similarity 89.0%; Pred. No. 2.1e-76;
Matches 348; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

OY 2358 ccagtcagcagagagagagacacactgctgctgtcagcagagcctacccctcg 2417
DB 1 ccagtcagcagagagagagacacactgctgctgtcagcagagcctacccctct 60
OY 2418 ccaaccagcctgctccagagatcacacaagagcacaagaactggaagtgccacg 2477
DB 61 ccaaccagcctgctccagagatcacacaagagcacaagaactggaagtgccacg 120
OY 2478 cgtccagagcagtgagctggtgtgtacactcttctgtgagagaagaattccatca 2537
DB 121 cgtccagagcagtgagctggtgtgtacactcttctgtgagagaagaattccatca 180
OY 2538 ggaagatgctgaagctcaagcttgacccctgagccactcaagagagcagcagcaaaa 2597
DB 181 ggaagatgctgaagctcaagcttgacccctgagccactcaagagagcagcagcaaaa 240
OY 2598 aggaattacagatatttcaagaagcgagtgacgaatttgcctgcgagcagtt 2657
DB 241 aggaattacagatatttcaagaagcgagtgacgaatttgcctgcgagcagtt 300
OY 2658 ttgagagatctggagcagcagagacagtgctcccatgtacgaagcagagatctgggca 2717
DB 301 ttgagagatctggagcagcagagacagtgctcccatgtacgaagcagagatctgggca 360
OY 2718 aagtgagagatcagcagcagccttgccctc 2748
DB 361 aagtgagagatcagcagcagccttgccctc 391

```

RESULT 6

XX	1D	A77754	standard; cDNA; 401 BP.
XX	AC	A77754;	
XX	DT	14-NOV-2000	(first entry)
XX	DE	cDNA encoding human colon tumour polypeptide, SEQ ID NO:33.	
XX	KW	Human colon tumour polypeptide; tumour antigen; cancer; vaccine;	
XX	OS	immunotherapy; diagnosis; progression; ss.	
XX	PN	Homo sapiens.	
XX	PD	WO200037643-A2.	
XX	PF	29-JUN-2000.	
XX	PR	23-DEC-1999; 99WO-US30909.	
XX	PR	23-DEC-1998; 98US-0221298.	
XX	PR	02-JUL-1999; 99US-0347496.	
XX	PR	22-SEP-1999; 99US-0401064.	
XX	PR	19-NOV-1999; 99US-0444242.	
XX	PR	02-DEC-1999; 99US-0454150.	
XX	PA	(CORI-) CORIXA CORP.	
XX	PI	Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;	
XX	PI	Wang T, Yuqiu J;	
XX	DR	WPI: 2000-442671/38.	
XX	PT	New colon tumor polypeptides used to inhibit the development of cancer,	
XX	PT	especially colon cancer, and for diagnosing and monitoring the	
XX	PT	progression of the cancer	
XX	PS	Claim 1; Page 96-97; 229pp; English.	
XX	CC	Sequences A77722-A78199 represent 478 cDNAs encoding proteins or	
XX	CC	portions of proteins which are associated with human colon tumors.	
XX	CC	The invention also specifically discloses 8 human colon tumour proteins	
XX	CC	(B11897-B11904). The nucleic acids, the polypeptides they encode, and	
XX	CC	antigen presenting cells (APCs, preferably dendritic cells) expressing	
XX	CC	such polypeptides may be used in vaccines that target tumour cells,	
XX	CC	especially colon tumour cells, thereby inhibiting the development of	
XX	CC	cancer. T-cells specific for the polypeptide expressed by the APC are	
XX	CC	used to remove tumour cells from biological samples, especially blood or	
XX	CC	fractions thereof. The sample or the isolated T-cells specific for the	
XX	CC	polypeptide can then be used to inhibit cancer development. CD4+ and/or	
XX	CC	CD8+ T-cells from a patient may be incubated with a polypeptide or	
XX	CC	nucleic acid of the invention, or an APC expressing such a polypeptide,	
XX	CC	to cause the proliferation of specific T-cells. The T-cells can be	
XX	CC	cloned and then administered back to the patient to inhibit cancer	
XX	CC	development. Nucleic acids encoding the polypeptides and antibodies	
XX	CC	against the polypeptides may be used to determine the expression level	
XX	CC	of a tumour protein of the invention, and therefore to determine whether	
XX	CC	cancer cells are present. Such diagnostic methods may also be used to	
XX	CC	monitor the progression of a cancer by repeating the processes at time	
XX	CC	intervals, and comparing the current result to previous results. The	
XX	CC	present sequence represents a cDNA encoding a human colon tumour	
XX	CC	polypeptide.	
XX	SO	Sequence 401 BP; 105 A; 88 C; 123 G; 85 T; 0 other;	
XX	QY	Query Match	11.2%; Score 317.8; DB 21; Length 401;
XX	QY	Best Local Similarity	89.1%; Pred. No. 1,8e-75;
XX	QY	Matches 343; Conservative	0; Mismatches 42; Indels 0; Gaps 0;
XX	QY	2364 agcagaagggacaggaacacactcgtcgtcgtcgaagcagcaggaacccaccccttcgcgaac	2423
XX	QY	1 agcagaagggacaggaacacactcgtcgtcgtcgaagcagcaggaacccaccccttcgcgaac	60

OY	2424	caagccgctgcctccgaagatcacaaagagcgaagaaacttgcgaagtgtccacgagcc	2403
Db	61	caagccctgcgcccgaagatcacaaagagcgaagaaacttgcgagctgcacgcgtcc	120
OY	2484	agcgcaatgcagctgtgtgtcactactttctctgtgtgaagaataattccatacagaag	2543
Db	121	agcgcaatgtggtgtgtgtcactactttttctctgtgtgaagaataattccatccgaag	180
OY	2544	tgtctgaaggtcctcaaaagcttgcacctgcgcccactctcaagagcagctcagcaaaagga	2603
Db	181	tgtctgaaggtcctcagaagcttgcacctgcgcccactctcaagagcagctcagcaaaagga	240
OY	2604	attccagatattattccaagaagagcgatgtgacgaatttcctctcgagagcagcttttgcg	2663
Db	241	atttaagattacttacttcaaaaagaacgagcatgtgatttccctgtgtgagcggtgtttgcg	300
OY	2664	agatcttgcgacgaagaaacagtgctccccaatgtaagaaagcaggaatccctgcgcaaaagc	2723
Db	301	agatcttgcgacgaagaaacagtgctccccaatgtaagaaagcaggaatccctgcgcaaaagc	360
OY	2724	agaagatcgaactgagaccttgcgcctc	2748
Db	361	agcgcatcgaatgagccctgcgtggctc	385

RESULT	7
XX	T11418
XX	T11418 standard; cDNA; 2383 BP.
XX	T11418;
XX	15-APR-1996 (first entry)
XX	p53 response protein PIGI-1 coding sequence.
XX	Response protein; PIGI-1; oncogenesis; cancer; tumour; p53; ss.
XX	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	93..701
XX	/*tag= a
XX	/product= p53 response protein PIGI-1.
XX	W09601907-A1.
XX	25-JAN-1996.
XX	10-JUL-1995; 95MO-U080597.
XX	12-JUL-1994; 94US-0274318.
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	Buckbinder L, Kley N, Seizinger BR, Talbott R;
XX	WPI: 1996-097636/10.
XX	P-PSDB; R89895.
XX	New isolated nucleic acid encoding p53 response protein PIGI-1
XX	used to develop prods. for the study, diagnosis and treatment of
XX	tumours and cancer
XX	Claim 3; Figure 6; 58pp; English.
XX	Recombinant production of PIGI-1 allows the study of the structure,
XX	function and role in oncogenesis of the protein. PIGI-1 and
XX	nucleic acid encoding it can also be used to develop products for
XX	use in treating tumours and cancer and in the diagnosis of cancer.
XX	Sequence 2383 BP; 561 A; 603 C; 657 G; 562 T; 0 other;

XX	18-SEP-2000	(first entry)
DT		
XX		
DE	Human CR1 cDNA.	
XX		
KW	CR2: human; antibody: cytokine response gene; cytosolic; anti-allergic;	
KW	immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;	
KW	cell differentiation; cancer; immune disease; rheumatologic disease;	
KW	transplant rejection; anti-infective; CR1; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	116..724
FT		/tag="a
FT		/product="CR1"
PN	US6057427-A.	
PD	02-MAY-2000.	
XX		
PE	05-JUN-1996;	96US-0652446.
XX		
PR	20-NOV-1991;	91US-0796066.
PR	10-AUG-1993;	93US-0104736.
PR	27-OCT-1994;	94US-0330108.
PR	05-JUN-1996;	96WO-US08992.
XX		
PA	(DART-) DARTMOUTH COLLEGE.	
XX		
PI	Beadling C, Smith KA;	
DR	WPI: 2000-338623/29.	
DR	P-PSDB: Y87952.	
XX		
PT	Novel antibody or antibody fragment which selectively binds to a	
PT	polypeptide encoded by cytokine response gene 2 -	
XX		
PS	Example IV; Column 75-78; 66pp; English.	
XX		
CC	This invention describes a novel isolated antibody or antibody fragment	
CC	(I) which selectively binds to a polypeptide encoded by cytokine response	
CC	gene 2 (CR2) and modulates CR2 activity. The products of the invention	
CC	have cytostatic, anti-allergic, immunosuppressive and antimicrobial	
CC	activity. The antibodies are useful as therapeutic agents for regulating	
CC	cellular proliferation and differentiation and for treating all kinds of	
CC	cancers, immune diseases such as allergic, autoimmune, and rheumatologic	
CC	diseases, transplant rejection, and as anti-infectives for fighting	
CC	viral, bacterial, parasitic and fungal infections. This sequence encodes	
CC	the human CR1 protein described in the invention.	
XX		
XX	Sequence 2406 BP; 565 A; 621 C; 656 G; 564 T; 0 other;	

	Query Match	2.1%	Score 58.8	DB 21	Length 2406
	Best Local Similarity	47.2%	Pred. NO. 1.1e-07		
	Matches 251	Conservative	0	Mismatches 127	Indels 9
				Gaps	2
QY	444	ggtggaccgaagctcttcaactctctgttgggtggaccagatggtcatcccttcgcga	503		
Db	297	ggtggagagagctgcgtcgaccctgcgtcgagagataaaatgtagtggctgtccacg	356		
QY	504	cttctctggagagggagaagatggtgagatacgctggaactctcggttctgttaatgggt	563		
Db	357	cttctctgaagacgaagcttcagttggaggaacctggaagcttgcgtctggcttggaggagt	416		
QY	564	tcaggcagatgaaacctggaaagatacacaacatttcgagttggcgcgaagcgaatcataaag	623		
Db	417	tca---agaagatccgatacgaatcacaagctgcctccagggcacaacccagatcttggag	473		
QY	624	ggtacatctggagacaacacggctgtctctccaaagcagatgaagccgcaccaaagactata	683		
Db	474	agttcaattg-----cagttgagggcccttaaaaggtcaacatttaccattgagaccgcgg	527		

Qy	684	tagagagtgctgcacgaagaacaacagatggtcgggtcaattgtttacccaaggaacagaccy	743
Db	528	agctgcacgaggaatggaactctgcagactctgccacaagccaacatgcttttattgcggtccaggga	587
Qy	744	agatccacggagatgcatggaagaanaatgctaccacaggtgtctcttgactctatgacattacc	803
Db	588	agacaagctaacctcgtatggaagaagactcctcaccacaagctcctctgaagtcgcctgttacc	647
Qy	804	tggaaatctgtagaagatgtggggggaaadaacaagcttaacatgaatgaacggggacttgga	863
Db	648	gggagcctcgtgtgcccaagccttcacgcgctctgtccactctgtccagctgcagcagctggacc	707
Qy	864	ggcctaaaggtctattgtgtgtactcctccacacttgatgaagaagaaggatggacgtgtg	923
Db	708	agccttcacacacacctgtgcttccacgagctgaggaagccacgacgggaagaagatggag	767
Qy	924	ccgacctcctaaagtcgaaactctcacccacacgctgtgtgctgtccagcaaac	975
Db	768	tcaccactcccgaggtggtgcctctgtgtggaggaagatctcgcaagc	819
RESULT	10		
ID	A39678	standard; cDNA; 606 BP.	
XX	A39678;		
XX	AC		
XX	AD		
XX	AE		
XX	AF		
XX	AG		
XX	AA		
XX	AB		
XX	AC		
XX	AD		
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XX	AC		
XX	AD		
XX	AE		

XX	RESULT 10
XX	A39678
XX	ID A39678 standard; cDNA; 606 BP.
XX	
XX	A39678;
XX	
XX	18-SEP-2000 (first entry)
XX	
XX	Cytokine response gene-related cDNA sequence (Seq ID 27).
XX	
XX	CR2; human; antibody; cytokine response gene; cytosolic; anti-allergic;
XX	immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;
XX	cell differentiation; cancer; immune disease; rheumatologic disease;
XX	transplant rejection; anti-infective; ss.
XX	
XX	Unidentified.
XX	
XX	US6057427-A.
XX	
XX	02-MAY-2000.
XX	
XX	05-JUN-1996; 96US-0652446.
XX	
XX	20-NOV-1991; 91US-0796066.
XX	10-AUG-1993; 93US-0104736.
XX	27-OCT-1994; 94US-0330108.
XX	05-JUN-1996; 96WO-US08992.
XX	
XX	(DART-) DARTMOUTH COLLEGE.
XX	
XX	Beadling C, Smith KA.
XX	
XX	WPI; 2000-338623/29.
XX	
XX	Novel antibody or antibody fragment which selectively binds to a
XX	polypeptide encoded by cytokine response gene 2 -
XX	Disclosure; Column 113-116; 66pp; English.
XX	
XX	This invention describes a novel isolated antibody or antibody fragment
XX	(1) which selectively binds to a polypeptide encoded by cytokine response
XX	gene 2 (CR2) and modulates CR2 activity. The products of the invention
XX	have cytosolic, anti-allergic, immunosuppressive and antimicrobial
XX	activity. The antibodies are useful as therapeutic agents for regulating
XX	cellular proliferation and differentiation for treating all kinds of
XX	cancers, immune diseases such as allergic, autoimmune, and rheumatologic
XX	diseases, transplant rejection, and as anti-infectives for fighting
XX	viral, bacterial, parasitic and fungal infections. This sequence is
XX	presented in the Seq ID list but is not described in the specification.
XX	
XX	Sequence 606 BP; 147 A; 172 C; 170 G; 117 T; 0 other;

XX 09-APR-1998.
 PD 06-OCT-1997; 97WO-US18259.
 PF 06-JUN-1997; 97US-0870815.
 PR 04-OCT-1996; 96US-0726228.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Glimeo CJ, Levinson DA;
 XX WPI: 1998-240085/21.
 DR P-PSDB: M59293.
 XX
 XX New activated T helper cell specific gene, RATH - used for
 PT developing products for treating e.g. autoimmune disorders,
 PT arthritis, graft rejection, asthma, allergy, infections or neoplasms
 XX
 PS Claim 1: Fig 1A-C: 127pp: English.
 XX
 CC This sequence encodes a novel member of the mouse regulator of G-protein
 CC signalling (RGS) gene family, RATH1.1. The encoded protein participates
 CC in the regulation, control and/or modulation of G-protein mediated
 CC signal transduction, involved in T cell activation, including T-helper
 CC (TH) cell and TH cell subpopulation activation. The protein can be
 CC used to develop products for treating autoimmune disorders, arthritis,
 CC graft rejection, asthma, allergy, infections or neoplasms.
 XX
 SQ Sequence 2272 BP; 548 A; 584 C; 625 G; 515 T; 0 other:

Query Match 1.8%; Score 50.8; DB 19; Length 2272;
 Best Local Similarity 50.3%; Pred. No. 0.0015;

Matches 183; Conservative 0; Mismatches 172; Indels 9; Gaps 2;

OY 444 ggtgagaccagcttaccctctctctgtgtgagaccagatgtgcatcctcttcgga 503
 DB 219 gatggagagagcttgcgtctgctgaacagtaaaatggggctgccttcacatg 278
 OY 504 ctcttcctgagagggagaaatgtgtgatacgtctgactctcgttctgttaatgggt 563
 DB 279 cctctctaaagcggagatcatcgtgaggaagaaactgagctcgtgtgctcgaggaagt 338
 OY 564 tcaaggcagatgaacctgaaagataccaaaacttgcgagtgcccaagaatctataaga 623
 DB 339 tca---agagagatcgcgtacgaccacaactggtccagggctcacacatcttgcag 395
 OY 624 ggtacatcagaaacacagcgttctcacaagcagctgaagcccgccacaaagactaca 683
 DB 396 agtacct-----ccgcagcgaagccctaaagagtgacatacagagacccgag 449
 OY 684 tagcagatgcatacgaagcaacagatcgctcgtgtcatgtttgacccagcagacgg 743
 DB 450 aactgaccacgaagcaaacaccacagctgcacactacacagtgctgagtgagtgaggga 509
 OY 744 agatccagcagatgtgaggaagaatgacctaccaggtgtcttgcattcgtacattacc 803
 DB 510 agaccgcacattgattgaggaagagactctatccgcgcttccctcaagatcaccaagcttacc 569
 OY 804 tggga 807
 DB 570 gcga 573

RESULT 13
 AS3800
 ID AS3800 standard; DNA: 7720 BP.
 AC AS3800;
 XX
 XX 19-DEC-2000 (first entry)
 XX

DE Genomic DNA encoding M68 TNF receptor related protein.
 XX
 KW M68: tumour necrosis factor; TNF; programmed cell death; apoptosis;
 KW receptor; immune response; cell differentiation; ligand; cancer;
 KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
 KW Grave's disease; idiopathic myxedema; autoimmune diabetes;
 KW thrombotic thrombocytopenic purpura; multiple sclerosis;
 KW liver diseases; autoimmune gastritis; ulcerative colitis;
 KW glomerulonephritis; pulmonary fibrosis; heart failure;
 KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
 KW osteoporosis; Alzheimer's disease; Parkinson's disease; stroke;
 KW myocardial infarction; human; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
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 FT /*label= Exon 1
 FT intron 6004..6139
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 FT exon 6140..6334
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 FT intron 6335..7091
 FT /*tag= d
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 FT exon 7092..7375
 FT /*tag= e
 FT /*label= Exon 3
 XX
 PN WO200046247-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000WO-US03037.
 XX
 PR 05-FEB-1999; 990US-0118902.
 PR 20-DEC-1999; 990US-0172754.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Bai C;
 XX
 DR WPI: 2000-506066/45.
 DR P-PSDB: Y97246.
 XX
 PT Isolated human M68 nucleic acids and proteins which are part of the
 PT tumor necrosis factor receptor (TNFR) family, useful for identifying
 PT modulators that may be used to treat various diseases e.g. cancer,
 PT osteoporosis, Alzheimer's disease
 XX
 PS Claim 19; Page 76-78; 80pp: English.
 XX
 CC The M68 protein is a member of a family of proteins which have
 CC roles in immune responses, cell death, cell proliferation and
 CC stimulation of cell differentiation. M68 lacks a transmembrane domain
 CC and is a secreted factor suggesting that it functions as a natural
 CC inhibitor for its ligand. The altered expression pattern of M68 in a
 CC multitude of tissues suggests that M68 may play a role in cancer by
 CC binding to its ligand and blocking apoptotic cell death induced by
 CC such a ligand. This anti-apoptotic role of M68 suggests that
 CC modulators of M68 will be useful in treatment of apoptosis-related
 CC diseases such as various forms of cancer and various bone disorders.
 CC M68 nucleic acids and proteins are therefore useful for treating
 CC conditions involving atypical apoptosis and for identifying
 CC modulators of M68. Modulators of M68 are useful for treatment of
 CC cancer and other diseases associated with abnormal levels of
 CC apoptosis including systemic lupus erythematosus, Hashimoto's
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
 CC liver diseases, autoimmune gastritis, ulcerative colitis,

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 18:57:37 ; Search time 136.23 Seconds
(without alignments)
3620.734 Million cell updates/sec

Title: US-09-587-574-6

Perfect score: 2825
Sequence: 1 cagccgtcgcgagatgattc.....accctgtctcagactacgc 2825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/1na/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/2/1na/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	58.8	2.1	2383	1	US-08-274-318-1 Sequence 1, Appl
2	58.8	2.1	2383	2	US-08-754-108-1 Sequence 1, Appl
3	58.8	2.1	2406	2	US-08-463-081B-1 Sequence 1, Appl
4	58.8	2.1	2406	2	US-08-461-379A-1 Sequence 1, Appl
5	58.8	2.1	2406	2	US-08-462-390B-1 Sequence 1, Appl
6	58.8	2.1	2406	3	US-08-463-074B-1 Sequence 1, Appl
7	58.8	2.1	2406	3	US-08-465-585C-1 Sequence 1, Appl
8	58.8	2.1	2406	3	US-08-465-585C-1 Sequence 1, Appl
9	57.2	2.0	606	2	US-08-463-081B-27 Sequence 27, Appl
10	57.2	2.0	606	2	US-08-461-379A-27 Sequence 27, Appl
11	57.2	2.0	606	2	US-08-462-390B-27 Sequence 27, Appl
12	57.2	2.0	606	3	US-08-463-074B-27 Sequence 27, Appl
13	57.2	2.0	606	3	US-08-465-585C-27 Sequence 27, Appl
14	57.2	2.0	606	3	US-08-652-446-27 Sequence 27, Appl
15	57.2	2.0	746	3	US-08-870-815-3 Sequence 3, Appl
16	57.2	2.0	746	4	US-08-949-004-3 Sequence 3, Appl
17	52.4	1.9	2272	2	US-08-726-228-1 Sequence 1, Appl
18	52.4	1.9	2272	3	US-08-870-815-1 Sequence 1, Appl
19	52.4	1.9	2272	4	US-08-949-004-1 Sequence 1, Appl
20	48.2	1.7	1505	1	US-07-915-246-1 Sequence 1, Appl
21	47.6	1.5	7218	1	US-08-232-463-14 Sequence 14, Appl
22	42.6	1.5	7218	1	US-08-232-463-14 Sequence 14, Appl
23	39.8	1.4	1848	1	US-08-635-137-1 Sequence 1, Appl
24	36.8	1.3	1704	2	US-08-748-483-2 Sequence 2, Appl
25	36.8	1.3	1704	1	US-08-528-199-5 Sequence 5, Appl
26	36.8	1.3	1704	1	US-08-528-199-5 Sequence 5, Appl
27	36.6	1.3	2580	4	US-09-050-863-2 Sequence 2, Appl

C	28	36.6	1.3	5452	2	US-09-130-114-1	Sequence 1, Appl
	29	36.6	1.3	10596	1	US-07-884-811-15	Sequence 15, Appl
	30	36.6	1.3	10596	1	US-07-885-971-15	Sequence 15, Appl
	31	36.6	1.3	10596	1	US-08-087-783A-15	Sequence 15, Appl
	32	36.6	1.3	10596	1	US-08-194-088B-15	Sequence 15, Appl
	33	36.6	1.3	10596	2	US-08-194-087-15	Sequence 15, Appl
	34	36.6	1.3	10596	5	PCT-US93-04648-15	Sequence 15, Appl
	35	36.4	1.3	1295	1	US-08-433-854-3	Sequence 3, Appl
	36	36.4	1.3	1295	1	US-08-174-745A-3	Sequence 3, Appl
	37	36.4	1.3	1295	2	US-08-195-947-3	Sequence 3, Appl
	38	36.4	1.3	1295	2	US-08-433-885-3	Sequence 3, Appl
	39	36.4	1.3	1295	2	US-08-433-908B-3	Sequence 3, Appl
	40	36.4	1.3	43280	2	US-08-804-227C-1	Sequence 1, Appl
	41	36.2	1.3	554	2	US-08-997-080-144	Sequence 144, App
	42	36.2	1.3	554	2	US-08-997-362-144	Sequence 144, App
	43	36.2	1.3	554	4	US-09-095-855-144	Sequence 144, App
C	44	36.2	1.3	2214	3	US-08-864-038A-1	Sequence 1, Appl
	45	36.2	1.3	2830	2	US-09-010-928B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-274-318-1
; Sequence 1, Application US/08274318
; Patent No. 5667987
; GENERAL INFORMATION:
; APPLICANT: Buckbinder, Leonard
; APPLICANT: Talbott, Randy
; APPLICANT: Seizinger, Bernd R.
; APPLICANT: Kley, Nikolai
; TITLE OR INVENTION: NO. 5667987e1 p53 Response Genes
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,318
; FILING DATE: 11-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogden, James M.
; REGISTRATION NUMBER: 32,962
; REFERENCE/DOCKET NUMBER: ON0127-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-727-3688
; TELEFAX: 206-727-3601
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-274-318-1

Query Match 2.1%; Score 58.8; DB 1; Length 2383;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;
444 ggtggcccaagttcttaccctctgttgggtgacccggatgtgcatctcttcggga 503
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Db 274 GGTGAGAGAGTCTGTCACCTGCTGCTGAGCAGTAAATGAGTGGCTGCTTCACG 333
QY 504 cttcccgaggagagaaatgltgtaacgtgagcttctgttctgtaataagt 563
Db 334 CTTTCTGAAACAGAGTTCACGAGGAAACCTGGAATTTGGCTGGCTGTGAGAGT 393
QY 564 tcaggcagatgaacctgaaggatataccaaacttgcagatgagcgaagaaactataa 623
Db 394 TCA---AGAAATCCGATCAGCTACCAAGCTGGCTCCAGGACACACAGATCTTTGAG 450
QY 624 ggtcatgtgaaacaacagcggttcttccaagcgtcgtgaagcccgcccaagcctaca 683
Db 451 AGTTGATTG-----CAGTAGAGGCCCTTAAAGAGTCAACATTGACATGACATGACCGCG 504
QY 684 tagcagatgcatcaagaagcaacagatcggtcgtcatgtttgacagagcacagacg 743
Db 505 AGCTGACGAGATGAACTGCAGACTGCCACAGCCACATGCTTTGATTCGGCTCAGGGGA 564
QY 744 agatccagcagatgtaggagaaatgctacacaggtgttcttgcatacttcaattacc 803
Db 565 AGACACGTAACCTGATGAGAGAGGACTCTTACCCACGCTTCTGAAAGTGGCTGCTTAC 624
QY 804 tggatattgtagagagtgaggagaaacacagcttacaatgtagaaggggactgggga 863
Db 625 GGGACCTGCTGCCCAACCTCAGCCGCCCTCTGCTGCTGCTGCACTGCTGCAAGCTGAGC 684
QY 864 gctcaaggtcttattgtgtctacccctccaccttgatgaagaagaggtgagcgtgtg 923
Db 685 AGCCTTCACACACCTGATGATCTCCACGGACAGTAGAGAACCCCGGGAAGAGGTGAG 744
QY 924 cgcagctcaagtgaactctcaaccacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
Db 745 TCACCATCCCGAGAGTGGCTGCCCTGTGTGGAGGACGAGGTTCGCAAGC 796

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RESULT 2

US-08-754-108-1
Sequence 1, Application US/08754108
Patent No. 5886149

GENERAL INFORMATION:

APPLICANT: Buckbinder, Leonard
APPLICANT: Talbott, Randy
APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai
TITLE OF INVENTION: No. 5886149el p53 Response Genes
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/754,108

FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/274,318
FILING DATE: 11-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bogden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: ONO127-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-727-3688
TELEFAX: 206-727-3601
INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-754-108-1

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Query Match 2.1%; Score 58.8; DB 2; Length 2383;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

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QY 444 ggtgaccagatcttcaactcttgttgggtgacagagatggtgatactcttcgga 503
Db 274 GGTGAGAGAGTCTGTCACCTGCTGCTGAGCAGTAAATGAGTGGCTGCTTCACG 333
QY 504 cttcccgaggagagaaatgltgtaacgtgagcttctgttctgtaataagt 563
Db 334 CTTTCTGAAACAGAGTTCACGAGGAAACCTGGAATTTGGCTGGCTGTGAGAGT 393
QY 564 tcaggcagatgaacctgaaggatataccaaacttgcagatgagcgaagaaactataa 623
Db 394 TCA---AGAAATCCGATCAGCTACCAAGCTGGCTCCAGGACACACAGATCTTTGAG 450
QY 624 ggtcaattgagaacaacagcggttctccaagcgtcgtgaagcccgcccaagcctaca 683
Db 451 AGTTGATTG-----CAGTAGAGGCCCTTAAAGAGTCAACATTGACATGACATGACCGCG 504
QY 684 tagcagatgcatcaagaagcaacagatcggtcgtcatgtttgacagagcacagacg 743
Db 685 AGCCTTCACACACCTGATGATCTCCACGGACAGTAGAGAACCCCGGGAAGAGGTGAG 744
QY 744 agatccagcagatgtaggagaaatgctacacaggtgttcttgcatacttcaattacc 803
Db 745 TCACCATCCCGAGAGTGGCTGCCCTGTGTGGAGGACGAGGTTCGCAAGC 796
QY 804 tggatattgtagagagtgaggagaaacacagcttacaatgtagaaggggactgggga 863
Db 864 gctcaaggtcttattgtgtctacccctccaccttgatgaagaagaggtgagcgtgtg 923
QY 924 cgcagctcaagtgaactctcaaccacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
Db 976 TCACCATCCCGAGAGTGGCTGCCCTGTGTGGAGGACGAGGTTCGCAAGC 796

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RESULT 3

US-08-463-081B-1
Sequence 1, Application US/08463081B
Patent No. 5871960

GENERAL INFORMATION:

APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRP Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLANSKI
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-463-081B-1

Query Match 2.1%; Score 58.8; DB 2; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

OY 444 ggtggaacagctcttaccctctgtgtggtgagcaagatggtacatcctctccgga 503
DB 297 GGTGAGAGAGTCGTTGACGCTGCTGAGCAGTAAATAAGAGTGCCTTCACG 356
OY 504 cttctcgtgagggaggaatggtggtatagctgactctggtctgtctgtaagggt 563
DB 357 CTTTCTTGAAAGACAGTTCAGTGTGAGGAGAACCTGAGTGGCTGTGAGGAGT 416
OY 564 tcaggcagatgagcttgaagatgacaaacttgcagtggtgcaagaatctataaga 623
DB 417 TCA---AGAGATCCGATCAGTACCAAGCTGGCTCCAGGGCAGACAGATCTTGAGG 473
OY 624 gttacattgagaacacagcgtgtgtctccaagcagctgaagccgcacaaagactaca 683
DB 474 AGTTGATTGG-----CAGTGAGGCCCTTAAAGAGGTCAACATTGACATGAGAGCCGCG 527
OY 684 ttcgagatgagctcaagaagaacagatcgctggtctgttgcacagagcagacg 743
DB 538 AGCTGACGAGGATGAACCTGACAGCTGCCACAGCCACATGCTTTGCGGCTCAGAGGGA 587
OY 744 agatccagcagtgatgaggaagaatgacctaccagtggtcttgaacttgaattacc 803
DB 588 ACACACATACCTGATGAGAGAGAGACTCTACCAAGCTTCTGTAAGTGCCTGCTTACC 647
OY 804 tggatatatgaggaagtgaggggggaacacacagctacatagtgaacggggagtgagg 863
DB 648 GGGAGCTGGCTGCCAAGCTCAGCGGCTGTGCACCTGTGCACAGCTCAGAGCTGAGGC 707
OY 864 gcttaaaaggtctatgtgtgctacatcccaacttgaataaagaagaggtgtaggtg 923
DB 708 AGCCCTCAGACACCTGAGTCTCCACGCGAGTGAAGAGACACCGGGAAGAGGTTGAG 767
OY 924 ccgacctcaagtgcaaacctcaccacacgltgtgtgtgtgttccagcaaac 975
DB 768 TCACCCATCCCGAGGTGGCTGCCCTGTGTGGAGGAGAGGTTTCTCAAGC 819

RESULT 4
US-08-461-379A-1
; Sequence 1, Application US/08461379A

Patent No. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
ADDRESS: (B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-461-379A-1

Query Match 2.1%; Score 58.8; DB 2; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

OY 444 ggtggaacagctcttaccctctgtgtggtgagcaagatggtacatcctctccgga 503
DB 297 GGTGAGAGAGTCGTTGACGCTGCTGAGCAGTAAATAAGAGTGCCTTCACG 356
OY 504 cttctcgtgagggaggaatggtggtatagctgactctggtctgtctgtaagggt 563
DB 357 CTTTCTTGAAAGACAGTTCAGTGTGAGGAGAACCTGAGTGGCTGTGAGGAGT 416
OY 564 tcaggcagatgagcttgaagatgacaaacttgcagtggtgcaagaatctataaga 623
DB 417 TCA---AGAGATCCGATCAGTACCAAGCTGGCTCCAGGGCAGACAGATCTTGAGG 473
OY 624 gttacattgagaacacagcgtgtgtctccaagcagctgaagccgcacaaagactaca 683
DB 474 AGTTGATTGG-----CAGTGAGGCCCTTAAAGAGGTCAACATTGACATGAGAGCCGCG 527
OY 684 ttcgagatgagctcaagaagaacagatcgctggtctgttgcacagagcagacg 743
DB 538 AGCTGACGAGGATGAACCTGACAGCTGCCACAGCCACATGCTTTGATGCGGCTCAGAGGGA 587
OY 744 agatccagcagtgatgaggaagaatgacctaccagtggtcttgaacttgaattacc 803

Db 588 AGACACCTACCTGATGAGAGAGACTCTACCCACGCTTCCTGAGTCGCTTACCC 647
QY 804 tgaatctgtgag 863
Db 648 GGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 707
QY 864 gctaaagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 923
Db 708 AGCCCTACACACTGATGATCTCCACGACGAGTGAAGAGCCGCGGAGAGAGAGT 767
QY 924 ccgaactcaagtgaactctcaccacggtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
Db 768 TCACCCATCCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819

RESULT 5
US-08-462-390B-1
Sequence 1, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding C88 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-462-390B-1

Query Match 2.1%; Score 58.8; DB 2; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

QY 444 ggtgacaaagtcttataactctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 503
Db 297 GGTGAGAGAGAGTCTGACCTGCTGAGCAGTAAATAATGAGTGTGCTGCTTCCAGC 356

QY 504 cttcccttgaag 563
Db 357 CTTTCTGAGAGACAGACTGTAGTGAAGAGAACTGAGTTCTGCTGCTGCTGCTGCTGCT 416
QY 564 tcagacagatgaactcttaagatataccttcttcttcttcttcttcttcttcttct 623
Db 417 TCA---AGAGATCTCGATTCACCTTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
QY 624 gttacattgagaacaacagcgttcttccaaagcagctgaagcccgcaacaagactaca 683
Db 474 AGTTCAATTTG-----CAGTGAAGCCCTTAAGAGTCAATATGACCATGAGACCGCG 527
QY 684 tacgagatgagatcaagaagaacagatcgtctgtgcatgtttgaccagacagacg 743
Db 528 AGCTGACGAGAGATGACACTGACACTGACACGACACACATGCTTGATGCTGCTGCTG 587
QY 744 agatcaagcagatgag 803
Db 588 AGACACGTAACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
QY 804 tgaatctgtgag 863
Db 648 GGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 707
QY 864 gctaaagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 923
Db 708 AGCCCTACACACTGATGATCTCCACGACGAGTGAAGAGCCGCGGAGAGAGAGT 767
QY 924 ccgaactcaagtgaactctcaccacggtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
Db 768 TCACCCATCCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819

RESULT 6
US-08-463-074B-1
Sequence 1, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding C81 Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

444 South Flower St. - Suite 1

```

; LENGTH: 2406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..722
; US-08-463-074B-1

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Query Match      2.1%; Score 58.8; DB 3; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

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OY 444 ggtgagcaagtccttacaccccttggtggtgagcaggaatgtgataccttcgcga 503
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DB 297 ggtgagagagtcgttcgactgctgagcagatgaaatgagtggtgcttcacag 356
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 504 ctttcctgagagggaggaatgtgtgatacgtctgactcttggttctgttaatgg 563
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 357 ctttcctgagagggaggaatgtgtgatacgtctgactcttggttctgttaatgg 563
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 564 tcagcagatgagcctgaggaatgatacacaacttgcgagtgcccaagaactataaga 623
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DB 417 tca---agaaatccgagatcagctacacagctgcccacagggcagacacagatcttgag 473
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 624 ggtacattgagaaacaacagcgtgtctcacaagcagctgaagcccgacacaagactaca 683
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 474 agttcatttg-----cagtgagggccctaaagagctcaaatgacattgagacccggcg 527
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 684 tacgagatgagcagcaagaagacagatcgctcgatcgttctgacagcagcagacagcg 743
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 528 acctgacgagatgaaactgacactgacacagccacacacacacacacacacacacacag 587
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 744 agatccagcagctgattgaggaatgctcctcacaagctgtctctgactctgacatttac 803
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 588 agacacagatcctgattgaggaatgctcctcacaagctgtctctgactctgacatttac 803
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 804 tggaaatgtgagagtgaggggggaagaacacagcttacaatgaaagggagctgggga 863
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 648 gggacctggtgctcccaagacgtcagccgctctgctcactgtgtccacactcagctgagac 707
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 864 gcttaaggtcttatgtgtctacccctcaccacttgatgaagaagggagtgagctgtg 923
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 708 acccttcacacacactgagctcctcagcgacagtgaggaagcagcagggagagaggttgag 767
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 924 ccgacctcaagtgcaaacctcaccacacgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 768 tcaccatccccgagtggtgctgctgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 819
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RESULT 7
US-08-465-585C-1
; Sequence 1, Application US/08465585C
; Patent No. 6027914
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vectors
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESSEE: (B) STREET: 444South Flower St. - Suite 190
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 900071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,585C
; FILING DATE: 5-JUNE-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 4894210
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..722
; US-08-465-585C-1

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Query Match      2.1%; Score 58.8; DB 3; Length 2406;
Best Local Similarity 47.2%; Pred. No. 2.5e-06;
Matches 251; Conservative 0; Mismatches 272; Indels 9; Gaps 2;

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OY 444 ggtgagcaagtccttacaccccttggtggtgagcaggaatgtgataccttcgcga 503
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DB 297 ggtgagagagtcgttcgactgctgagcagatgaaatgagtggtgcttcacag 356
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 504 ctttcctgagagggaggaatgtgtgatacgtctgactcttggttctgttaatgg 563
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 357 ctttcctgagagggaggaatgtgtgatacgtctgactcttggttctgttaatgg 563
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 564 tcagcagatgagcctgaggaatgatacacaacttgcgagtgcccaagaactataaga 623
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 tca---agaaatccgagatcagctacacagctgcccacagggcagacacagatcttgag 473
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 624 ggtacattgagaaacaacagcgtgtctcacaagcagctgaagcccgacacaagactaca 683
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 474 agttcatttg-----cagtgagggccctaaagagctcaaatgacattgagacccggcg 527
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 684 tacgagatgagcagcaagaagacagatcgctcgatcgttctgacagcagcagacagcg 743
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 528 acctgacgagatgaaactgacactgacacagccacacacacacacacacacacacacag 587
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 744 agatccagcagctgattgaggaatgctcctcacaagctgtctctgactctgacatttac 803
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 588 agacacagatcctgattgaggaatgctcctcacaagctgtctctgactctgacatttac 803
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OY 804 tggaaatgtgagagtgaggggggaagaacacagcttacaatgaaagggagctgggga 863
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 648 gggacctggtgctcccaagacgtcagccgctctgctcactgtgtgtgtgtgtgtgtgtgt 707
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 864 gcttaaggtcttatgtgtctacccctcaccacttgatgaagaagggagtgagctgtg 923
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 708 acccttcacacacactgagctcctcagcgacagtgaggaagcagcagggagagaggttgag 767
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OY 924 ccgacctcaagtgcaaacctcaccacacgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 975
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 768 tcaccatccccgagtggtgctgctgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 819
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```

```

RESULT 8
US-08-652-446-1

```

Sequence 1, Application US/08652446
Patent No. 6057427

GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Reading, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSER: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SRD ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 116..722
US-08-652-446-1

444 South Flower St. - Suite 1900

ATTORNEY/AGENT INFORMATION:
NAME: Yviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-463-081B-27

Query Match 2.0%; Score 57.2; DB 2; Length 606;
Best Local Similarity 51.4%; Pred. No. 3.4e-06;
Matches 187; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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OY 444 ggtgaccagtccttaccaccccttctgtgtggtgaccagatggtgcatcctcttcgga 503
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DB 182 ggtgaccagtccttaccaccccttctgtgtgaccagatggtgcatcctcttcgga 241
OY 504 ctttcctgagagagagaaatgtgtgatacgtctgactcttggtcttgaatggt 563
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 ctttcctgagagagagaaatgtgtgatacgtctgactcttggtcttgaatggt 301
OY 564 tcaggcagatgacctgaaagatatacaaaacttgcgagtgccaaagaatctataaga 623
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DB 302 tca---AGAGATCCGATACGATACCACTGCGCTCCAGGGCACCCAGATCTTTGAGG 358
OY 624 ggtacatgagaacaacagcgtgtctcccaagcagtcgagccgcacaaagactaca 683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 359 AGTTGATTG-----CACTGAGGCCCTTAAGAGGTCAACATTCATGAGACCCGGG 412
OY 684 tacgagatgcatcagaagaacagatcggtctggtcattgttgaccagagacagc 743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 413 AGCTGACGAGATGAACCTGACAGACTGCCACAGCCCATGCTTTGTCGGCTCAGGGGA 472
OY 744 agatccagcagtgatgagagaaatgctaccaggtgttcttgacttgcattacc 803
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 AGACACGTACCTGATGGAAGAGACTCTACCCACGCTTCTGGAAGTCCCTGCTTACC 532
OY 804 tggga 807
    |||
DB 533 GGGA 536
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RESULT 10
US-08-461-379A-27
Sequence 27, Application US/08461379A
Patent No. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
ADDRESS: (B) STREET:One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Yviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-461-379A-27

Query Match 2.0%; Score 57.2; DB 2; Length 606;
Best Local Similarity 51.4%; Pred. No. 3.4e-06;
Matches 187; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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OY 444 ggtgaccagtccttaccaccccttctgtgtggtgaccagatggtgcatcctcttcgga 503
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DB 182 ggtgaccagtccttaccaccccttctgtgtgaccagatggtgcatcctcttcgga 241
OY 504 ctttcctgagagagagaaatgtgtgatacgtctgactcttggtcttgaatggt 563
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 ctttcctgagagagagaaatgtgtgatacgtctgactcttggtcttgaatggt 301
OY 564 tcaggcagatgacctgaaagatatacaaaacttgcgagtgccaaagaatctataaga 623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 302 tca---AGAGATCCGATACGATACCACTGCGCTCCAGGGCACCCAGATCTTTGAGG 358
OY 624 ggtacatgagaacaacagcgtgtctcccaagcagtcgagccgcacaaagactaca 683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 359 AGTTGATTG-----CACTGAGGCCCTTAAGAGGTCAACATTCATGAGACCCGGG 412
OY 684 tacgagatgcatcagaagaacagatcggtctggtcattgttgaccagagacagc 743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 413 AGCTGACGAGATGAACCTGACAGACTGCCACAGCCCATGCTTTGTCGGCTCAGGGGA 472
OY 744 agatccagcagtgatgagagaaatgctaccaggtgttcttgacttgcattacc 803
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 AGACACGTACCTGATGGAAGAGACTCTACCCACGCTTCTGGAAGTCCCTGCTTACC 532
OY 804 tggga 807
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DB 533 GGGA 536
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RESULT 11
US-08-462-390B-27
Sequence 27, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
ADDRESS: (B) STREET:One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482

US-08-465-585C-27
Sequence 27, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, R. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 900071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465, 585C
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-585C-27

Query Match 2.0%; Score 57.2; DB 3; Length 606;
Best Local Similarity 51.4%; Pred. No. 3.4e-06;
Matches 187; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

444 ggtagcaccagcttctacccctcctggtgagcagatggtacatacctctccgga 503
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 182 GGTGAGAGAGCTGTCGACGCTGCTGACGAGTAATAATGAGTGCTGCTTACG 241
504 cttccctgagagggagaaatggtgagacagctgagctctggttggtaattggat 563
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 CTTCTCTGAAGACAGAGTCACTGAGAGAACCTGAGTCTGCTGCTGAGAGAG 301
564 ttagcagatgaaacctgaaagataccaaccttgcgagtgagcacaagaactataaga 623
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 302 TCA--AGAGAGATCCGATCAGCTGAGCTGCTCCAGGACACACAGATCTTTGAGG 358
624 ggtacatgaagacaacagcgttctcacaagcgtgaagcccgccacaagaactaca 683
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 359 AGTTGATTG-----CATGAGGCCCTTAAGAGAGTCAACATGACATGAGAGACCCGCG 412
684 ttagcagatgcaatcagaagacaagacagatcggtcggtcattgttgacagagcagacgg 743
413 AACTGACGAGAGATGAACCTGACGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA 472
744 agatcagcagcagatgtaggggaaatgctacacagtgctcttgacttctgacattacc 803
||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

DB 473 AGACAGTACCTGATGAGAGAGACTCTACCCAGCTTCTGAGATGCGCTTACC 532
QY 804 tgga 807
|||
DB 533 GGGA 536

RESULT 14
US-08-652-446-27
Sequence 27, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 18:41:56 ; Search time 3054.04 Seconds
(without alignments)
8080.928 Million cell updates/sec

Title: US-09-587-574-6

Perfect score: 2825
Sequence: 1 cagccgtcgcgattgattt.....accctgtctcagcctacgc 2825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Result	Score	Match	Length	ID	Description
1	480	17.0	798	140 BE872155	BE872155 601446262
2	437	15.5	591	102 A1818109	A1818109 WK27C05.x
3	429.8	15.2	732	140 BE882875	BE882875 601509279
4	420.2	14.9	621	122 AW962356	AW962356 EST374429
5	392.2	13.9	543	177 A1220032	A1220032 9978B02.x
6	375.2	13.3	548	7 AA46378	AA46378 z558B07.f
7	370.4	13.1	427	149 BF521997	BF521997 UT-R-Y0-8
8	367.6	13.0	471	169 BF812711	BF812711 RC3-C1019
9	363	12.8	521	168 BF757617	BF757617 MR2-CT059
10	341.6	12.1	463	103 A1912345	A1912345 tz24C04.x
11	334.8	11.9	1068	231 CNS03YD0	A1266841 Tetraodon
12	330.8	11.7	830	230 CNS03YD0	A1172875 Tetraodon
13	327	11.6	399	8 AA489748	AA489748 aa43B02.f
14	325.6	11.5	487	18 A1307112	A1307112 q189F01.x
15	323.2	11.4	460	20 A1419942	A1419942 tg40D11.x
16	314.4	11.1	459	18 A1722864	A1722864 q143B03.x
17	301.6	10.7	308	142 BF021386	BF021386 ux56a02.x
18	293.8	10.4	444	13 AA937585	AA937585 of71h02.s

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	19	290.6	10.3	545	13	AA155099
C	20	285	10.1	495	139	BE755017
C	21	276.8	9.8	447	13	AA503395
C	22	271.8	9.6	418	103	AI858567
C	23	266.8	9.4	902	231	CNS03G20
C	24	261.4	9.3	409	8	AA489644
C	25	257	9.1	375	5	AA305361
C	26	256.4	9.1	413	19	AI336613
C	27	247	8.7	363	18	AI262837
C	28	240	8.5	408	23	AI660139
C	29	236.2	8.4	257	135	BB523213
C	30	219.6	7.8	345	24	AI742962
C	31	214.6	7.6	383	112	AA202598
C	32	208	7.4	651	141	BE894571
C	33	207.8	7.4	391	13	AA684421
C	34	206.6	7.3	282	134	BB448134
C	35	201.6	7.1	595	230	CNS03314
C	36	179.4	6.4	299	19	AI163868
C	37	175.4	6.2	986	150	BF588224
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C	40	170	6.0	584	219	AZ315171
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C	43	166	5.7	539	3	AA198605
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C	45	154	5.5	428	8	AA502360
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BF5893324 602010155
BF595312 U1-R-EL-F
BE854108 w027g03.y
AZ315171 mx023u1j6A
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AA506657 f03a11.s
AA502360 ne2c011.s

BE872155	798 bp	EST	20-OCT-2000
LOCUS			
DEFINITION	6014462626.F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850502.5', mRNA sequence.		
ACCESSION	BE872155		
VERSION	BE872155.1	GI:10320931	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 798)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		

FEATURES

Source

1. .798

BASE COUNT

218 a	229 c	207 g	144 t
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ORIGIN	Query Match	17.0%;	Score 480;	DB 140;	Length 798;
	Best Local Similarity	81.7%;	Pred. No. 1.5e-112;		
	Matches 629;	Conservative	0;	Mismatches 130;	Indels 11; Gaps
QY	571 gataaacctgaagatataccaaacatttcgagatgagcgaagaacatctataagatgatac 630				
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QY	631 ttggaatacaacaggttgctccgaagagcttgaagccgcacaaagaaactataatcagga 690				
Db	61 TGAAGAACAAAGACACTCTCTCCAAAGAGCTGAAGCCTCGACCAAGACCTACATATAGAGA 120				
QY	691 ttgagatcaagaagaacacagatcgccgcgagatgatttgacagagcagaaccagatataca 750				
Db	121 TGGCATTAAGAGACAGCAGATGATTTATTCATCATAGTTTGACACAGCGCAGACGAGATATCA 180				
QY	751 ggcagtgatggaagaaatgctcctacaagtgatgcttgacttcgtacattcattcctggaata 810				
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QY	871 ggtcttatgtggtaacctcccaacttgaatggaagaaggagtgagctgtgcccagact 930				
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QY	931 caagtgcacaaactcaccacacgctggatgctgtgtcgttcacaaactcttcgggacacgc 990				
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QY	991 gagtgtgagatccacggaacacagctctgaagaagatctcaggtctctcaat--gagaaga 1047				
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QY	1048 cccagatcaatccatatacaagtaggttcgcgatactg--tccttgacacagcacaacagcgca 1106				
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QY	1107 acgacagacagagtt--atccagacgacgaactacacagacagatltccatgtccatgacgagaa 1164				
Db	541 ACGACAGTGAAGATATCATGATGCATGGCGTGAAGGGCTGATTCATATGTCATGACGAGAC 600				
QY	1165 tagcgtatgagtagagtcctcctc--accgcataggggagtaagaagaag--ctccagaga 1219				
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QY	1220 gagtgatctcgagctgtggaagcgcaatggcgaagtgctctactcaatttcctcgaagac 1279				
Db	661 ACATGGAATGCGACAGGGGAGCGCCACCGGCAAGTGCCATATCCCCATCCCCCAATCCC 720				
QY	1280 caccgcctgcacaaagagatgacgcctgtgtgaaacctgtgccttcgcgcgc 1329				
Db	721 ACGCAAGCGCCACAGAGGGAAGACCCCCCGGAACCGCGGACACCCCGGAC 770				
RESULT 2	AI1818109	591 bp	mRNA	EST	21-DEC-1999
LOCUS	AI1818109/c				
DEFINITION	W27005.x1 NCI-GAP-Bru2 Homo sapiens cDNA clone IMAGE:2413544 3				
ACCESSION	AI1818109				
VERSION	AI1818109.1	GI:5437188			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 591)				

Query Match	14.9%	Score 420.2	DB 122	Length 621
Db	181	CGCTGCTCCAGGCGAAGGACCGACACGACATCTGTGGGGGGGCAACAGGGGAG	240	
Qy	2213	tcctgcctcagtcgcccgggtcacc-cattttccagaagcccttgcaatgctcccttacc	2211	
Db	241	CCCCGGCAGCAGCCCGGTGCCCCACGCTGTTTCAACCCAGACACCTCGCATGCCCTTCAC	300	
Qy	2272	cccccccaaaacttggcaagtcataaggaagaacgctgacgagctggcagaaggtgtgaa	2331	
Db	301	CCCAACCCAAACACCTGGCTCAGCTGGAGGAGGCGCTGTCCAGAGCTAGCTGAGGTTCGA	360	
Qy	2332	gccccaaagaacagcggctgctgctgctgagcagcaagaggaacaggaacccactgcgtgc	2391	
Db	361	GCCCCCAAAACACACCGGTGCTGTGTGGCCAGTCAAGCAGAGGAGCAGGAATTCATTGGCCAC	420	
Qy	2392	tgtctagcagcagcagcctcacccttcgccaaccgaagcctgctcagaagatcacaaga	2451	
Db	421	TGTTCAAGCAGGGAGGC- AACCTTCTTCAATCAACGACCTGGCTCCAGAAATCACAAAGA	479	
Qy	2452	gcccaaa-aaacttggcagaatgttccaaagcgtccagcagcagtgactgttgcactact	2510	
Db	480	GCCAAACAAAACCTGCGCAGGTGTCAGCCCTCCACAGCCAGTGAAGTGTGTCATTACT	539	
Qy	2511	ttctctgtgagaagaataatcacaagaagatgctgaagc-ccaagcttgaacct-	2568	
Db	540	TTTTCTGTGGGAGAAATTCATACCGGAGGATGCTGAAGGCTTCAGAGCTTGACCTT	599	
Qy	2569	-gggcaccttcaagcagcagctcagcacaagaagaatactacglatatltcaagaag	2627	
Db	600	GGCGCACTTTAAAAAGACACCTCAGCGCAAAAGAAATTAATGATTACTTCAAAAAG	659	
Qy	2628	cgaagtacgaatctgctgcgcgaagcagcttttgag	2662	
Db	660	CAACGATGAGTTGCTGTGAGCGCGGTGGAAGAG	694	
RESULT 4				
LOCUS	AW9623356	621 bp	mRNA	EST 01-JUN-2000
DEFINITION	EST3744429	MAGE	resequencences, MAGC Homo sapiens	CDNA, mRNA sequence.
ACCESSION	AW9623356			
VERSION	AW9623356.1	GI:8152190		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 621)			
	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holtz			
	,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and			
	Quackenbush,J.			
TITLE	Assessment of gene expression patterns in a model of colon tumor			
JOURNAL	metastasis using a 19,200 element cDNA microarray			
COMMENT	Unpublished (2000)			
	Contact: John Quackenbush			
	The Institute for Genomic Research			
	9712 Medical Center Dr., Rockville, MD 20850, USA			
	tel: 301 838 3528			
	Fax: 301 838 0208			
	Email: johnq@tigr.org			
	Plate: 174			
	Seq primer: Reverse.			
FEATURES	Location/Qualifiers			
SOURCE	1..621			
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	/clone_lib="MAGE resequencences, MAGC"			
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[illegible]

FEATURES

source

High quality sequence stop: 224.

Location/Qualifiers

1. 543

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/db_xref="taxon:9606"

/clone="IMAGE:184131"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pMT73D-Pac (pharmacia) with

a modified polylinker. Site 1: Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NDH19W, testis NT, and B-cell

NCL-GAP, GCB1) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,

726408-728711, and 729096-731399. Subtraction by Bento

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ACCESSION

AA446378

VERSION

AA446378.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 548)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.

Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie

, T., Waterston, R. and Wilson, R.

TITLE

Washu-Merck Est Project 1997

JOURNAL

Unpublished (1997)

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LUNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 490.

Location/Qualifiers

1. 548

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:774229"

/lab_host="DH10B"

/dev_stage="8-9 weeks"

/note="Vector: pMT73D-Pac (Pharmacia) with a modified

polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week

(total) fetus material with a Not I - oligo(dT) primer [5'

GTGTACCAATCTGAGAGGAGGAGGCGCGCTTAATTTTCTTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pMT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo.

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IMAGE:774229 5', mRNA sequence.

AA446378

AA446378.1 GI:2159043

EST.

human.

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 548)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.

Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie

, T., Waterston, R. and Wilson, R.

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

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1. 548

/organism="Homo sapiens"

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/clone="IMAGE:774229"

/lab_host="DH10B"

/dev_stage="8-9 weeks"

/note="Vector: pMT73D-Pac (Pharmacia) with a modified

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GTGTACCAATCTGAGAGGAGGAGGCGCGCTTAATTTTCTTTTCTTTT 3'].

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(Pharmacia), digested with Not I and cloned into the Not I

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Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

ACCESSION

AA446378

VERSION

AA446378.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 548)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.

Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie

, T., Waterston, R. and Wilson, R.

TITLE

Washu-Merck Est Project 1997

JOURNAL

Unpublished (1997)

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LUNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 490.

Location/Qualifiers

1. 548

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:774229"

/lab_host="DH10B"

/dev_stage="8-9 weeks"

/note="Vector: pMT73D-Pac (Pharmacia) with a modified

polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week

(total) fetus material with a Not I - oligo(dT) primer [5'

GTGTACCAATCTGAGAGGAGGAGGCGCGCTTAATTTTCTTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pMT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

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Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

Soares and M. Fatima Bonaldo.

ACCESSION

AA446378

VERSION

AA446378.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 548)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

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Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie

, T., Waterston, R. and Wilson, R.

TITLE

Washu-Merck Est Project 1997

JOURNAL

Unpublished (1997)

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

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IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 490.

Location/Qualifiers

1. 548

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:774229"

/lab_host="DH10B"

/dev_stage="8-9 weeks"

/note="Vector: pMT73D-Pac (Pharmacia) with a modified

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(total) fetus material with a Not I - oligo(dT) primer [5'

GTGTACCAATCTGAGAGGAGGAGGCGCGCTTAATTTTCTTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pMT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo.

Oy	2657	ttctgagagatcctggacgcagacagtcctcccatgtcgaaggacgatcctggc	2716
Db	373	TTTTAGGAGAGATCTGGAGGATGAGACCGTGTCTCCCGATGTGAAGGCCGATTCGTGGGC	432
Oy	2717	aagatggagagatcgacttgaaccttgaccgcc	2748
Db	433	AAAAAAAAAAGCAAGCATGATTGCTTGAGCAGCGGTG	372

REFERENCE	AUTHORS	TITLE	JOURNAL MEDLINE COMMENT
BFS21997	1 (pages 1 to 427)	mRNA	EST
BFS21997	UI-R-Y0-acc-b-09-0-UI-R1 UI-R-Y0 Rattus norvegicus cDNA clone	11-DEC-2000	
BFS21997	UI-R-Y0-acc-b-09-0-UI 5', mRNA sequence.		
BFS21997.1	GI:11629964		
EST.			
Norway rat.			
Rattus norvegicus			
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
1 (pages 1 to 427)			
Bernaldo,M.F., Lennon,C. and Soares,M.B.			
Normalization and subtraction: two approaches to facilitate gene			
discovery			
Genome Res. 6 (9), 791-806 (1996)			
9704447			
Contact: Soares, MB			
Program for Rat Gene Discovery and Mapping			
University of Iowa			
451 Eckstein Medical Research Building Iowa City, IA 52242, USA			
Tel: 319 335 8255			
Fax: 319 335 9565			
Email: meoares@blue.weeg.uiowa.edu			
cDNA Library Preparation: M.B. Soares Lab Clone distribution:			
clones will be available through Research Genetics (www.resgen.com)			
This clone is also available through the I.M.A.G.E. Consortium at			
LNL (info@lmg.lnl.gov). IMAGE ID= 1791410			
Seq primer: M13 Forward.			
Location/Qualifiers			
I. .427			
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/strain="Sprague-Dawley"			
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/clone="UI-R-Y0-acc-b-09-0-UI"			
/Clone_LID="UI-R-Y0"			
/dev_stage="adult"			
/lab_host="DH10B (Life Technologies)"			
/note="Vector: pUT73D-Pac (Pharmacia) with a modified			
polylinker. Site.1: Not I; Site.2: Eco RI; The UI-R-Y0			
library is a subtracted library derived from an			
individually-tagged normalized whole-eye (minus the lens)			
library. The driver for the subtraction consisted of a			
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,			
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of			
3-5 nucleotides present between the Not I site and the			
oligo-dT track which allows identification of the library			
of origin of a clone within the mixture. The subtracted			
library (UI-R-Y0) was constructed as follows: PCR			
amplified cDNA inserts from previous library clones from			
which 3' ESTs had been derived were used as a driver in a			
hybridization with the normalized whole-eye library in			
the form of single-stranded circles. The remaining			
single-stranded circles (subtracted library) was purified			
by hydroxyapatite column chromatography, converted to			
double-stranded circles and electroporated into DH10B			
bacteria (Life Technologies) to generate the UI-R-Y0			
library. This procedure has been previously described			
(Bernaldo, Lennon and Soares, Genome Research 6: 791-806,			
1996)."			

BASE COUNT	118 a	126 c	113 g	70 t
ORIGIN				
Query Match				
Best Local Similarity	92.6%			
Matches	389;	Conservative	0;	Mismatches 31; Indels 0; Gaps 0;
Score	370.4;			
DB	149;			
Length	427;			
Query	2234	caccattaccacgaagaccctgtcaatgcctcccttaccaccacacacacttggcacag	2293	
Db	8	CACCCATTACCCAGAGACCCCTGCATGCTCCCTCCCTACCCACCCACACCTTGGCGCAG	67	
Query	2294	ctagaggaagagctgtgcgcgaagcttggcagaagtgtctaaagccccagaagaagcgtgtcgc	2353	
Db	68	CTAGAGGAAGCTGTGCCGAGGCTGGCCGAGGCTGTAAAGCCCCACAAACAGAGGTGCTTC	127	
Query	2354	gtggcgaatcagcagaaggagacagaaccactgtgcctgtctgtcagaagcagaccaccc	2413	
Db	128	GTGGCCTATCAGACAGAGGACAGAACCCACGACACAGTTCAGGACGAGACCCACATCC	187	
Query	2414	ctgcgcaacccaagcctgtgtccagaagaatcaaaagaagccaaagaactgtgcaagtgc	2473	
Db	188	TTCTCCACCCGAGGCTGCTTCAAGAAATCATCAAAAGACCCAAAGACACTGCTGTGTGC	247	
Query	2474	cacgcgtcccaagcgcagcagcgtgtgttcaactcttttctgtggaagaataattcca	2533	
Db	248	CACGCATCCCAAGCCAGGAGCTGATGTTCTTACCTCTTTTGTGGAGAAATAATCCA	307	
Query	2534	tacaagaagatgcttgaagtcctaaagcttgacccttgggcacttcaagaagcagctcagc	2593	
Db	308	TACAGAGAGATGCTGAAGCCGACAGCCTTGACTGTGGCCACTTCAAGAGACAGCTCAC	367	
Query	2594	aaaaagggaaaattacaggtatattatttcaagaagcgcagtgacgaatttgcgtgcgagca	2653	
Db	368	AAAAAGGAAATATACAGGTATTACTTCAAGAGGCGAGTACGAAATTTGCTGTGGAGCA	427	
RESULT	8			
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LOCUS	RC3-C10195-221100-021-a10	C10195	Homo sapiens	cdna, mRNA sequence.
DEFINITION	BE812711			
ACCESSION	BE812711.1	GI:12142597		
VERSION				
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 471)			
AUTHORS	Dias Neto, E., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,			
	Nagai, M.A., Carvalho, A.F., Matsukuma, B., Bala, G.S., Simpson, D.H.,			
	Goldman, G.H., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare			
	Brustein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare			
	, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and			
	Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed			
	sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20020663			
COMMENT	Contact: Simpson A.J.G.			
	Laboratory of Cancer Genetics			
	Ludwig Institute for Cancer Research			
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,			
	Brazil			
	Tel: +55-11-2704922			
	Fax: +55-11-2707001			
	Email: asimpson@ludwig.org.br			
	This sequence was derived from the FAPESP/LICR Human Cancer Genome			
	Project. This entry can be seen in the following URL			
	(http://www.ludwig.org.br/scripts/gethtml2.pl?ref=RC3&et=RC3-C10195			
	221100-021-a10&et=2000-11-22&et4=1)			
	Seq primer: puc 18 forward			
	High quality sequence start: 4			


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Db 487 ACCTCCAGAGAAATGCTTCCGACAGTTCGAAGCC 521
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RESULT 10
AI912345 463 bp mRNA EST 16-DEC-1999
LOCUS t23404.x1 NCI CGAP ut2 Homo sapiens cDNA clone IMAGE:2289510 3'
DEFINITION similar to TR:070240 070240 AXIL.; mRNA sequence.
ACCESSION AI912345
VERSION AI912345.1 GI:5632200
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 463)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 2487 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 414.
Location/Qualifiers
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:2289510"
/clone.lib="NCI-CGAP_ut2"
/tissue.type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab.host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
BASE COUNT 108 a 148 c 148 g 58 t 1 others
ORIGIN
Query Match 12.1%; Score 341.6; DB 103; Length 463;
Best Local Similarity 83.7%; Pred. No. 5.4e-77;
Matches 386; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Oy 1697 tgcctccctcttgaggagagctctctgaccaaacagacgagacgttcaccac 1756
|||||
Db 2 TCCTCCCTCTCTGGGGGCAAGGCTTTGTGACCAACAGACGACGAAATGTCACAC 61
|||||
Oy 1757 cactatattccacagacgagcgtctcccaagacgaagagagatcgaggacagaccaca 1816
|||||
Db 62 CACTACATCCACACACATCCCTCCCAAGACCAAGAGAGATCGAGCGAGCGCAGC 121
|||||
Oy 1817 cagagagtcgctgctctgctcctggggaacagattattgtctaccacaaatgcaaa 1876
|||||
Db 122 CAGCGGGTCACTACTGCTTCGCCCTGGGGCAGCAGATATTACTGCTACTCGAAATGCAAA 181
|||||
Oy 1877 agcacccagagctcagacgagcctctgctggggaacagatttctgagcagcagagtggt 1936
|||||
Db 182 AGCCACATCCAGGCTCCGGAACATGCGCAGCAGCAGTTCGCGCAGCAGAGGACAGT 241
|||||
Oy 1937 accctgcacaaacgaaatgcaaaagggacaggaacgcggctctgacatgtcgcccaaggat 1996

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```

Db 242 ACCTTCCCAACGCAATGCAAGCAGCAGAGCCGGGCTGCGCTGCGCCGCAAGGAA 301
|||||
Oy 1997 ggaaggatgtccagtgacgaggggggccccagcttcctgagggaagagacggtca 2056
|||||
Db 302 GGAGGGGCCCCCGCGGACCTGCGCCCTGACGCTTCCCGGAGAGAAAGACAGGTGG 361
|||||
Oy 2057 caggatgtctgacgagtgatgtgttgagagtgagcgagcagaagtcagaagcccatgt 2116
|||||
Db 362 CAGGATGTCTGCGAGTGATGCTGGAGAGTGAAGCGGACAGCAAGCCCAAGCCCATAGT 421
|||||
Oy 2117 gcccaagcataaagaagactaccatgtgagtcgccc 2157
|||||
Db 422 GCCCAAGCACAANAAAGGCGTACCCCTTGAGTGTGCGCCG 462
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RESULT 11
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LOCUS Tetradon nigroviridis genome survey sequence PUC-ori end of clone
DEFINITION 069C20 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL266841.1 GI:7988628
VERSION AL266841.1
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percormorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradon.
1 (bases 1 to 1068)
Roest-Crollius,H., Jallou,O., Dasilva,C., Fizeses,C., Fisher,C.,
Bonneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
2 (bases 1 to 1068)
Roest-Crollius,H., Jallou,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Fizeses,C., Mincker,P., Brothier,P., Queller,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 1068)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
Location/Qualifiers
FEATURES
source 1..1068
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="069C20"
/clone.lib="G"
/note="Genoscope sequence ID : C0B0609BBI0SP1-end :
PUC-ori"
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ORIGIN
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Best Local Similarity 64.9%; Pred. No. 3.7e-75;
Matches 537; Conservative 0; Mismatches 272; Indels 19; Gaps 2;

Oy 113 agagacaagccgcatgtgcgagaggaactgtgaagaagaagaagagaggaagaaana 172
|||||
Db 59 AGAGAGAAAGAGCGGCGAGCGAGAGAGAGCTCCCGCTGACATTAGAGAGAGATTA 118

```


QY	173	agcaaaacaaaatccaaacatccagtcagagcgtctccctccatcgaatgtagcgccggtta	232
Db	119	AGCAGCAGCYCGGGGCTCCGACTCTCCGGCGGGCTGGCGCGTCAGACCCATGAGCCA	178
QY	233	gtgactctccctccagaatcccaagcagcgtctcccgagatgtctcccgccgccggtt	292
Db	179	GGCGCTTGGCGACACACATCGC--CGGAGTTTCAGAAATATGCCCCCTGCACCCCGGTC	236
QY	293	ccggagaaagaaggagaaacccacgctgtcagcctagctgtgtggcaagtccacgtccacc	352
Db	237	CCGGGGGAGGAGGCGAGGCGCCCTCGTACCCAGCAAAACGGCAGATGAAGAAGCGCTG	296
QY	353	aaacctatgcccgttctcctaagc-----tagcggaatgaagatg	395
Db	297	GAACTTCCCAAAAGCTGGCGGCTTCGCTCACATCGGCTCCGCCAGAGAGGAGAAAGAGACG	356
QY	396	gactgggggaagcccgagagggggagccctcccccagaatccctcttgaccaggttgaccagat	455
Db	357	GGCTTCGGGGAACCCGAGAGGACAGCCCTCTCCCGGACTCTCCGCTTCCCGCTGGACAAAGT	416
QY	456	ctttacacctctctgtttggtgtagcagaatgtgtgatacactcttcgcagacttccgtgaga	515
Db	417	CTTTGCACTCCCTTCGGGGAGACCAGAGCGGCGCTCTTCTTCAGGACCTCTTGAGGC	476
QY	516	gggagaaatgtgtgatacgtctgacttctggtttctgttaatgggtltaaggcagatga	575
Db	477	GAGGAAATGTGTGGACACTTTTGACCTTCGTGGTCCGCTCCAAAGGTTTCCGGCAGATGG	536
QY	576	accggaagagataccaaaactttgaggtggccaaagaaactataagataggtatcatgaga	635
Db	537	ACCTCAAGGATACCAAAAAGCAGAGAGTTGGCCAAAGCAATTTGCAAGCGTTACATCGAAA	596
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Db	597	GCAACAGGCTGTGGCCAAACAGCTGAAGCCCGCACCAAAACCTTCATCCGGGATACCA	656
QY	696	tcaagaagcaacagatcgtgcctcggtatglttgaccagcgacagacccgaatccagcgag	755
Db	657	TCAAGAAACACACACATGCACTCGGCCATGTTCCGACACAGGGCGAGATGAGATCCAGCCA	716
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QY	816	ggagctgggggggaaacacagactacatgagtaaacyggggagctggyggagcctaaggtct	875
Db	777	GGACCGGGGGGAGAACCCCAATCACTCAACCCCAACGCGCTGGGAGCACTGTAAGGCAG	836
QY	876	tatgtgctactctcccaacttgataagaagaagaggtggaogtvg	923
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RESULT 12	CNS01YDU/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
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	AL172875									
	AL172875.1	GI:7810932								
	GSS: genome survey sequence.									
	Tetradon nigroviridis.									
	Tetradon nigroviridis									
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Eucacanthomorpha; Holacanthopterygii; Acanthopterygii; Percormorpha;									
	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.									
	1 (bases 1 to 830)									
	Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saudin,W., Bernot,A. and									

TITLE	Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
JOURNAL	Unpublished																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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AUTHORS	Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Benoit, A., Fzimes, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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COMMENT	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases. This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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Matches	508; Conservative 4; Mismatches 247; Indels 12; Gaps 2;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:34:09 ; Search time 4956.99 seconds
(without alignments)
1097.836 Million cell updates/sec

Title: US-09-587-574-7
Perfect score: 369
Sequence: 1 tggaccaaatctctacaccc.....acattacctggaatatgtg 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: gb_ba3:*
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94: gb_rnd:*
95: gb_rnd2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	369	100.0	2825 9	A98521 Sequence 6
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4	369	100.0	191041 69	AC024114 Mus muscu
5	365.8	99.1	3016 94	AF205889 Mus muscu
6	337	91.3	3216 94	AF017757 Rattus no
7	308.2	83.5	2538 88	AF205888 Homo sapi
8	308.2	83.5	3072 88	AF078165 Homo sapi
9	308.2	83.5	184263 85	AC004805 Homo sapi
10	227.2	61.6	3485 8	AB032263 Dando rer
11	163.4	44.3	3156 8	AF009012 Gallus ga

12 161.2 43.7 3411 88 AF009674
c 13 161.2 43.7 23786 91 HS415C1
c 14 161.2 43.7 35054 91 HS33B10
c 15 161.2 43.7 39170 85 AC005202
c 16 161.2 43.7 133069 70 AC026836
c 17 161.2 43.7 187272 74 AC069076
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19 149 40.4 3460 9 AF017756
20 148.8 40.3 3066 8 AB032662
21 147.4 39.9 3761 94 AF009011
22 119 32.2 2121 8 AF140243
23 64.8 17.6 910 7 AF011361
24 56.8 15.4 2638 93 HS027655
25 35.2 13.0 606 9 AR035823
26 35.2 15.0 606 9 AR035850
27 27 2132 93 HS094829
28 55.2 15.0 2383 10 165400
29 55.2 15.0 2383 93 HS070426
30 55.2 15.0 2406 9 AR035805
31 55.2 15.0 2406 9 AR035832
32 54 14.6 1505 94 AF215669
33 54 14.6 1688 94 AF215670
34 52 14.1 606 94 MMU70427
35 52 14.1 2272 9 AR064044
36 50.4 13.7 838 94 MMU72881
37 50.4 13.7 995 94 MMU67189
38 50.4 13.7 2250 94 MMU94828
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42 47 12.7 186051 64 AC015683
43 46.6 12.6 325 8 AF090083
44 45.6 12.4 543 88 AF300649
45 45.6 12.4 765 88 AF297015S1

ALIGNMENTS

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LOCUS Sequence 7 from Patent WO911780.
ACCESSION A98522
VERSION A98522.1 GI:6781608
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 369)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 7 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
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source Location/Qualifiers
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BASE COUNT 101 a 82 c 99 g 87 t
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Best Local Similarity 100.0%; Pred. No. 3, 6e-94;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 ttctcggagagggagaaatgtgtgatacgtgataccttcggttcttgaatgggttc 120
Db 1 ttctcggagagggagaaatgtgtgatacgtgataccttcggttcttgaatgggttc 120

Db 61 TTCTGTGAGAGGAGGAATAATGTGTGATACGCTTGACTTCTGTGTTGTTGTAATGGGTTTC 120
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Db 181 TACATTGGAACAACAAGCTTGTCTCCAAAGCACTGAAGCCGCCCAAGACCTTACATA 240
OY 241 cgaagtgcataaagaacaacagatcgcctgcgtgcatatgtttgaccaggacaacaggag 300
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Db 301 ATCCAGCAGATGATGAGAAATGCTTACCAGAGTGTTGACTTGTGACATTACTCTG 360
OY 361 gaatatgtg 369
Db 361 GAATATGTG 369

RESULT 2
A98521 2825 bp DNA PAT 26-JAN-2000
LOCUS Sequence 6 from Patent WO911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

Query Match 100.0%; Score 369; DB 9; Length 2825;
Best Local Similarity 100.0%; Pred. No. 4, 4e-94;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 121 aggcagatgaaacctgaagataccaaacttgcaggtggccaagcaatctataaagg 180
Db 121 AGGCAGATGAACCTGAAGATACCAAACTTTCGAGTGGCCAAAGCAATCTATMAAGG 625
OY 181 taccattggaacaacagcgtttgtctccaagcagcgtgaagccgcgcacaaagactaata 240
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OY 241 cgaagtgcataaagaacaacagatcgcctgcgtgcatatgtttgaccaggacaacaggag 300
Db 241 CGAGATGCAATCAACCAACCAACAGATCGCTGCGTGCATGTTGACCAAGCAGACCGAG 300
OY 301 atccagcagatgagtgagaaatgctcaccagagtggttcttgacttcgaattactctg 360
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Db 746 ATCCAGCAGTATGAGGAAATGCTTACACAGTGTCTTGTGACTTGTGACATTACTG 805

QY 361 gaataatgtg 369
|||||

Db 806 GAATATGTG 814

RESULT 3

AF073788 2825 bp mRNA ROD 13-JUL-1998

LOCUS Mus musculus conductin mRNA, complete cds.

DEFINITION AF073788

ACCESSION AF073788.1 GI:3309246

VERSION

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A., Wurttele, M., Grimm, J., Asbrand, C., Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W.
Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta
Science 280 (5363), 596-599 (1998)

TITLE

JOURNAL 2 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A. and Birchmeier, W.
Direct Submission
Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany

FEATURES

source location/Qualifiers

1..2825

/organism="Mus musculus"

/db_xref="taxon:10090"

215..2737

/function="induces degradation of beta-catenin"

/codon_start=1

/product="conductin"

/protein_id="AAC26047.1"

/db_xref="gi:3309247"

/translation="MSSAVLVTLPLDPSSPFREDAPRPVPEGEETPPCOPSVGKVO
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IKKQDLSVDFDQATQIAVMEENAVOFLSDYLEVVRSGGNTAVMSGGLSL
KVLGCLPTLNEEEMTCADLKCKLSPVVGSLSTLRATSDSVCEAENGFSEFK
SDPVNPVAGSGVYVAPATSDSELSDALDMSMTDSVCEVPPVPMGSKKQLQ
REMRHSVANGOVSLPHPPRTIRLPEKMTVPVPAFAELIRLKLKLEESRSLLE
ERLQOIRDEKEKESSEALSSNDGAPVOHPALALPSSGYEEDPOTILDDHLSRLVKT
GCOSRGVCRYSRPSRSPDHNNHNOCHTLLSTGGKILPPAAKPLUGGKSFUTKOT
TKVHNHTIHHAVPKTEELAEATONVRCCLPGGTDYTCYSKCSHPKAEPLPGE
QFCGSRGGLTPRNKAGTEPGLALSARDGMSAAGDQLPEEDRSQDWOMLMS
EROSKSKPHSAOSIKRSYPLESARAPEGRVSRHNLGDSVARSVARHPTODPAM
PLTPPTNLALOEACRLAEYSKPOKORCVASOORDNHSAGACAGSPRANSLA
PDHKEPKLASVALOASLIVYTFPGCEETPRYRMKAOSITLGHKEQLSKNGNY
RYPRKASDERACGAVFEIMDETIVLPMTESGRILKGYERID"

BASE COUNT 703 a 815 c 813 g 494 t

ORIGIN

Query Match 100.0% Score 369 DB 94 Length 2825
Best Local Similarity 100.0% Pred. No. 4.4e-94
Matches 369: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 566 AGGACATGATACCTGAAGATACCAAACTTTGCGATGGGCCAAAGCAATCTAAGAG 625

QY 181 tacattgagaacaacagcgtgtcttccaagcagctgaagccgcacccaagactacata 240
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Db 626 TACATTGAGAACACACGCGTGTCTCCAAAGCAGCTGAAGCCGCCACCAAGACTACATA 685

QY 241 cgaatgagcatcaagaagaacacagctcgctggtatgtttgacaggacagaccagag 300
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Db 686 CGAGATGATCAAGAAAGCAACAGATGCGTCCGCTATGTTTACACGACACAGACCGAG 745

QY 301 atccagcagtgatgaggaagaatgcctaccagtgcttcttgactctgacattacctg 360
|||||

Db 746 ATCCAGCAGTATGAGGAAATGCTTACACAGTGTCTTGTGACTTGTGACATTACTG 805

QY 361 gaataatgtg 369
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Db 806 GAATATGTG 814

RESULT 4

AC024114 191041 bp DNA HTG 06-NOV-2000

LOCUS AC024114/C

DEFINITION Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT

ACCESSION AC024114.8 GI:11094615

VERSION

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE

ORGANISM house mouse.

Mus musculus

REFERENCE 1 (bases 1 to 191041)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Meltzer, M. L., Lewis, L. R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carllock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hognes, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kover, C., Liu, J., Liu, W., Louisedge, H., Lozada, R. J., Martin, R., Massey, E., McLeod, M. P., Mel, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, B., Perez, L., Relfer, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Worley, K. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 191041)
Worley, K. C.
Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 4, 2000 this sequence version replaced gi:9929587.

COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: MACA

Center clone name: RP23-278J12

----- Summary Statistics

Sequencing vector: M13: 108821

Chemistry: dye-primer Bodipy: 95% of reads

Chemistry: dye-terminator Big Dye: 5% of reads

Assembly program: Phrap: version 0.990329

Consensus quality: 158769 bases at least Q40

Consensus quality: 172780 bases at least Q30

Consensus quality: 179030 bases at least Q20

Estimated insert size: 180377; sum-of-ctrls estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (See http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 19344: contrig of 19344 bp in length
* 19345 19444: gap of unknown length
* 19445 33763: contrig of 14319 bp in length
* 33764 33863: gap of unknown length
* 33864 47738: contrig of 13875 bp in length
* 47739 47839: gap of unknown length
* 47839 59611: contrig of 11773 bp in length
* 59612 67897: contrig of 8186 bp in length
* 67898 67997: gap of unknown length
* 67997 77929: contrig of 9932 bp in length
* 77930 78029: gap of unknown length
* 78030 86605: contrig of 8576 bp in length
* 86606 86706: gap of unknown length
* 86706 93904: contrig of 7199 bp in length
* 93905 94004: gap of unknown length
* 94005 104236: contrig of 10232 bp in length
* 104237 104337: gap of unknown length
* 104337 113241: contrig of 8905 bp in length
* 113242 113341: gap of unknown length
* 113342 120171: contrig of 6830 bp in length
* 120172 120271: gap of unknown length
* 120272 125989: contrig of 5718 bp in length
* 125990 126089: gap of unknown length
* 126090 131869: contrig of 5780 bp in length
* 131870 131970: gap of unknown length
* 131970 139294: contrig of 7325 bp in length
* 139295 139394: gap of unknown length
* 139395 146006: contrig of 6612 bp in length
* 146007 146106: gap of unknown length
* 146107 150788: contrig of 4682 bp in length
* 150789 150888: gap of unknown length
* 150889 156925: contrig of 6037 bp in length
* 156926 157025: gap of unknown length
* 157026 161170: contrig of 4145 bp in length
* 161171 161270: gap of unknown length
* 161271 164311: contrig of 3041 bp in length
* 164312 164411: gap of unknown length
* 164412 167354: contrig of 2943 bp in length
* 167355 167454: gap of unknown length
* 167455 171291: contrig of 3837 bp in length
* 171292 171391: gap of unknown length
* 171392 174233: contrig of 2842 bp in length
* 174234 174333: gap of unknown length
* 174334 177744: contrig of 3411 bp in length
* 177745 177844: gap of unknown length
* 177845 179402: contrig of 1558 bp in length
* 179403 179502: gap of unknown length
* 179503 182420: contrig of 2918 bp in length
* 182421 182520: gap of unknown length
* 182521 184923: contrig of 2403 bp in length
* 184924 185023: gap of unknown length
* 185024 187054: contrig of 2031 bp in length
* 187055 187154: gap of unknown length
* 187155 188272: contrig of 1118 bp in length
* 188273 188372: gap of unknown length
* 188373 189634: contrig of 1262 bp in length
* 189635 189734: gap of unknown length
* 189735 191041: contrig of 1307 bp in length.

Location/Qualifiers

source 1. 191041
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-278J12"
BASE COUNT 49790 a 43523 c 42989 g 51816 t 2923 others
ORIGIN

Query Match 100.0%; Score 369; DB 69; Length 191041;
Best Local Similarity 100.0%; Pred. No. 6,7e-94;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggacaaagcttaccactccctgtgtggtgacaaagatggtacactctccgagact 60
Db 111421 TGGACCAAGCTCTTAACTACCTCTGTGGGATCGACGATGTGATACCTCTTCGGACT 111362
QY 61 ttccctggagagggaaatggtggtatagctgtgactctgtgtgtgtaaggttc 120
Db 111361 TTCCCTGGAGAGGGAAATGTTGTGATAGCTGTGACTTCTGTGTTGTTGTAATGGGTTT 111302
QY 121 aggcagatgaacctgaagatataccaaacttgcgagtgcgcaagcaatctataagag 180
Db 111301 AGGCAGATGAACCTGAAGATACCAAACTTTCGAGTGGCCAAAGCAATCTATAGAGG 111242
QY 181 tacattggaacaacagcgtgtctcaagacgtgaagccgcacaaagactacata 240
Db 111241 TACATTGGAACAACAGCGTGTCTCAAGACGTCGAGCCGCCACCAAGACCTACATA 111182
QY 241 cgaagtgcacatcaagaacaacagatgcgtcgtgcatggtttgaccagagcagacgag 300
Db 111181 CGAGTGCACATCAAGAACCAACAGATGCGTGTGTCATGTTGACACGACACAGCCGAG 111122
QY 301 atccagcagtgatgagaaatgctaccagagtgcttctgtgactctgaaattacctg 360
Db 111121 ATCCAGCAGTGATGAGAAATGCTTACCAAGTCTTGTACATTGACATTACTCG 111062
QY 361 gaatatgtc 369
Db 111061 GAATATGTG 111053

RESULT 5
AF205889 3016 bp mRNA ROD 03-JAN-2000
LOCUS AF205889
DEFINITION Mus musculus Axin2 (Axin2) mRNA, complete cds.
ACCESSION AF205889
VERSION AF205889.1 GI:6653585
KEYWORDS
SOURCE
house mouse.

ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 3016)
Zhang, T., Ragotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
Jenkins, N.A., Warburton, D. and Costantini, F.
Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation

TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3016)
AUTHORS Zhang, T. and Costantini, F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HHSC 1416, New York, NY 10032, USA
Location/Qualifiers

FEATURES
source
1. 3016
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/map="between Wnt3 and Pkca"
1. 3016
/gene="Axin2"
gene

FEATURES

CDS

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/product="Axin2"
/protein_id="AA022800.1"
/db_xref="GI:6653586"
/translation="MSSAVLVTLPLDPSSSFREDAPRPVPEEGEETPPCPGSGVKVQ
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KCVDTLDFWFCNKGFRQNLKDTKTLRYAKAIYKRIENNSVSKOLKPAKTYIRDG
IKKQOIGSVMPDQAOETLQAVMEENAYOVFLSDIYLYEVRSRGENTAYMSNGLGSL
KVLGCLPTLNEEEMTCADLCKLSPTVYGLSKTLRATASVSTETAENGFERSFKR
SDPVPYHVGSGVFPAPATSAWSELSALDSDMSMTDSSVDGIPPRMSKKOLO
REMRHSVANGOVSLPHFPRTHRLPKEMTPVPEPAFAELISRLKLELSRHSLE
ERLQOIRDEEEKESSEALSRDGA PVQHPALPLPSGYEEDPOTLIDHLSRVLYKTP
GOSPGVGRISPRSRSPDHNNHOOHTLHOCFTLPTGKLPVACPPLGKSSLYKOT
TKHHNHYIHHNAVPRKTEIEAETORVRCJCPGCTDYCYSKCSKHPAEPLPE
OFCGSRGCTLPKRNAGKTEPGLALASRDGMSAAGAPOLPEEGDSODVOMWMLSE
EROSKSRHSAOSIRKSYPLESARAPEERSRHLLGASGHSVARAHPTODPAM
PLTPPNTLQLEACRILAEYSKPOKORCCVAAQOORNRHNSAAGACAGSPANSLA
PDHKEPKKLASVHALQASSELVYTFPGCEIEIPYRMILKAQSLTIGHREQLSKGNVY
RYFKASDERACGAVFEIWDDEVLPMEYGRILGKVERID"

BASE COUNT 766 a 858 c 837 g 555 t

ORIGIN

Query Match 99.1%; Score 365.8; DB 94; Length 3016;
Best Local Similarity 99.5%; Pred. No. 3.6e-93;
Matches 367; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tggaccaagctcttaacacccctgtgttggtgaccagaatgagcatatccttcgcgact 60
DB 286 TGGACCAAGCTCTTTACACTCTTGTGGTGACAGAGATGTCATACCTTCCGCGACT 345
QY 61 ttccctggagaggaagaatgctgtgatacgccttgactcttgcttgtaagtgttc 120
DB 346 TTCCTGGAGAGAAAGAAATGTGTGATACGCTGACTTGGTTGCTGTATAGGTTTC 405
QY 121 aggcagatgaacctgaagaatataccaaactttgcgagtggtgccaagaacataagagg 180
DB 406 AGGCAGATGAACTGGAAGATATACCAAACTTGGAGTGCCCAACCAACTTAAAGAGG 465
QY 181 tacattgagaacaacagcgttgtctccaagcagctgaagccgcaccaagaactcata 240
DB 466 TACATTGAGAACACACGCGTGTCTCCAAAGCACTGAAGCCGCCCAAGACTTACATA 525
QY 241 cgaagatgcatcaagaagaacagatcggctcgtgcatggtttgacacagacagacgag 300
DB 526 CGAGATGGCATCAAGAAGACAGATCGGCTCGTCAATGTTTACACGACGACGAG 585
QY 301 atccagagcagtgatgaggaagaatgctctaccaggtgttcttgactctgacattactg 360
DB 586 ATCCAGGCAAGTGTATGAGGAATAATGCTTACAGAGTGTCTTGACATTTACCTG 645
QY 361 gaatatgtg 369
DB 646 GAATATGTG 654

RESULT 6
AF017757 3216 bp mRNA ROD 24-APR-1998
LOCUS Rattus norvegicus GSK-3beta Interacting protein Axin mRNA, complete
DEFINITION cds.
ACCESSION AF017757
VERSION AF017757.1 GI:3080758
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3216)
Yamamoto,H., Kishida,S., Uochi,T., Ikeda,S., Koyama,S., Asashima,M.

TITLE and Kikuchi,A.
Axin, a member of the Axin family, interacts with both glycogen
synthase kinase 3beta and beta-catenin and inhibits axis formation
of Xenopus embryos
JOURNAL Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
MEDLINE 98226558
REFERENCE 2 (bases 1 to 3216)
AUTHORS Yamamoto,H., Ikeda,S., Murali,H., Kishida,S. and Kikuchi,A.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,
Japan

FEATURES
source Location/Qualifiers
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
85..2601
/note="GSK-3beta Interacting protein; Axin like protein"
/codon_start=1
/product="Axin"
/protein_id="AAC40089.1"
/db_xref="GI:3080759"
/translation="MSSAVLVTLPLDPSSSFREDAPRPVPEEGEETPPCPGSGVKVQ
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IKKQOIGSVMPDQAOETLQAVMEENAYOVFLSDIYLYEVRSRGENTAYMSNGLGSL
KVLGCLPTLNEEEMTCADLCKLSPTVYGLSKTLRATASVSTETAENGFERSFKR
SDPVPYHVGSGVFPAPATSAWSELSALDSDMSMTDSSVDGIPPRMSKKOLO
REMRHSVANGOVSLPHFPRTHRLPKEMTPVPEPAFAELISRLKLELSRHSLE
ERLQOIRDEEEKESSEALSRDGA PVQHPALPLPSGYEEDPOTLIDHLSRVLYKTP
GOSPGVGRISPRSRSPDHNNHOOCHLLPTGKLPVACPPLGKSSLYKOTK
TKHHNHYIHHNAVPRKTEIEAETORVRCJCPGCTDYCYSKCSKHPAEPLPE
OFCGSRGCTLPKRNAGKTEPGLALASRDGMSAAGAPOLPEEGDSODVOMWMLSE
EROSKSRHSAOSIRKSYPLESARAPEERSRHLLGASGHSVARAHPTODPAM
PLTPPNTLQLEACRILAEYSKPOKORCCVAAQOORNRHNPATGAGPVSFNSPLASE
DHKEPKKLASVHALQASSELVYTFPGCEIEIPYRMILKAQSLTIGHREQLSKGNVY
YFKASDERACGAVFEIWDDEVLPMEYGRILGKVERID"

BASE COUNT 860 a 914 c 872 g 570 t

ORIGIN

Query Match 91.3%; Score 337; DB 94; Length 3216;
Best Local Similarity 94.6%; Pred. No. 5.3e-85;
Matches 349; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 tggaccaagctcttaacacccctgtgttggtgaccagaatgagcatatccttcgcgact 60
DB 316 TGGACCAAGCTCTTTGACACTCTTGTGGGGAGACCAAGATGTCATACCTTCCGCGACT 375
QY 61 ttccctggagaggaagaatgctgtgatacgccttgactcttgcttgtaagtgttc 120
DB 376 TTCCTGGAGAGGAGAAATGTGTGATACCTCGACTTGGTTGCTTCAATGAGGTTTC 425
QY 121 aggcagatgaacctgaagaatataccaaactttgcgagtggtgccaagaacataagagg 180
DB 436 AGGCAGATGAACTTGAAGATATACCAAACTTGGAGTGCCCAAGCAACTTAAAGAGG 495
QY 181 tacattgagaacaacagcgttgtctccaagcagctgaagccgcaccaagaactcata 240
DB 496 TACATTGAGAACAAAGTGTGTCTCCAAAGCACTGAACCCGCCACCAAGACTTACATA 555
QY 241 cgaagatgcatcaagaagaacagatcggctcgtgcatggtttgacacagacagacgag 300
DB 556 AGAGATGGCATCAAGAAGACAGATCGGCTCGTCAATGTTTGAACGAGGCGAGG 615
QY 301 atccagagcagtgatgaggaagaatgctctaccaggtgttcttgactctgacattactg 360
DB 616 ATTCAGGCGGTGATGAGGAATAATGCTTACAGAGTGTCTTGACTTGTGACATATACCTC 675
QY 361 gaatatgtg 369
DB 676 GAATATGTG 684

RESULT 7
AF205888 2538 bp mRNA PRI 03-JAN-2000
LOCUS Homo sapiens AXIN2 (AXIN2) mRNA, complete cds.
DEFINITION AF205888
ACCESSION AF205888.1 GI:6653583
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2538)
AUTHORS Zhang, T., Pagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N. G.,
Jenkins, N. A., Warburton, D. and Costantini, F.
TITLES Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2538)
AUTHORS Zhang, T. and Costantini, F.
TITLES Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HMSC 1416, New York, NY 10032, USA
FEATURES
source
1. .2538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q24"
/tissue-type="brain; lymphoblast"
/note="Similar to Esrs 823683 and 446378"
1. .2538
/gene="AXIN2"
110. .2443
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/codon_start=1
/product="AXIN2"
/protein_id="AAF22799.1"
/db_xref="GI:6653584"
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CVDTLDFWACNGFRONLKDPTKLRVAKAIYKRYIENNSIVSKOLPARKTYLRDGI
KKQQLDSIMFOAQTEIOSVEMENAYOMFLSDIYEVRSRGENTAYMSGUGLSK
VVCGLPLTNEEEMTCADFCKLSPTVYGSLSKLRATASVSTETVDSGYRSFKRS
DPVAVHIGSGVYFAPATNSDEISDALTDMSMTDSSVDGIPRYVSGSKOLOR
EMHSYKANGRVSLPHPRTRRLKEMPVPAFAELISRLKILLESRSLSER
RLQOIRDEDEREGSELTINSREGAPTDHPLSLSGSTEEDPOTLLDHLRYLTKRG
COSPGVGRYSRSPRSDPHHHHHSQYHSLPPGKLPAPASPGACPLGSGKGVTKO
TTKRVHHHYIHHNAVPTKTEIEAATORVACFCPGSGEYCYCKSKSHKAPETMP
EOPGASOTKRAYPLESARSSPGERASRHHLMGNSGHPRTTPRAHLFTQDSAMPSTLP
PNTLAHLEACRLAEVSKPPKORCVASQORDNHSATVOTGATPFSNPFLADEHK
EPKTLGVHAQASLEIVYVTFPGCEETPYRMLKAOSLTIGHFKEQLSKKNVNYFRK
KASDFRCAGAFEEIWEDEVILPMYEGRIILKVERID"

BASE COUNT 617 a 724 c 724 g 473 t
ORIGIN
Query Match 83.5%; Score 308.2; DB 88; Length 2538;
Best Local Similarity 89.7%; Fred. No. 7.6e-77;
Matches 331; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 tggacaagcttcaacacctgtgtgagtgacagagatgagtcataccttcgcgagact 60
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DB 338 TGGACCAAGTCTTACACCTTATTGGCGCATCAAGACGGTGCTTACTGTTCCGAAT 397
|||||

QY 61 ttccctgagagagagaatggtgatacgtcgtgaccttgcgttgcgttaatgggttc 120
|||||
DB 398 TTCCCTGAGAGAGGAAATGCTGATACCTTAGACTTCTGTTGCCGCAATGATTC 457
|||||

QY 121 aggcagatgagaaactatccaaactttgcgagatgagtgccaaagcaatctataagag 180
|||||
DB 458 AGGCAGATGAACTTACCAAACTTACGAGTAGGCCAAAGCGATTCACAAAGG 517
|||||

QY 181 tacattgagaacaacagcgtgtgtctccaaagcagctgaagcccgcccaagaacctata 240
|||||
DB 518 TACATTGGAACAACAGCAATGTCTCCCAAGCAGCTGAGAGCTCGCACCAAGACCTACATA 577
|||||

QY 241 cgagatgcatcaagaagaacagatgcgtcgcgtcatggttgcacccagcagacgag 300
|||||
DB 578 AGAGATGGCATCAAGAAACACAGATGATTGATTCATCATGTTTGACCAAGCGCGACGAG 637
|||||

QY 301 atccagcagctgagtgaggaatgctccaccagctgtcttcctgacttcgatacttacc 360
|||||
DB 638 ATCCAGCTGGTGATGAGAGAAATGCCCTACCAAGATGTTTGTGACTTTCGATATATACCTC 697
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QY 361 gaatatgtg 369
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DB 698 GAATATGTG 706
|||||

RESULT 8
AF078165 3072 bp mRNA PRI 21-MAR-1999
LOCUS AF078165
DEFINITION Homo sapiens conductin mRNA, complete cds.
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3072)
AUTHORS Mai, M., Qian, C., Yokomizo, A., Smith, D. I. and Liu, W.
TITLES Cloning of the human homolog of conductin (AXIN2), a gene mapping
to chromosome 17q23-q24
JOURNAL Genomics 55 (3), 341-344 (1999)
MEDLINE 99168905
REFERENCE 2 (bases 1 to 3072)
AUTHORS Mai, M., Qian, C., Smith, D. I. and Liu, W.
TITLES Direct Submission
JOURNAL Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic,
200 First Street SW, Rochester, MN 55905, USA
FEATURES
source
1. .3072
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q23-q24"
/note="AXIN2"
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/translation="MSSAMLYTCLPDPSSSFREDAPRPVYGEGETPPCOGVGKQ
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KKQQLDSIMFOAQTEIOSVEMENAYOMFLSDIYEVRSRGENTAYMSGUGLSK
KVVCGYLPNTNEEEMTCADFCKLSPTVYGSLSKLRATASVSTETVDSGYRSFKR
SDPVNPHYIGSGVYFAPATNSDEISDALTDMSMTDSSVDGIPRYVSGSKOLOR
REHRSYKANGRVSLPHPRTRRLKEMPVPAFAELISRLKILLESRSLSER
RLQOIRDEDEREGSELTINSREGAPTDHPLSLSGSTEEDPOTLLDHLRYLTKRG
COSPGVGRYSRSPRSDPHHHHHSQYHSLPPGKLPAPASPGACPLGSGKGVTKO
TTKRVHHHYIHHNAVPTKTEIEAATORVACFCPGSGEYCYCKSKSHKAPETMP
EOPGASOTKRAYPLESARSSPGERASRHHLMGNSGHPRTTPRAHLFTQDSAMPSTLP
PNTLAHLEACRLAEVSKPPKORCVASQORDNHSATVOTGATPFSNPFLADEHK
EPKTLGVHAQASLEIVYVTFPGCEETPYRMLKAOSLTIGHFKEQLSKKNVNYFRK
KASDFRCAGAFEEIWEDEVILPMYEGRIILKVERID"

BASE COUNT 769 a 838 c 883 g 582 t
ORIGIN
Query Match 83.5%; Score 308.2; DB 88; Length 3072;
Best Local Similarity 89.7%; Fred. No. 7.7e-77;


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complement(20034..20330)
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repeat_region 21450..21626
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complement(21627..21702)
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repeat_region 21967..22020
/rpt_family="Alu"
repeat_region 22100..22407
/rpt_family="Alusx"
repeat_region 22424..22475
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/rpt_family="Alusx"
complement(24676..24839)
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complement(25689..25985)
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repeat_region complement(26521..26812)
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26971..27250
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complement(27279..27602)
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repeat_region complement(31308..31532)
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complement(34112..34294)
/rpt_family="FRAM"
repeat_region complement(34460..34767)
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35143..35452
/rpt_family="Alusx"
35464..35745
/rpt_family="AluO"
complement(35781..35902)
/rpt_family="FLAM.C"
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40069..40101
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41491..41619

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/rpt_family="Alusq"
repeat_region complement(43274..43341)
/rpt_family="L2"
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/rpt_family="LIME"
repeat_region complement(46499..46811)
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repeat_region complement(46812..47117)

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 Best Local Similarity 89.7%; Pred. No. 1.2e-76;
 Matches 331; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 1 tggaccagctcttacacccctctgttggtgagcagagatggtgcatacctcctcgact 60
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DB 2327 TGGACCAAGTCTTACACTCCTTATGCGCATCAAGACGCTTACCTGTTCCGAAC 2268
|||
QY 61 ttcttgagagaggaatggtgatacgtgactcttggttgatggttc 120
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DB 2267 TTCTGAGAGGAGAAATGCTGATACCTTACACTTCTGTTGCTCGATGATTC 2208
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QY 121 aggcagatgaacccgaaagatatacacaacttgcgagtgagcgaagaatctataagag 180
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DB 2207 AGGCAGATGAACTCGAAGATACCAAACTTACGAGTAGCCAAAGCATCAAAAG 2148
|||
QY 181 tacattggaacaacagcgtgtgtccaaagcgtgaagccgcacaaagactata 240
|||
DB 2147 TACATTGGAACAACAGCATGTCTCCAAAGCAGCTGAGCCTGCCACCAACCTTACATA 2088
|||
QY 241 cgaatgagcatcaagaagaacagatgcgctcgatgtttgacagagcagaccag 300
|||
DB 2087 AGAGTGGCATCAAGAACAGACAGATGATTCATCATGTTGACCAAGCCACACCGAG 2028
|||
QY 301 atccagcagatgatgaggaatgactacacaggtgtcttgactctgacattacctg 360
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DB 2027 ATCCAGTCGGTGAAGAGGAGAAATGCCATCACAGATGTTTGATTCGATATATACCTC 1968
|||
QY 361 gaatatgtg 369
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DB 1967 GAATATGTG 1959
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RESULT 10
 AB032263 3485 bp mRNA VRT 01-AUG-2000
 LOCUS
 DEFINITION Danio rerio mRNA for axln2, complete cds.
 ACCESSION AB032263
 VERSION AB032263.1 GI:7229079
 KEYWORDS
 SOURCE
 ORGANISM

Danio rerio cDNA to mRNA.
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Rasbora; Danio.

REFERENCE
 1 (sites)
 Shimizu,T., Yamanaoka,Y., Ryu,S.L., Hashimoto,H., Yabe,T.,
 Hirata,T., Bae,Y.K., Hibl,M. and Hirano,T.
 Cooperative roles of Bozozok/Dharma and Nodal-related proteins in
 the formation of the dorsal organizer in zebrafish
 Mech. Dev. 91 (1-2), 293-303 (2000)

JOURNAL MEDLINE
 REFERENCE 2 (bases 1 to 3485)
 Hirano,T., Hibl,M. and Shimizu,T.
 Direct Submisson
 TITLE Submitted (09-SEP-1999) to the DDBJ/EMBL/Genbank databases. Toshio
 Hirano, Biomedical research center, Osaka Univ. Med. school,
 Department of Molecular Oncology, 2-2, Yamadaoka, Suita, Osaka

Db 750 AAAAGCTTCAAAAAGACTGTGTCATGAACTGACAGATGACCTGACATGCTTGACAG 809
Qy 289 gcaagaccgagatccagcgagtgatgagagaaatgcctccagtgcttctactct 348
Db 810 GCCCAACTGAGTTCGATGATGAGAGACATACCTCTTGCTTCTTAAGTCG 869
Qy 349 gacattaccctgaata 365
Db 870 GATATTATTGGAATA 886
RESULT 12
AF009674 3411 bp mRNA PRI 15-JUL-1997
LOCUS Homo sapiens axin (AXIN) mRNA, partial cds.
DEFINITION AF009674
ACCESSION AF009674.1 GI:2252819
VERSION
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3411)
AUTHORS Vasicek,T.J., Zeng,L., Guan,X.-J., Zhang,T., Costantini,F. and
Tilghman,S.M.
TITLE Two dominant mutations in the mouse Fused gene are the result of
transposon insertions
Genetics (1997) in press
2 (bases 1 to 3411)
AUTHORS Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L.
3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F.
TITLE The mouse Fused locus encodes Axin, an inhibitor of the Wnt
signaling pathway that regulates embryonic axis formation
Cell 90 (1), 181-192 (1997)
JOURNAL 97373830
MEDLINE 3 (bases 1 to 3411)
REFERENCE Vasicek,T.J., Tilghman,S.M., Costantini,F., Zeng,L., Perry,W.L. III
AUTHORS and Zhang,T.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1997) Biological Technology Millennium
Pharmaceuticals, Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
FEATURES
source
1..3411
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/dev_stage="ubiquitously expressed in development and in
adults"
1..3411
/gene="AXIN"
/note="Fused is the classical dominant mouse tail kink
mutation due to an lap insertion in the Axin gene"
1..2704
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/function="may inhibit embryonic axis formation"
/note="contains RGS domain and Daugherless similarity;
may inhibit embryonic axis formation"
/codon_start=2
/product="axin"
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LDLVEPGSASPPPYLKWESLHSLDDDDGLSTFELKQSCADLDWFRCTG
FRKLEPCDSNEERIKLARAYRYILDNNIVSRQTPARKSPKIGKIMQLDIPAM
FDOATETQATMENTYPSFLKSDYLEYTRIGSPKVSQDSGSGTGKIGSYLP
TLNDEEMKCDODDEDGRDAPGRPKLLETAPRVSRRSSRRSEGEFRYGSW
REPAPRYVNGYALAPATSDSEOSTISDADLTSTDSYVQGIPIRYRKHRE
MOESAQVGRVPLPHIRTYRVEKVEKFADELHRLHLEAVORTREAEKLEERL
KRVMEEGEDGDPSSGPGCHKLPAPAMHHPPLRCWTWACGLDAHEENDESI
LDEHVRVLTGTGROSPPGHRSPDSGHVAKMPVALGGAASGHKHPKSGAKLDAAG

BASE COUNT 752 a 1010 c 1066 g 582 t 1 others
ORIGIN
Query Match 43.7%; Score 161.2; DB 88; Length 3411;
Best Local Similarity 68.3%; Pred. No. 3.8e-35;
Matches 258; Conservative 0; Mismatches 108; Indels 12; Gaps 2;
Qy 1 tgaaccaagcttaccctccttggtgagacagatggtgcatccttcctgagct 60
Db 365 TGGGCTGATGCTACTGATTCCTCCTGATGACCAAGATGAGATGATGATGAGT 424
Qy 61 ttccctgagagagaaatggtgatacgtctgacttctggttcttgtaaggttc 120
Db 425 TTCCGTGAAGCAGAGAGGCGTGCAGCTTCTGCTGCTTCTGCTGCTGCTGCT 484
Qy 121 agcagatg-----aacctgaagataccaaacttcgagtgagcgaagaacac 171
Db 485 AGGAGCTGGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
Qy 172 tataagagttaca---ttgaacaacaagcgtgtctccaaagcagctgaagccgcaac 228
Db 545 TACCGAAGTACTCTTGTGATTAACATGCAATCGTCCCGACAGACCAACGACCC 604
Qy 229 aagacatacagatgagatgataaagaagaacagctgctgctgctgctgctgctg 288
Db 605 AAGAGCTTCAAAAGGGCTGATCATGAGCAAGTGAAGTGAAGTGAAGTGAAGT 664
Qy 289 gcaagaccgagatccagcgagtgatgagagaaatgcctccagtgcttctactct 348
Db 665 GCCCAGACCGAATTCAGCCACATGAGAGAAACACTTCCCTCTTCTTAAGTCT 724
Qy 349 gacattaccctgaata 366
Db 725 GATATTATTGGAATAAT 742
RESULT 13
HS415C1 23786 bp DNA PRI 23-NOV-1999
LOCUS Human DNA sequence from cosmid 415C1 from a contig from the tip of
DEFINITION the short arm of chromosome 16, spanning 2mb of 16p13.3. Contains
EST and CpG Islands.
298272
ACCESSION 298272.1 GI:3036780
VERSION 16p13.3; CPG.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 23786)
AUTHORS Smye,R. and Lightning,J.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1997) Chromosome 16 Project Group
(http://www.sanger.ac.uk/HGP/Chr16/) Sanger Institute, Wellcome Trust
Genome Campus, Hinxton, Cambridge, CB10 1SA, UK. E-mail
enquiries: humquery@sanger.ac.uk Clone requests:
clonerequest@sanger.ac.uk
COMMENT On Apr 8, 1998 this sequence version replaced gi:2578104.
IMPORTANT: This sequence is the entire insert of clone 415C1. The
true left end of clone 415C1 is at 1 in this sequence. The true
right end of clone C33B10 is at 8634.
The true left end of clone C36768 is at 23683.
415C1 is from a 400kb clone contig on 16p.
Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit,
Institute of Molecular Medicine, Oxford.
415C1 came from the Los Alamos flow sorted human Chromosome 16


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repeat_region /note=.889
/note="MER44A repeat: matches 313. .178 of consensus"
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3050. .3155
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3151. .3242
/note="2 copies of 46 mer 90 & conserved"
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repeat_region /note="Aluub repeat: matches 193. .1 of consensus;
incomplete repeat"
4966. .5259
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5436. .5537
/note="2 copies of 51 mer 100 & conserved"
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5808. .5917
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repeat_region /note=.6036
5863. .6036
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8003. .8030
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/note="Alusg repeat: matches 1. .302 of consensus"
10596. .10635
/note="20 copies of 2 mer 85 & conserved"
repeat_region /note=.10973
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11081. .11376
/note="AluY repeat: matches 1. .294 of consensus"
12188. .12327
/note="AluJo repeat: matches 1. .139 of consensus;
incomplete repeat"
12311. .12631
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12636. .12935
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13215. .13515
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13229. .13232
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13562. .13568
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13665. .13834
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13835. .14153
/note="AluYb repeat: matches 308. .1 of consensus"
14154. .14286
/note="Alusg repeat: matches 133. .1 of consensus;
incomplete repeat"
14288. .14581
/note="AluJo repeat: matches 294. .4 of consensus"
15755. .>16037
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19202. .>19484; Paired with EST AA007530 matching this
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16208. .16246
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16517. .16816
/note="AluY repeat: matches 1. .301 of consensus"
17136. .17272
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incomplete repeat"
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17273. .17565
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17990. .19134
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EST AA007531 matching this clone; contains 11 repeat"
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15755. .>16037; Paired with EST AA007530 matching this
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20762. .21055
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21089. .21390
/note="AluY repeat: matches 1. .301 of consensus"
21713. .21738
/note="13 copies of 2 mer 92 & conserved"
22862. .23161
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23220. .23259
/note="AluY repeat: matches 41. .1 of consensus; incomplete
repeat"
23226. .23280
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23317. .23434
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23443. .23751
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23752. .23914
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24246. .24281
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25305. .26209
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25932. .26608
/note="PTRS repeat: matches 1533. .2438 of consensus"
27641. .27943
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27954. .28248
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28372. .28666
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28586. .28587
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28605. .28608
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28699. .29009
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29654. .29955
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32740. .33035
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33038. .33342
/note="AluY repeat: matches 1. .301 of consensus"
34019. .34290
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ORIGIN
Query Match 43.7%; Score 161.2; DB 91; Length 35054;
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XX Claim 18; Fig 3; 22pp; German.
PS
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Mingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polypsis Coll (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;

Query Match 100.0%; Score 369; DB 20; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1.1e-110; Indels 0; Gaps 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggaccaagcttactactctctgtgtggtgacccagatgtgtacatcttccggact 60
Db 232 tggaccaagcttactactctctgtgtggtgacccagatgtgtacatcttccggact 291
QY 61 ttccctgagagggagaaatgtgtgatacgcgtgactctgtgttctgtatgtgttc 120
Db 232 ttccctgagagggagaaatgtgtgatacgcgtgactctgtgttctgtatgtgttc 351
QY 121 aggcagatgaacccgtgaagatacacaactttgagagtgccaaagcaatctataagg 180
Db 352 aggcagatgaacccgtgaagatacacaactttgagagtgccaaagcaatctataagg 411
QY 181 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacccaagaactata 240
Db 412 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacccaagaactata 471
QY 241 cgaatgagcatcaagaagaacagatcgctcgatcatgtttgaccagagcaacagcgag 300
Db 472 cgaatgagcatcaagaagaacagatcgctcgatcatgtttgaccagagcaacagcgag 531
QY 301 atccagcagatgatgaggaagaatccctacagagtgcttctgacttgcatttacttg 360
Db 532 atccagcagatgatgaggaagaatccctacagagtgcttctgacttgcatttacttg 591
QY 361 gaatatgtg 369
Db 592 gaatatgtg 600

RESULT 2
X23369
ID X23369 standard; cDNA; 2825 BP.
XX
AC X23369;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human conductin DNA.
XX
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Mingless signalling pathway; Adenomatous Polypsis Coll; APC;
KW tumour suppressor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 215..2737
FT /*tag= a
FT /*product= "Conductin"
FT misc_signal 446..814
FT /*tag= b
FT /note= "regulator of G-protein signalling region as
FT described in Claim 19"

FT protein_bind 1241..1402
FT /*tag= c
FT /bound_moiety= GSK-3beta
FT /note= "as described in Claim 20"
FT 1403..1609
FT /*tag= d
FT /bound_moiety= beta-catenin
FT /note= "as described in Claim 21"
FT misc_feature 2561..2713
FT /*tag= e
FT /note= "Disvelled homology region as described in
FT Claim 22"
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XX W09911780-A2.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-DE02621.
XX
XX 02-SEP-1997; 97DE-1038205.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX Behrens J, Birchmeier W;
XX
XX WPI: 1999-214706/18.
XX
XX P-PSDB: W93569.
XX
XX "Tumor-suppressing protein conductin - used for treatment and
XX diagnosis of tumors
XX
XX Claim 18; Fig 2; 22pp; German.
XX
XX This invention describes a novel human conductin protein which has
XX anti-tumour activity. Detecting the presence or amount of conductin,
XX at protein or nucleic acid levels, is used to diagnose tumours, while
XX agents that (re)activate conductin are used for tumour therapy.
XX Conductin binds to beta-catenin and induces its cytoplasmic degradation,
XX resulting in blockade of the Wnt/Mingless signalling pathway in
XX vertebrates. Conductin also binds to Adenomatous Polypsis Coll (APC)
XX fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;

Query Match 100.0%; Score 369; DB 20; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1.1e-110; Indels 0; Gaps 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggaccaagcttactactctctgtgtggtgacccagatgtgtacatcttccggact 60
Db 446 tggaccaagcttactactctctgtgtggtgacccagatgtgtacatcttccggact 505
QY 61 ttccctgagagggagaaatgtgtgatacgcgtgactctgtgttctgtatgtgttc 120
Db 506 ttccctgagagggagaaatgtgtgatacgcgtgactctgtgttctgtatgtgttc 565
QY 121 aggcagatgaacccgtgaagatacacaactttgagagtgccaaagcaatctataagg 180
Db 566 aggcagatgaacccgtgaagatacacaactttgagagtgccaaagcaatctataagg 625
QY 181 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacccaagaactata 240
Db 626 tacattggaacaacagcgtgtgtctcccaagcagctgaagccgcacccaagaactata 685
QY 241 cgaatgagcatcaagaagaacagatcgctcgatcatgtttgaccagagcaacagcgag 300
Db 686 cgaatgagcatcaagaagaacagatcgctcgatcatgtttgaccagagcaacagcgag 745
QY 301 atccagcagatgatgaggaagaatccctacagagtgcttctgacttgcatttacttg 360
Db 746 atccagcagatgatgaggaagaatccctacagagtgcttctgacttgcatttacttg 805

QY 361 gatatatg 369
 |||||
 DB 806 gatatatg 814

RESULT 3
 X09012
 ID X09012 standard; DNA: 3411 BP.

AC X09012:

DT 14-JUN-1999 (first entry)

XX Human axin gene.

XX Axin: cancer; breast cancer; colorectal cancer;
 KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 2..2704
 FT CDS /*tag= a
 FT /product= Axin

XX W09902179-A1.

XX 21-JAN-1999.

XX 09-JUL-1998; 98WO-US14414.

XX 10-JUL-1997; 97US-0890865.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Constantini F, Zeng L;

XX WPI: 1999-120510/10.

XX P-PSDB: W96264.

XX Newly isolated nucleic acid encoding "axis inhibition" protein
 PT (Axin) - useful for detecting, diagnosing and treating cancer

XX Disclousure: Figure 10A-10B; 95pp; English.

CC Nucleic acids encoding mutant and wild type Axin and
 CC oligonucleotides derived from them are useful for detecting
 CC mutations in the Axin gene and for determining whether a subject is
 CC likely to develop cancer (including breast, colorectal,
 CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
 CC type Axin and homologues of Axin are useful for treating subjects
 CC who are likely to develop cancer (thyroid carcinomas). The nucleic
 CC acids are also useful for diagnosing cancer and for detecting
 CC mutations in cancerous cells. Wild type Axin, its antisense
 CC molecule and identified compounds form pharmaceutical compositions
 CC in the treatment of cancer. The compositions are also useful for
 CC treating cancer by inhibiting tumorigenesis (by inducing degradation
 CC of beta-catenin). The nucleic acid encoding Axin acts through
 CC negative regulation of the Wnt pathway in the Nleuwkoop Center.

XX Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;

Query Match 43.7%; Score 161.2; DB 20; Length 3411;

Best Local Similarity 68.3%; Pred No. 1.3e-42;

Matches 258; Conservativity 0; Mismatches 106; Indels 12; Gaps 2;

QY 1 tggaccagcttaccactctgtgtggcgcagagatggtacacactctccggaact 60
 ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
 DB 365 tggcctgagctactcgtcctcctgctgagtgaccagaagtggataagcctgttcgaact 424

QY 61 ttcctggagaggagaatgtgtgatacctggaactctgttctgttaatggctc 120
 ||||| ||| ||| ||| ||||| ||||| ||||| ||| ||| |||
 DB 425 ttcctgaagcagagaggtgtgctgctggaactctggaactctgttctgtcctgcaactgcttc 484
 QY 121 aggcagatg-----aacctgaaggaatacacaacttgcagatggcacaagcaatc 171
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 DB 485 aggaagctgagccctgtgacatcgaacgagagaagagctgaagctgagctgagagcacc 544
 QY 172 tataagaggtaca---tgaagaacaagcgtgtctccaagcagctgaagccgcacc 228
 || | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 DB 545 taccgaaagatacttctgatacaatgcatcgtgtcccgcaagcacaagcacc 604
 QY 229 aagacctacatacagatgtgcatcaagaagcaacagatcgctcgctcatgtttgacag 288
 |||| | ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 605 aagagcttcataaaggctgcatacgaagcagctgatacctcctgcaatgttgacag 664
 QY 289 gacagaccgagatccagcagatgtagaggaataatgctacagatgttctgactct 348
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 665 gccacgaccgaatccagcagcatgtagaggaataacactatccctcctctaagtct 724
 QY 349 gacattaccctggaatat 366
 || ||||| ||||| |||||
 DB 725 gatattacttggaaatat 742

RESULT 4

X09013
 ID X09013 standard; DNA: 3761 BP.

XX X09013;

XX 14-JUN-1999 (first entry)

XX Murine axin gene.

XX

XX Axin: cancer; breast cancer; colorectal cancer;
 KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
 KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
 KW beta-catenin; ss.

XX Mus musculus.

XX

XX Key Location/Qualifiers
 FH 1..2981
 FT CDS /*tag= a
 FT /product= Axin

XX W09902179-A1.

XX 21-JAN-1999.

XX 09-JUL-1998; 98WO-US14414.

XX 10-JUL-1997; 97US-0890865.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Constantini F, Zeng L;

XX WPI: 1999-120510/10.

XX P-PSDB: W96265.

XX Newly isolated nucleic acid encoding "axis inhibition" protein
 PT (Axin) - useful for detecting, diagnosing and treating cancer

XX

XX Claim 7; Figure 9A-9B; 95pp; English.

CC Nucleic acids encoding mutant and wild type Axin and
 CC oligonucleotides derived from them are useful for detecting
 CC mutations in the Axin gene and for determining whether a subject is
 CC likely to develop cancer (including breast, colorectal,
 CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
 CC type Axin and homologues of Axin are useful for treating subjects

Db 567 acacgtaccctgatgagagaagcctaccacagcttccctgaagtgcgctgtaccg 626
 QY 361 ga 362
 Db 627 ga 628

RESULT 8
 T43376
 ID T43376 standard; cDNA; 2406 BP.
 AC T43376;
 XX 11-MAR-1997 (first entry)
 DE Human cytokine response gene CRI.
 XX Cytokine response gene CRI; interleukin-2; IL-2;
 KW ligand-stimulated gene expression; diagnosis; therapy; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 116..724
 FT /*tag= a

XX PN M09639427-A1.
 XX 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US09194.
 XX
 PR 05-JUN-1995; 95US-0465585.
 PR 05-JUN-1995; 95US-0461379.
 PR 05-JUN-1995; 95US-0462337.
 PR 05-JUN-1995; 95US-0462390.
 PR 05-JUN-1995; 95US-0463074.
 PR 05-JUN-1995; 95US-0463081.
 XX
 PA (DART-) DARTMOUTH COLLEGE.
 XX
 PI Beadling C, Smith KA;
 XX
 DR WPI: 1997-043062/04.
 DR P-PSDB; W08133.
 XX
 PT Cytokine response proteins and genes - used in the detection and
 FT therapy of diseases caused by a mutation in the CR coding region
 XX
 PS Disclosure; Page 11-12; 81pp; English.
 XX
 CC 8 Clones (T43376-83) contg. interleukin-2 (IL-2)-induced genes were
 CC isolated from a human IL2 receptor-positive T blast cell cDNA
 CC library following IL-2 stimulation. 6 Of these ligand-induced genes
 CC (CRI, 2, 3, 5, 6, 8) are novel. CRI expression is rapidly and
 CC transiently induced by IL-2, and mRNA expression is suppressed by
 CC elevated intracellular cAMP. It encodes an intracellular protein
 CC (W08133) that shows homology to GOS8 and BL-34. CR genes and
 CC polypeptides (W08133-40) can be used as diagnostic or therapeutic
 CC agents; CR gene sequences can be used to detect and treat allelic
 CC mutations.
 CC
 XX Sequence 2406 BP; 565 A; 621 C; 656 G; 564 T; 0 other;

Query Match 15.08; Score 55.2; DB 18; Length 2406;
 Best Local Similarity 51.14; Pred. No. 5.7e-08;
 Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;
 QY 1 tggaccagcttaccctctgtgtgggagacagatggtgcatcccttcgcagact 60
 DB 299 tggagagatcgttcgacctgctgagcagtaataatgagtgctgcttccacgct 358

QY 61 ttctcgagagggagaatgtgtgatacgtgacttctgttctgttaatgggttc 120
 Db 359 ttctcgagagagagttcagtgagagaaacctggagttctggtcgcttgaggaagttc 418
 QY 121 agcagatgaaccttgaagatcaccaaaacttgcgagtgcccaagaatctataaagg 180
 Db 419 a---agaagatcgcagctacccaagctgctcccaagggcacccagatctttgaggag 475
 QY 181 tacattggaacaacagcgttctccaagcagctgaagccgccaccaagactata 240
 Db 476 ttcatltg-----cagtgagggccctaagaaggtlcaacattgacatgagaccgcgag 529
 QY 241 cgagatggcatcaagaagcaacagatcggtcgtctcatgttttgccagagcacagacgag 300
 Db 530 ctgaagagatgaacctgcgactgcgcacagccacagatgttgcgctcagggaag 589
 QY 301 atccagcagtgatgaggaagaaatgcctaccaggtgttcttgactctgaattactcg 360
 Db 590 acacgtaccctgatgaggaagactctaccacagcttccctgaagtgctgcgttaccg 649

QY 361 ga 362
 Db 650 ga 651

RESULT 9
 A39660
 ID A39660 standard; cDNA; 2406 BP.
 XX
 AC A39660;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE Human CRI cDNA.
 XX
 KW CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic;
 KW immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;
 KW cell differentiation; cancer; immune disease; rheumatologic disease;
 KW transplant rejection; anti-infective; CRI; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 116..724
 FT /*tag= a
 FT /product= "CRI"

XX PN US6057427-A.
 XX
 PD 02-MAY-2000.
 XX
 PF 05-JUN-1996; 96US-0652446.
 XX
 PR 20-NOV-1991; 91US-0796066.
 PR 10-AUG-1993; 93US-0104736.
 PR 27-OCT-1994; 94US-0330108.
 PR 05-JUN-1996; 96WO-US08992.
 XX
 PA (DART-) DARTMOUTH COLLEGE.
 XX
 PI Beadling C, Smith KA;
 XX
 DR WPI: 2000-338623/29.
 DR P-PSDB; Y87952.
 XX
 PT Novel antibody or antibody fragment which selectively binds to a
 PT polypeptide encoded by cytokine response gene 2
 XX
 PS Example IV; Column 75-78; 66pp; English.
 CC
 CC This invention describes a novel isolated antibody or antibody fragment
 CC (I) which selectively binds to a polypeptide encoded by cytokine response

CC gene 2 (CR2) and modulates CR2 activity. The products of the invention
 CC have cytotoxic, anti-allergic, immunosuppressive and antimicrobial
 CC activity. The antibodies are useful as therapeutic agents for regulating
 CC cellular proliferation and differentiation and for treating all kinds of
 CC cancers, immune diseases such as allergic, autoimmune, and rheumatologic
 CC diseases, transplant rejection, and as anti-infectives for fighting
 CC viral, bacterial, parasitic and fungal infections. This sequence encodes
 CC the human CR1 protein described in the invention.

XX Sequence 2406 BP; 565 A; 621 C; 656 G; 564 T; 0 other:

Query Match 15.0%; Score 55.2; DB 21; Length 2406;
 Best Local Similarity 51.1%; Pred. No. 5.7e-08;
 Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggacaaagcttctacactccttctgtggtgagcagagatggtacatcttcaggact 60
 DB 299 tggagagagctgtctgacactgtctgagcagtaaaatggagtgctgtccacagct 358
 QY 61 ttcctggagagagagaaatgtgtgatacgtcgtgactctgtgttctgttaatggttc 120
 DB 359 ttcctggagagagagatctcagtgtagagaaacctgaggttctgtgtgctgtgagagttc 418
 QY 121 aggcagatgaacctgagatgacaaacttgcagatgagcacaagcaatcataagag 180
 DB 419 a---agaaatctcgatcagctacacagctgcctccagggcacacagatcttgagag 475
 QY 181 tacattgagaaacacagcgttctccaaagcagctgaagccgcagcaacactacata 240
 DB 476 ttcatttg-----cagtgagggccctaaaggttcaacatgacatgagaccgcgag 529
 QY 241 cgaatgcatcaagaagaacacagatcggtcgtgcatgtttgacacagacagcgag 300
 DB 530 ctgacgagagatgaacctgcagactgcacagacacacatgcttgatgcggtcagggagag 589
 QY 301 atccagagcagtgatggagaaatgctcctacaggggtgttcttgaactctgaacttacc 360
 DB 590 acacgtaccctgtagagagaaagactctcaccagcgttcttgaaagtcgcttaccgag 649
 QY 361 ga 362
 DB 650 ga 651

RESULT 10
 V34779
 ID V34779 standard; DNA; 2272 BP.

AC V34779;
 DT 11-SEP-1998 (first entry)
 DE Mouse RATH1.1 DNA.

XX RATH1.1; RGS gene family; regulator of G-protein signalling; murine;
 KW regulation; activation; modulation; signal transduction; T Cell;
 KW T helper cell; treatment; autoimmune disorders; arthritis; infection;
 KW graft rejection; asthma; allergy; neoplasm; ss.

OS Mus sp.

XX Key Location/Qualifiers
 FH 41..646
 FT /*tag-
 FT CDS /product= RATH1.1

XX MO9814579-A1.

XX 09-APR-1998.

XX 06-OCT-1997; 97WO-US18259.

XX

PR 06-JUN-1997; 97US-0870815.
 PR 04-OCT-1996; 96US-0726228.

XX (MILL-) MILLENNIUM PHARM INC.

XX Gimeno CJ, Levinson DA;

XX WPI; 1998-240085/21.

DR P-PSDB; W59293.

PT New activated T helper cell specific gene, RATH - used for
 PT developing products for treating e.g. autoimmune disorders,
 PT arthritis, graft rejection, asthma, allergy, infections or neoplasms
 PS Claim 1; Fig 1A-C; 127pp; English.

XX This sequence encodes a novel member of the mouse regulator of G-protein
 CC signalling (RGS) gene family, RATH1.1. The encoded protein participates
 CC in the regulation, control and/or modulation of G-protein mediated
 CC signal transduction, involved in T cell activation. Including T-helper
 CC (TH) cell and TH cell subpopulation activation. The protein can be
 CC used to develop products for treating autoimmune disorders, arthritis,
 CC graft rejection, asthma, allergy, infections or neoplasms.

SQ Sequence 2272 BP; 548 A; 584 C; 625 G; 515 T; 0 other:

Query Match 13.7%; Score 50.4; DB 19; Length 2272;
 Best Local Similarity 50.3%; Pred. No. 2.1e-06;
 Matches 182; Conservative 0; Mismatches 171; Indels 9; Gaps 2;

QY 1 tggacaaagcttctacactccttctgtggtgagcagagatggtacatcttcaggact 60
 DB 221 tggagagagcttctgacttgcgtcgaacagtaaaatggggtgctgcctccatgcc 280
 QY 61 ttcctggagagagaaatgtgtgatacgtcgtgactctgtgttctgttaatggttc 120
 DB 281 ttcctaaagaggaatctcagtgagagaaacctggaatctgtgtgctcgcgagagttc 340
 QY 121 aggcagatgaacctgagatgacaaacttgcagatgagcacaagcaatcataagag 180
 DB 341 aagaagat---ccgatcagcaccacaaactgcggtccagggctcacacatcttgagag 397
 QY 181 tacattgagaaacacagcgttcttccaaagcagctgaagccgcacacagactacata 240
 DB 398 tacat-----ccgcagcgaagcccttaagaggtgaacatgacatcagagaccgagaa 451
 QY 241 cgaatgcatcaagaagaacacagatcggtcgtgcatgtttgacacagacagacgag 300
 DB 452 ctgaccaaagaacaaactacaagctgcactacacagatgcttgatgtgctcagggagag 511
 QY 301 atccagcagtgatggagaaatgctcctaccaggtgttcttgaactctgaacttacc 360
 DB 512 accgcacattgtagagagagactctcctacgcgcttctcctcaagtcacagactatcgc 571
 QY 361 ga 362
 DB 572 ga 573

RESULT 11
 V38084
 ID V38084 standard; cDNA; 745 BP.

AC V38084;

DT 14-SEP-1998 (first entry)

DE Human regulator of G-protein signalling encoding cDNA.

XX Human; regulator; G-protein signalling; HRGS; cancer; inflammation;
 KW hypertension; cardiovascular shock; arrhythmias; asthma; ss.

XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 70..615
 FT CDS /*tag= a
 FT /product= "regulator of G-protein signalling"
 XX
 PN M09820128-A1.
 XX
 PD 14-MAY-1998.
 XX
 PD 06-NOV-1997; 97MO-US18476.
 XX
 PR 08-NOV-1996; 96US-0748483.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Goli SK, Hillman JL;
 DR WPI: 1998-286944/25.
 DR P-PSDB: W62075.
 XX
 PS Claim 5; Fig 1; 66pp; English.
 CC The present sequence encodes human regulator of G-protein signalling
 CC (HRGS). The HRGS regulates G-protein signalling in cancer cells and
 CC may be useful in the treatment of any cancer, especially cancers of the
 CC brain and thyroid. Products of the present invention can also be used
 CC for treating other conditions associated with uncontrolled cell
 CC signalling such as inflammation. The products can also be used to
 CC modulate HRGS activity in response to disorders involving the
 CC sympathetic nervous system including hypertension, cardiovascular shock,
 CC arrhythmias and asthma. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 745 BP; 221 A; 174 C; 169 G; 179 T; 2 other;

Query Match 10.3%; Score 38; DB 19; Length 745;
 Best Local Similarity 48.1%; Pred. No. 0.014;
 Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

QY 1 tggaccagcttctaacctcctgtgtggtgacagagatgtgcatccttcgcgact 60
 DB 250 tggcgtgattcccttgacaacactcctgcagacaactatgacttgcagttcctcaaaagt 309
 QY 61 ttccctggagggaggaatgtgtgatacgcctgactctgtgttctgttaatggttc 120
 DB 310 ttccctgaagcttgatcaagtgaagaaaccttgagcttcgtgattgctgtgagattac 369
 QY 121 aggcagatgaacctgaagataccaaaacttgcagatggccaaagcaatctataagag 180
 DB 370 aagaagatcaa---gtccctgcgcagaagtgtgtagaaggaagcaaatattatgaagaa 426
 QY 181 tacattggaacaacacagcgtgtctccaagcagctgaagccgcgccaagaactacata 240
 DB 427 ttcatcaaacagagagcctcctaagaagtgatattgaccacttcaactaaggacataca 486
 QY 241 cgaagatgcatacaagaacagatcgctgcgtgcatgattgaccagcagaagccgag 300
 DB 487 atgaagaacctggttgaac-----cttccttgagcagccttgaatgagccagaagaa 540
 QY 301 atccagagagatgagaaatgctcctacagaggtcttcttgacattacactg 360
 DB 541 atccatgcccctgagtaagaagaatctctgctcctgcttggcgtctgagtttatacag 600
 QY 361 gaat 364
 DB 601 gagt 604

RESULT 12
 AS2090
 ID AS2090 standard; cDNA; 1164 BP.
 XX
 AC AS2090;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Murine RGS protein coding sequence.
 XX
 KW RGS; regulators of G-protein signalling; GTPase activating protein; GAP;
 KW G-alpha protein; cell adhesion; chemotaxis; vulnery; immunosuppressor;
 KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
 KW cytosolic; hepatotropic; anti-anaemic; modulator; gene therapy; ss.
 XX
 OS Mus sp.
 XX
 FH Location/Qualifiers
 FT 134..841
 FT CDS /*tag= a
 FT /product= RGS_protein
 XX
 PN M0200046236-A2.
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000MO-US02977.
 XX
 PR 04-FEB-1999; 99US-0244314.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Hodge MR, Yowe D;
 DR WPI: 2000-532893/48.
 DR P-PSDB: Y97154.
 XX
 PT Novel regulator of G-protein signalling nucleic acids and polypeptides,
 PT useful as diagnostic and investigative tools and to treat G-protein
 PT signalling disorders
 PS Claim 1; Page 102-104; 105pp; English.
 CC The RGS (regulators of G-protein signalling) protein genes, clones h16395
 CC and m1975, were identified in human and murine spleen cDNA libraries. The
 CC C-terminal location of the RGS domain is consistent with RGSs known to
 CC act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-1
 CC linked receptors support rapid adhesion and directed migration of
 CC leukocytes and other cell types. The novel RGS proteins may be used to
 CC modulate cell adhesion and chemotaxis, e.g. for aiding wound repair.
 CC The RGS proteins, related cDNAs and anti-RGS antibodies are useful for
 CC modulation, diagnosis and treatment of immune and respiratory disorders.
 XX
 SQ Sequence 1164 BP; 406 A; 202 C; 222 G; 334 T; 0 other;

Query Match 10.3%; Score 38; DB 21; Length 1164;
 Best Local Similarity 48.1%; Pred. No. 0.017;
 Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

QY 1 tggaccagcttctaacctcctgtgtggtgacagagatgtgcatccttcgcgact 60
 DB 380 tggcgtgattcccttgacaacactcctgcagacaactatgacttgcagttcctcaaaagt 439
 QY 61 ttccctggagggaggaatgtgtgatacgcctgactctgtgttctgttaatggttc 120
 DB 440 ttcttaaacatgaattcagtgaggaacattgatttggcgtcgtgaggaacttc 499
 QY 121 aggcagatgaacctgaagataccaaaacttgcagatggccaaagcaatctataagag 180

Db 500 a---agaaatgcagaagacatcaacaatcatcctaaagaagcaatcattagagaa 556
 QY 181 tacattgagagaacaacgcgtgtgtctccaagcactgaagccgccacaagactacata 240
 Db 557 ttcaattcaagaatg-----tgcgcccaagaagttacaattgatttcatcactaaagaa 610
 QY 241 cgaatgtgcacacagaagacagatcgctcgtctcattgtttgacagacagacagag 300
 Db 611 gtaattgctaaagacatcgcccccagccactctccacagttttgataagcacaagaagcaga 670
 QY 301 atccagagcagtgatgaggaagaatgacctaccaggtgtcttctgactctgaattacatcg 360
 Db 671 gttgaccagctcattgagacaatgacagtataaagcgtttttgaaatctgagactactta 730
 QY 361 gaat 364
 Db 731 caat 734

 RESULT 13
 Z36910 ID Z36910 standard; cDNA; 1691 BP.
 AC Z36910;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE cDNA encoding a regulator of G protein signalling RGS5.
 XX
 KW Activator of G protein signalling; AGS; ras-related G protein;
 KW GTP hydrolysis; G protein activity; pheromone response pathway;
 KW G protein-coupled signal transduction; G-gamma selectivity;
 KW cellular signal transduction; regulator of G protein signalling;
 KW RGS5; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..590
 FT /tag= a
 FT /product= "regulator of G-protein signalling"
 XX
 PN W0958670-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99MO-US10151.
 XX
 PR 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Cismowski M, Duzic E;
 XX
 DR WPI; 2000-072337/06.
 DR P-PSDB; Y53931.
 XX
 PT A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 XX
 PS Claim 73; Page 139-140; 162pp; English.
 XX
 CC The present sequence encodes a regulator of G protein signalling (AGS)
 CC protein, RGS5. The specification also describes an activator of G
 CC protein signalling (AGS) protein. The AGS cDNA sequence was isolated
 CC from a human liver cDNA library. The AGS protein exhibits homology to
 CC ras-related G proteins, and contains alterations in conserved amino
 CC acids consistent with a deficiency in GTP hydrolysis activity. AGS
 CC stimulates G protein activity, G protein-coupled signal transduction
 CC and the pheromone response pathway in a receptor-independent manner.
 CC The AGS protein also shows G-gamma selectivity, as measured by growth
 CC assays in yeast expressing various mammalian G-gamma constructs, and

CC tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
 SQ Sequence 1691 BP; 548 A; 343 C; 305 G; 495 T; 0 other;

 Query Match 10.3%; Score 38; DB 21; Length 1691;
 Best Local Similarity 48.1%; Pred. No. 0.02;
 Matches 175; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

 QY 1 tggaccaagcttaactcctctgttggtggtgacagagatggtatccttcggact 60
 Db 225 tggcgtgattccctcgacaactctctcgagacaactatggaacttgcagttcaaaagt 284
 QY 61 ttccctgagagggagaatggtgatacgctgactctcgtttgttctgtaatgggttc 120
 Db 285 ttctctgaagcttgatcattcattgaggaagaaaccttgagttcgttgatgcttgagattac 344
 QY 121 aggcagatgaacctgaagataccacaacttgcagatggccaaagaacatcataagagg 180
 Db 345 aagaagatcaaa---gtccctgcagaagatgctgagaaggaagcaaatltatgaagaa 401
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 Db 576 gaat 579

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 X51745 ID X51745 standard; DNA; 1923 BP.
 AC X51745;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE DNA encoding a human secreted protein.
 XX
 KW Human secreted protein; cancer; immune disorder; infection;
 KW inflammatory disorder; skin disorder; tumor; atherosclerosis;
 KW restenosis; autoimmune disorder; Alzheimer's disease;
 KW peripheral neuropathy; trauma; spinal cord injury; allergy;
 KW hematopoietic disorder; skeletal disorder; neurological disorder;
 KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
 KW transplant rejection; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09911293-A1.
 XX
 PD 11-MAR-1999.
 XX
 PF 03-SEP-1998; 98MO-US18360.
 XX
 PR 12-SEP-1997; 97US-0058974.
 PR 05-SEP-1997; 97US-0057626.
 PR 05-SEP-1997; 97US-0057663.
 PR 05-SEP-1997; 97US-0057669.
 PR 12-SEP-1997; 97US-0058666.

PR 12-SEP-1997; 97US-0058667.
PR 12-SEP-1997; 97US-0058973.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
PI Rosen GA, Ruben SM, Shi Y;
XX WPI; 1999-204988/17.
DR P-PSDB; Y12958.
XX
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. neurological disorders,
PT tumours, immune disorders, inflammation or haematological disorders
XX
XX Claim 1; Page 175-176; 215pp; English.
XX
XX X51701-55 encode human secreted proteins. The polynucleotides and
CC their corresponding secreted polypeptides are useful for preventing,
CC treating or ameliorating medical conditions, e.g. by protein or gene
CC therapy. Pathological conditions can also be diagnosed by determining
CC the amount of the new polypeptides in a sample or by determining the
CC presence of mutations in the new polynucleotides. Specific uses are
CC described for each polynucleotide, based on which tissues they are
CC most highly expressed in, and include developing products for the
CC diagnosis or treatment of cancer, immune disorders, infection,
CC inflammatory disorders, skin disorders, tumours, atherosclerosis,
CC restenosis, autoimmune disorders, Alzheimer's disease, peripheral
CC neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
CC disorders, skeletal disorders, neurological disorders, arthritic
CC disorders, asthma, immunodeficiency diseases, AIDS and transplant
CC rejection. The polypeptides are also useful for identifying their
CC binding partners.
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XX Sequence 1923 BP; 604 A; 400 C; 363 G; 553 T; 3 other;
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Best Local Similarity 10.3%; Score 38; DB 20; Length 1923;
Matches 175; Conservative 48.1%; Pred. No. 0.022;
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QY 361 gaat 364
DB 796 gagt 799

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AC C41294;
XX
DT 17-OCT-2000 (first entry)
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DE Zea mays DNA fragment SEQ ID NO: 31364.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
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XX Zea mays subsp. mays.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.

Mon Jun 11 07:52:19 2001

us-09-587-574-7.rng

Page 12

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GenCore version 4.5
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Title: US-09-587-574-7

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Gap 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 605242

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	55.2	15.0	606	2	US-08-461-379A-27 Sequence 27, Appl
3	55.2	15.0	606	2	US-08-462-390B-27 Sequence 27, Appl
4	55.2	15.0	606	3	US-08-463-074B-27 Sequence 27, Appl
5	55.2	15.0	606	3	US-08-465-585C-27 Sequence 27, Appl
6	55.2	15.0	606	3	US-08-652-446-27 Sequence 27, Appl
7	55.2	15.0	746	4	US-08-870-815-3 Sequence 3, Appl
8	55.2	15.0	746	4	US-08-949-004-3 Sequence 3, Appl
9	55.2	15.0	2383	2	US-08-274-318-1 Sequence 1, Appl
10	55.2	15.0	2383	2	US-08-754-108-1 Sequence 1, Appl
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12	55.2	15.0	2406	2	US-08-461-379A-1 Sequence 1, Appl
13	55.2	15.0	2406	2	US-08-462-390B-1 Sequence 1, Appl
14	55.2	15.0	2406	3	US-08-463-074B-1 Sequence 1, Appl
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18	52	14.1	2272	3	US-08-870-815-1 Sequence 1, Appl
19	52	14.1	2272	4	US-08-949-004-1 Sequence 1, Appl
20	38	10.3	744	2	US-08-748-483-2 Sequence 2, Appl
21	34.6	9.4	7218	1	US-08-232-463-14 Sequence 14, Appl
22	33	8.9	5057	2	US-08-365-486A-12 Sequence 12, Appl
23	33	8.9	5108	1	US-07-642-002-1 Sequence 1, Appl
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25	29.8	8.1	3441	2	US-08-742-753-1 Sequence 1, Appl
26	29.8	8.1	3632	1	US-08-424-788-4 Sequence 4, Appl
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c 38	28.6	7.8	1244	2	US-08-974-653-1	Sequence 1, Appl
c 39	28.6	7.8	1244	4	US-09-283-011-1	Sequence 1, Appl
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c 42	28.6	7.8	2427	2	US-08-678-039A-39	Sequence 39, Appl
c 43	28.6	7.8	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 44	28.6	7.8	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 45	28.6	7.8	246240	2	US-08-724-394A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-463-081B-27
Sequence 27, Application US/08463081B
Patent No. 5871960 5837487
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OR INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Vytiana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DAFT-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-463-081B-27
Query Match 15.0%; Score 55.2; DB 2; Length 606;

Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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RESULT 2

US-08-461-379A-27
Sequence 27, Application US/08461379A
Patent No. 5871961

GENERAL INFORMATION:

APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia
(B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 8 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-461-379A-27

Query Match

15.0%; Score 55.2; DB 2; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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Db 535 GA 536
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RESULT 3

US-08-462-390B-27
Sequence 27, Application US/08462390B
Patent No. 5882894

GENERAL INFORMATION:

APPLICANT: Smith, K. A. & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia
(B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/330,108
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 27-OCT-1994
FILING DATE: 10-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-462-390B-27

Query Match 15.0%; Score 55.2; DB 2; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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OY 361 ga 362
DB 535 GA 536

RESULT 4

US-08-463-074B-27
Sequence 27, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736

444 South Flower St. - Suite 1900

FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-463-074B-27

Query Match 15.0%; Score 55.2; DB 3; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

OY 1 tggaccaagcttctaacctcctgtgtggtgacccagatggtgacatacctctccgact 60
DB 184 tggacagagctcttgcacctgctgctgacacagtaaaatgagtgctctccacgct 243
OY 61 ttcctgagagaggaagaaatgltgtaacgtctgactctgtgttctgttaatggttc 120
DB 244 TTCCTGAAGACAGAGTTCAGTAGAGGAGAACCTGAGATTCTGCTGCGCTGTGAGGATTG 303
OY 121 aggcagatgaactgaagataaccaaactttgcagatggtgccaagaactataagag 180
DB 304 A--AGAAATCCGATCAGCTACCAAGCTGCGCTCCAGGGCACACAGATCTTTGAGGAG 360
OY 181 tcatatgagaacacagcgltgttccaaagcagctgaagcccgccacagaactacata 240
DB 361 TTCATTG-----CAGTAGGCCCCCTTAAGAGGTCAACATTGACCATGAGACCCCGAG 414
OY 241 cgaagatgcatcaagaagaacagatcggtcgtgcatgtttgaccaggcacaagaccag 300
DB 415 CTGACGAGATGAACTGCAAGCTGCACAGACCAATGCTTGATGATCGGCTCAGGGGAG 474
OY 301 atccagcagatgtagggagaaatgctctaccaggtgttcttgactctgacattacctg 360
DB 475 ACACGTACCTGATGAGAGAGACTCTTACCCACAGCTTCTCTGAAGTCCGCTTACCGG 534
OY 361 ga 362
DB 535 GA 536

RESULT 5

US-08-465-585C-27
Sequence 27, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CRI Polypeptide, Vector
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

444South Flower St. - Suite

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-585C-27

Query Match 15.0%; Score 55.2; DB 3; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

OY 1 tggaccgaagtttaccactcttctgtgtggtgacccagatggtgacatcttccgagact 60
DB 184 TGGAGAGAGTGTTCGACCTGCTGCTGAGCAGTAAATAATGAGTGGCTGCTTCACGCT 243
OY 61 ttccctggagaggaagaatgltgtgatacgcctggaactctgttcttgaatggttc 120
DB 244 TTCCTGAAGACAGAGTTTACGTAGAGAGAACTGGAGTTCTGGCTGGCTGTGAGAGATTG 303
OY 121 aggcagatgaacctgaagatcacaacacttgcagatgagccaaagcaatcatalaagsg 180
DB 304 A--AGAGATCCGATCCAGTACCAAGCTGACCAAGGACACACAGATCATCTTTAGAGAG 360
OY 181 tacattggaacaacagaggttcttccaagcagctggaagcccgccacaagaactaata 240
DB 361 TTCAATTG-----CAGTGAAGGCCCTTAAGAGGTCAACATTGACCATGAGACCGCGAG 414
OY 241 cgaagatgcatcaagaacaacagacagatcgctgcgtgcatgtttgacagagcaagacgag 300
DB 415 CTGACGAGAGATGAACCTTCACAGACTGCCACAGGCACATGCTTTGATGCGGCTCAGGGAG 474
OY 301 atccagagcagatgaggaagaatgacctaccaggtgttcttgaactctgaacttaactc 360
DB 475 ACAGGTACCTGATGAGAGAGAGACTCTACCCACGCTTCTGTAAGTCCCTGCTTACCGG 534
OY 361 ga 362
DB 535 GA 536

RESULT 6
US-08-652-446-27
Sequence 27, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:

ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSEE: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-652-446-27

Query Match 15.0%; Score 55.2; DB 3; Length 606;
Best Local Similarity 51.1%; Pred. No. 8.4e-09;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

OY 1 tggaccgaagtttaccactcttctgtgtggtgacccagatggtgacatcttccgagact 60
DB 184 TGGAGAGAGTGTTCGACCTGCTGCTGAGCAGTAAATAATGAGTGGCTGCTTCACGCT 243
OY 61 ttccctggagaggaagaatgltgtgatacgcctggaactctgttcttgaatggttc 120
DB 244 TTCCTGAAGACAGAGTTTACGTAGAGAGAACTGGAGTTCTGGCTGGCTGTGAGAGATTG 303

REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-461-379A-1

Query Match 15.0%; Score 55.2; DB 2; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

1 tggaccagcttttaccactcttctgtgtgagaccagatgtgacatcttccgagct 60
299 TGGAGAGAGTGTGACCTGCTGAGCAATAAATGAGTGGCTTCACGCT 358
61 ttccctgagagaggaatgtgtgatacgtctgactctgttctgttaattgtgtc 120
359 TTCCTGAAGACAGAGTTCAGTGAAGAGAACTGAGTCTGCTGCGCTGAGAGATT 418
121 aggcagatgaacctgaagatatacaaaacttgcagatgagccaaagaactatagagg 180
419 A---AGAGATCCGATCAGTACCAAGCTGAGGCTCAAGGACACACAGATCTTTAGAG 475
181 tacattggaacaaagatgtgtctccaaagcagctgaagcccgacccaagaactacata 240
476 TTCAATTG-----CAGTGAGGCCCTTAAGAGTCAACATTGACCATGAGACCCGCGAG 529
241 cgagatgcatcaagaagaacaagatcgctcgatcgttgcacaggaagaacagcgag 300
530 CTGACGAGAGATGAACCTGCACTGACACAGCCACATGCTTTGATCGGCTCAGGGGAG 589
301 atccagcagatgagaggaatgtctcctcaagcagatgtcttctgactctgacattactg 360
590 ACAGCTACCTGATGAGAGAGATCTCTACCCACGCTTCTGAAGTCCGCTCTTACCGG 649
361 ga 362
650 GA 651

RESULT 13
US-08-462-390B-1
Sequence 1, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B

FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-462-390B-1

Query Match 15.0%; Score 55.2; DB 2; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

1 tggaccagcttttaccactcttctgtgtgagaccagatgtgacatcttccgagct 60
299 TGGAGAGAGTGTGACCTGCTGAGCAATAAATGAGTGGCTTCACGCT 358
61 ttccctgagagaggaatgtgtgatacgtctgactctgttctgttaattgtgtc 120
359 TTCCTGAAGACAGAGTTCAGTGAAGAGAACTGAGTCTGCTGCGCTGAGAGATT 418
121 aggcagatgaacctgaagatatacaaaacttgcagatgagccaaagaactatagagg 180
419 A---AGAGATCCGATCAGTACCAAGCTGAGGCTCAAGGACACACAGATCTTTAGAG 475
181 tacattggaacaaagatgtgtctccaaagcagctgaagcccgacccaagaactacata 240
476 TTCAATTG-----CAGTGAGGCCCTTAAGAGTCAACATTGACCATGAGACCCGCGAG 529
241 cgagatgcatcaagaagaacaagatcgctcgatcgttgcacaggaagaacagcgag 300
530 CTGACGAGAGATGAACCTGCACTGACACAGCCACATGCTTTGATCGGCTCAGGGGAG 589
301 atccagcagatgagaggaatgtctcctcaagcagatgtcttctgactctgacattactg 360
590 ACAGCTACCTGATGAGAGAGATCTCTACCCACGCTTCTGAAGTCCGCTCTTACCGG 649
361 ga 362
650 GA 651

RESULT 14
US-08-463-074B-1
Sequence 1, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
(B) STREET: One Westlakes-Berwyn
444 South Flower St. - Suite 1

STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/96,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-463-074B-1

Query Match 15.0%; Score 55.2; DB 3; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggaccagctcttaccacccctgtgtgggtgaccgagatgagcattcttcggact 60
DB 299 tggacagagctcgttcgacctgctgctgacacagtaaaatggatggcttccacgct 358
QY 61 ttcctcgaagaggaagaatgtgtgatacgtcgtgacttctgttctgtaagtgttc 120
DB 359 ttccgtaagacagagttcgtgagaggaagaaacttgagttctgcttgctgtaagagtttc 418
QY 121 aggcagatgaacctgaagataccaacatttgcagatggtgccaagaacataaagagg 180
DB 419 a---AGAAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACAGATCTTTGAGGAG 475
QY 181 tacattggaagaacaagcgtgtgtctccaagcagctgaagcccgcccaagaacctacata 240
DB 476 ttcatTTTG-----CAGTcAGGcCCCTTAAGAGTCAACATTGACCATGAGACCCCGGAG 529
QY 241 cgaagatgcatcaagaagaacacagatcgctcgtatcatgtttgaccaggcacagaccgag 300
DB 530 ctgacagagatgaacctgcagacatgcccacacacacacacacacacacacacacacac 589
QY 301 atccagcagatgagtgaggaagaaatgcctacacagtgcttcttgactctgacattactcy 360
DB 590 ACACGTACCCCTGATGAGAAAGACTCTACCCACGCTTCTGTAAGTCCGCTCTTACCGG 649
QY 361 ga 362
DB 650 GA 651

RESULT 15
US-08-465-585C-1

Sequence 1, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 900071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/96,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..722
US-08-465-585C-1

Query Match 15.0%; Score 55.2; DB 3; Length 2406;
Best Local Similarity 51.1%; Pred. No. 1.6e-08;
Matches 185; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 1 tggaccagctcttaccacccctgtgtgggtgaccgagatgagcattcttcggact 60
DB 299 tggacagagctcgttcgacctgctgctgacacagtaaaatggatggcttccacgct 358
QY 61 ttcctcgaagaggaagaatgtgtgatacgtcgtgacttctgttctgtaagtgttc 120
DB 359 ttccgtaagacagagttcgtgagaggaagaaacttgagttctgcttgctgtaagagtttc 418
QY 121 aggcagatgaacctgaagataccaacatttgcagatggtgccaagaacataaagagg 180
DB 419 a---AGAAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACAGATCTTTGAGGAG 475
QY 181 tacattggaagaacaagcgtgtgtctccaagcagctgaagcccgcccaagaacctacata 240
DB 476 ttcatTTTG-----CAGTcAGGcCCCTTAAGAGTCAACATTGACCATGAGACCCCGGAG 529
QY 241 cgaagatgcatcaagaagaacacagatcgctcgtatcatgtttgaccaggcacagaccgag 300
DB 530 ctgacagagatgaacctgcagacatgcccacacacacacacacacacacacacacacac 589

QY 301 atccaggcagtgatggaggaaatgcctaccaggtgttcttgacttctgacatttacctg 360
 Db 590 ACACGTACCTGTGATGAGAGGAGACTCCTACCCACGCTTCTGAAGTCGCGCTGCTTACCGG 649
 QY 361 ga 362
 Db 650 GA 651

Search completed: June 7, 2001, 00:26:30
 Job time: 19733 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:39 ; Search time 3054.04 Seconds
(without alignments)
1055.527 Million cell updates/sec

Title: US-09-587-574-7

Perfect score: 369
Sequence: 1 tggaccacagctcttacacctc.....acattaccctggaatatgtg 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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 187: em_gss_rod3:*
 188: em_gss_rod4:*
 189: em_gss_rod5:*
 190: em_gss_vit1:*
 191: em_gss_vit2:*
 192: em_gss_vit3:*
 193: em_gss_vit4:*
 194: em_gss_vit5:*
 195: em_gss_vit6:*
 196: em_gss_vit7:*
 197: em_gss_vit8:*
 198: em_gss_vit9:*
 199: em_gss_vit10:*
 200: em_gss_vit11:*
 201: em_gss_vit12:*
 202: em_gss_vit13:*
 203: em_gss_vit14:*
 204: em_gss_vit15:*
 205: em_gss_vit16:*
 206: em_gss_vit17:*
 207: em_gss_vit18:*
 208: em_gss_vit19:*
 209: em_gss_vit20:*
 210: em_gss_vit21:*
 211: em_gss_vit22:*
 212: em_gss_vit23:*
 213: em_gss_vit24:*
 214: em_gss_vit25:*
 215: em_gss_vit26:*
 216: em_gss_vit27:*
 217: em_gss_vit28:*
 218: em_gss_vit29:*
 219: em_gss_vit30:*
 220: em_gss_vit31:*
 221: em_gss_vit32:*
 222: em_gss_vit33:*
 223: em_gss_vit34:*
 224: em_gss_vit35:*
 225: em_gss_vit36:*
 226: em_gss_vit37:*
 227: em_gss_vit38:*
 228: em_gss_vit39:*
 229: em_gss_vit40:*
 230: em_gss_vit41:*
 231: em_gss_vit42:*
 232: em_gss_vit43:*
 233: em_gss_vit44:*
 234: em_gss_vit45:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	247.4	67.0	1068 231	CNS03YWO AL266841 Tetraodon
2	237.4	64.3	830 230	CNS01YDU AL172875 Tetraodon
3	218.6	59.2	902 231	CNS03GZ0 AT243621 Tetraodon
4	207.2	56.2	798 140	BE872155 601446262
5	162	43.9	975 230	CNS03J34 AL226201 Tetraodon
6	161.2	43.7	651 141	BE894571 601433182
7	147.4	39.9	585 140	BE854108 ux27903.Y
8	147.4	39.9	585 140	BE854108 ux27903.Y
9	147.4	39.9	585 140	BE854108 ux27903.Y
10	126.8	34.4	475 147	BE406997 UI-R-BQ2-AA198606 mu15604.T
11	120.2	32.6	406 169	BE802488 CM0-C1009
12	114.8	29.7	935 106	AL526136 AL526136
13	109.6	29.7	491 105	AL045145 DKFZPA340
14	108.6	29.4	364 140	AL044979 DKFZPA340
15	103.8	28.1	217 150	BE559312 UI-R-E1-f
16	99.2	26.9	1029 232	CNS051XC
17	94.6	25.6	303 109	AV138493 AV138493
18	86.4	23.4	565 170	BE892872 OVI-MT013

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source 1..830
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="218017"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG218AH09LP1-end : T7"

BASE COUNT 119 a 282 c 268 g 155 t 6 others
ORIGIN

Query Match 64.3% Score 237.4; DB 230; Length 830;
Best Local Similarity 77.5% Pred. No. 7.6e-60;
Matches 286; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

```
OY 1 tggaccagcttctacccctctgtgtgacacagatgtgtacatctctccggact 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 tggaccagcttctacccctctgtgtgacacagatgtgtacatctctccggact 527
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 ttccctggagaggaagaatgtgtgatacgtctgactctgtgtctgtatgtgttc 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 ttccctggagaggaagaatgtgtgatacgtctgactctgtgtctgtatgtgttc 467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 aggcagatgaacctgaagataccacacatttgcagatggccaaacacatataagag 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 aggcagatgaacctgaagataccacacatttgcagatggccaaacacatataagag 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 tacattggaaacaaaggtgttctccaagcagctggaagcccgccacacacacata 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 tacattggaaacaaaggtgttctccaagcagctggaagcccgccacacacacata 347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 241 cgaagatgcatcaagaagaacacagatcgctgcgtgacatgtttgacagacagacag 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 aggcagacgctcaaaagcagacagatcgctgcgtgacatgtttgacagacagacag 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 301 atccagcagtgatgaggaagaatgtctaccagatgttcttgaactctgacattact 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 gtttcagaccacatgagagagagccttaccagacatttctgacattactgac 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 361 gaatatgtg 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 gacttagctg 218
```

RESULT 3
CNS03G20/c 902 bp DNA GSS 17-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
DEFINITION 025B16 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL243621.1 GI:7964633
VERSION AL243621
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

REFERENCE 1 (bases 1 to 902)
AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Fizesmes,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 902)
AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Fizesmes,C., Winkler,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using
JOURNAL Tetraodon nigroviridis DNA sequence
REFERENCE Unpublished

3 (bases 1 to 902)

FEATURES
source 1..902
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="025B16"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG025DA08SP1-end :
PUC-ori"

BASE COUNT 197 a 233 c 243 g 227 t 2 others
ORIGIN

Query Match 59.2% Score 218.6; DB 231; Length 902;
Best Local Similarity 80.1% Pred. No. 3e-54;
Matches 257; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
OY 49 ctttcggacttcttcaggagaggaagaatgtgtgtaagcgtggaacttctgttct 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 ctttcgagacttcttggacagagaaatgcgacatttggacttctgttctgccc 836
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 109 tgaatgggttcagcagatgaacctgaagataccacacatttgcagatggccaaagca 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 tgcacagcttccggacagatgacattcagatgacacacacagagaggtggccaaagca 776
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 169 atcctaaaggtatcatgtgaagaacacagcgtgttctccaagcagctgaagccgcac 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 atttcgaagccttcatcgtgaagaacacagcgtgtgacacacacacacacacac 716
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 229 aagacctacacagagatgagcagcagcagcagcagcagcagcagcagcagcag 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 aaaccttcatccggatgacatgacacacacacacacacacacacacacacacac 656
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 289 gcacagaccgagatccagcagtgatgaggaagaatgtctaccagatgttcttactct 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 gcgcagatgagatccagacacacacacacacacacacacacacacacacacacac 596
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 349 gacattaccctggaatatgtg 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 gacgttacccttggatgactg 575
```

RESULT 4
BE872155 798 bp mRNA EST 20-OCT-2000
LOCUS BE872155
DEFINITION 601446262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850502 5',
RNA sequence.

ACCESSION BE872155 GI:10320931
VERSION BE872155
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 798)
AUTHORS Mammalian; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC <http://mgi.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM9569 row: k column: 15
High quality sequence stop: 544.
Location/Qualifiers
1.798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3850502"
/clone.lib="NIH_MGC_65"
/tissue.type="adenocarcinoma"
/lab.host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; Ncti; Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 218 a 229 c 207 g 144 t

ORIGIN

Query Match 56.2%; Score 207.2; DB 140; Length 798;
Best Local Similarity 90.6%; Pred. No. 7e-51;
Matches 221; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 126 gatgaacctgaagataccaacatttgagtgccaaagcaactataaggtacat 185
|||||
DB 1 GATGAACCTGAAGATACCAAACTTACGATGACCAAGCATCTCAAAAGTACAT 60
|||||
QY 186 tgaagacaacagtgctgtctccaagcagctgaagccgcacaagaactacataagaga 245
|||||
DB 61 TGAAGAACACAGCATGCTCTCCAAAGCAGCTGAAGCCTGCACCAAGCATCTCAATGAAGA 120
|||||
QY 246 tggcatcaagaagaacagatcgctcgatcatgttgcacagacagacagacagatcca 305
|||||
DB 121 TGGCATCAAGAAGACACAGATTGATTCATCATGTTTGACACAGCGCAGACAGATCCA 180
|||||
QY 306 ggcagtgatgaggaagaatgacctacagagtgcttcctgaacttcgacatttaactggaata 365
|||||
DB 181 GTCGGTGAATGAGAAATGCTTACAGATGTTTGTGACTTGTGATATATATACCTCGAATA 240
|||||
QY 366 tgtg 369
|||||
DB 241 TGTG 244

RESULT 5
CNS033J4 975 bp DNA GSS 15-MAY-2000
LOCUS Tetradon nlgroviridis genome survey sequence PUC-ori end of clone
DEFINITION 209617 of library G from Tetradon nlgroviridis, genomic survey
sequence.
ACCESSION AL226201
VERSION AL226201.1 GI:7885113
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nlgroviridis
ORGANISM Tetradon nlgroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurpterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Petcomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodon.
1 (bases 1 to 975)
Roest-Crolius,H., Jallion,O., Dasilva,C., Fzames,C., Fisher,C.,
Bouneau,L., Ballault,A., Quetler,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nlgroviridis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fzames,C., Wncker,P., Brotlier,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nlgroviridis DNA sequence

TITLE Unpublished
JOURNAL 3 (bases 1 to 975)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nlgroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetradon>.

FEATURES
source
1.975
/organism="Tetradon nlgroviridis"
/db_xref="taxon:99883"
/clone="209617"
/clone.lib="G"
/note="Genoscope sequence ID : C0AG209AD09SP1-end :
PUC-ori"

BASE COUNT 201 a 276 c 316 g 145 t 37 others

ORIGIN

Query Match 43.9%; Score 162; DB 230; Length 975;
Best Local Similarity 68.8%; Pred. No. 2e-37;
Matches 249; Conservative 11; Mismatches 95; Indels 7; Gaps 3;

QY 1 tggacaagctcttacactctctgtgttgtagcagagatgtgcatacctctccgact 60
|||||
DB 621 TGGACCAAGTCCCTGCACCTTCGCTGGGACACAGACGGCGCTCGCTTCAGAGAT 680
|||||
QY 61 ttcctgagagaggagaatgtgtgatacgtgacttcgtgttctgttaatggctc 120
|||||
DB 681 TTCCTGAGCGGGACGACGCCGCCGACACCTGTGACTTGTGTTCCGCTCAACGGCTTC 740
|||||
QY 121 aggcagatgacatgagatgatacaaatcttcgagtgccaaagacatctaagg 180
|||||
DB 741 AGCGAGTGAACCTGAAGATGCCAAACCTTGCGCTGSCCAAGCATCTTCAAAGCG 800
|||||
QY 181 tacattgagaacaacagcgtgtctccaagcagctgaagccgcacaagaactacata 240
|||||
DB 801 TACGTGACAGCAAGACCGTGTCTCCAGGAMMMAMMMNNMNCAMCADACTTCATC 860
|||||
QY 241 cgaatgcatcaagaagaacagatcgctcgatcatgtttgacacagacagaccgag 300
|||||
DB 861 AGCGAMAGSTTMA--GAGAGACAGATGATTCCG-CATGTTCCACAGCCCVKGGAGGT 917
|||||
QY 301 atccagcagtgatgaggaagaatgacctacagtgcttcgtacttcgacttgaattactg 360
|||||
DB 918 TCAGAGACATGAGAGGGA----GCTACCAAGCTTCTGACTCGGACATATACYTG 973
|||||
QY 361 ga 362
|||||
DB 974 GA 975

RESULT 6
BE894571 651 bp mRNA EST 20-OCT-2000
LOCUS BE894571 601433182F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918285 5',
DEFINITION mRNA sequence.
ACCESSION BE894571
VERSION BE894571.1 GI:10357078
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (pages 1 to 651)
NTH-MGC <http://mgc.ncl.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)
Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
source	1. .651

BASE COUNT	162 a	171 c	188 g	130 t
ORIGIN				

Query Match	43.7%;	Score 161.2;	DB 141;	Length 651;
Best Local Similarity	68.3%;	Pred. No. 3e-37;		
Matches 258; Conservative	0;	Mismatches 108;	Indels 12;	Gaps 2

QY	61	tttttgaagagggaagaatgtgtggaatcagctgactgtgttgcgtttaatggttc	120
Db	126	TTCTGTGAAGCAGGAGGGCTGTCCGCACTTCTGTGACTTCTGGTTTGGCTCTCACTGGGCTTC	185
QY	121	aggcagatg-----aacctgaagagatatacaaaaactttgagatgagtgcaaaagcaatc	171
Db	186	AGGAAGGTGGAGGCCCTGTGTGACTGTGAACGAGAGAAAGAGCGCTGGAAGCTGGCGAAGGCATC	245
QY	172	tataagaggtaca---ttgagaacaacagcgttgtctccaaagaagcgtgaagccgcgcacc	228
Db	246	TACCGAAAGTACACTTCTTGATTAACATAGCATGCTGTGTCCCGCGAGACCAAGCCAGCCACC	305
QY	229	aagaactacatcacgagatgycatcaagaagaacaacagatgycctcgtgtcatgtttgaccag	288
Db	306	AAGAAGCTTCTAAAGGGCTGCATCATGAAACACACTGTATCATCTCTGCCAATGTTTGACAG	365
QY	289	gacacagaccagaatccacgagcgtgcatgagagaagaatgacctacagtgcttctgactctc	348
Db	366	GCCCAAGCCGAATTCAGGSCCACTATGTGAGGAACACACCTATTCCTTCCTTTAAGTCT	425
QY	349	gacatttaccctggaatat	366
Db	426	GATATTATTATTGGAAATAT	443

RESULT	7
BE854108/c	
LOCUS	
DEFINITION	
	BE854108 585 bp mRNA EST 27-SEP-2000
	ux27g03.y1 Scores_NMAX_maxillary_Process Mus musculus cDNA clone
	IMAGE:3511540 5' similar to TR:070239.070239 RAXIN. ; mRNA
	sequence.

ACCESSION	BE854108
VERSION	BE854108.1
KEYWORDS	GI:10312720
SOURCE	EST. house mouse.

Seq primer: -40RP from Glibco
High quality sequence stop: 472.

BASE COUNT	129 a	157 c	142 g	156 t	1 others
ORIGIN					

Query Match	39.9%	Score 147.4	DB 140	Length 585
Best Local Similarity	66.0%	Pred. No. 3.7e-33		
Matches 249	Conservative	0	Mismatches 116	Indels 12
				Gaps 2

Db	442	TTCTGAAAGCAGGAGGGCTGTGCTGACCTGCTGACCTTTCGGTTTGGCTCGAAGGGCTTC	363
OY	121	aggcagat-----gaacctgaagatataccaaaacttgcgagttgcccagaagcaatc	171
Db	382	AGGAAGCTTGAGCCCTGTGACTCAATAGAGAAAAGAGCGCTGAAGCTGCACAAAGCCATC	323
OY	172	tataaaggttaca---ttggaacaanaaggtgtgtctccaagaagtcgaaagccgcgacc	228
Db	322	TACCGAAGATGATCCCTGGATGACAAATGGCATTTGTGTCCAGACAAACCAAGCCAGCCACT	263
OY	229	aagaccacatacagatactgcatcaagaagaacacagatactgctcgtgtcatgtttgaccag	288
Db	262	AAGAGCTTTCATTAAGGACTGTGTTCATTAACACAGCATATATCTGCCATGTTTGACAG	203
OY	289	gcacacacagagatccagagcattgatactggagaaatactgctaccagatgltcttacttctc	348
Db	202	GCACAGACAAATAATCCAGTCCACCATGAGAGAGAAATACCTAACCTTCCTTTTAAGTCT	143
OY	349	gacattactctgataa	365
Db	142	GACATTTATTTGGAGTA	126

RESULT	8
LOCUS	BF582324
DEFINITION	602101113f1 NC1_CGAF_CO24 Mus musculus cDNA clone IMAGE:422469 5'
ACCESSION	BF582324
VERSION	BF582324.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 956)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
source	1. .956

BASE COUNT	258 a	234 c	288 g	176 t
ORIGIN				

Query Match	39.98	Score 147.4	DB 150	Length 956
Best Local Similarity	66.08	Pred. No. 4.3e-33		
Matches 249, Conservative	0	Mismatches 116	Indels 12	Gaps 2

QY	1	tgagccaaagctcttaacccctcttgaggagcaagaatgtagaacctctccagat	60
Db	86	TGGGCTCAGTCACGCTATTCCTTACTGATGACCAAGATGGATCAGCCTTCAGACAT	145
QY	61	tctctgagagagagaaatgltgtagaacgtggaactctggtctcttlaatgggttc	120
Db	146	TTCTTGAAGCAGAGGGCGCTGCTGATGACCTCTGGACTTCGTGTTGGCTCAGATGGCTTC	205
QY	121	agcgagat-----gaacctgaagagataccaaaacttcgagatggccaagaacatc	171
Db	206	AGGAAGCTTTCAGCCCTGTGACTCAAAATGAGAAAAGGCGCTGAAGCTGGGAAAGGCATC	265
QY	172	tataaagggtaca---ctgaagaacaacaggtgtctccaagaagcctgaagccgcagacc	228
Db	266	TACCGAAAGTTCATCCTCGATAGCAATGGCATTTGTCTCAGACAAACCAAGCCACCT	325
QY	229	aagaactacatacagaatggcatcaagaagacaacagaatcgagctgtgtcatgtttgacag	288
Db	326	AAGAGCTTACATAAAGAGACTGTGTCATGAACAGACAGATTAATCCTGCATGTTTGAACAG	385
QY	289	gcacaaagccagatcccaagcgagtgatgagagaaatgtcctaccagatgtctctgaacttc	348

D _b	386	GCAAGACAGAAATCCAGTCACCATGAGAGAAATACCTACCTCTTCTTAAGCT	445
Q _Y	349	gacatttacctgata	365
D _b	446	GACATTTATTTGGAGTA	462

RESULT	9
AA198606/c	
LOCUS	
DEFINITION	539 bp mRNA EST 19-FEB-1997 m15d04.tl Soares thymus 2Nbdt Mus musculus cDNA clone IMAGE:639463 5' end of cDNA to sequence human B-cell activation promoter p132

ACCESSION	AA198606	
VERSION	AA198606.1	GI:1794333
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.
MGI:39155
Possible reversed clone: similarity on wrong strand
Seq primer: -2813 rev2 from Amersham
High quality sequence stop: 436.

FEATURES	Location/Qualifiers
source	1. .539

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="639463"
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/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand
cDNA was primed with a Not I - oligo(dT) primer [5',
TGTATCCCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTTTT
3']; Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

```

Query Match	38.9%	Score 143.6	DB 3	Length 539
Best Local Similarity	65.4%	Pred. No. 4,9e-32		
Matches 246	Conservative 0	Mismatches 119	Indels 11	Gaps 2

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533	tgggcttgatctactgcattccttacctgtagtgcacgaatggatggatcagcctgtttcaggaat	474	

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		/clone_lib="434 (synonym: htes3)"			
		/tissue_type="testis"			
		/dev_strage="adult"			
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BASE COUNT		131 a 127 c 139 g 94 t			
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Best Local Similarity 67.5%; Prid. No. 6e-22;					
Matches 189; Conservative 0; Mismatches 79; Indels 12; Gaps 2;					
QY	99	ctggttcttgctgaatgggtctcagcagatg-----aacctgaagatataccaaac	149		
Db	1	ctggcttccctcctcactgctctcaggaagctgagccctctgctcgaacgagagagag	60		
QY	150	tttgagtgatggccaagaatctataagaagtgaca---ttgagaacaacagctgtctc	206		
Db	61	gctgaagctggcgagagagcactctaccgaaagatgacttctgattacatgcatgctgtgc	120		
QY	207	caagcagctgaagcccgcccaaccaagaacctacacgagatgcatcagaagaagcaacagat	266		
Db	121	ccggcagacaccaaagccagccaccacagagcttcatgaaaggctgcatcagatgaaacacgtgatt	180		
QY	267	cgagtcgagctgattgttgaccagagcaacagcagatcagagcagatgaggaagaatgac	326		
Db	181	cgatcctccatgctgttgacacagagccagacgcaaaatccagagcactatgagagaaacac	240		
QY	327	ctaccaggtgtctctgactctcagactctacacattaccctggaatat	366		
Db	241	ctatccctcccttcccttgaagctcgaattattattttggaattat	280		
RESULT 14					
LOCUS		AL0044979		364 bp mRNA EST 29-FEB-2000	
DEFINITION		DKFZp434C044.F1.434 (synonym: htes3) Homo sapiens cDNA clone			
ACCESSION		DKFZp434C044.5, mRNA sequence.			
VERSION		AL0044979			
KEYWORDS		AL0044979.1 GI:5433164			
SOURCE		EST.			
ORGANISM		human.			
		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 364)			
AUTHORS		Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.			
TITLE		EST (Wambutt, et al.)			
JOURNAL		Unpublished (1999)			
COMMENT		Contact: Wambutt R			
		MIPS			
		Am Kioferspitz 18a D-82152 Martinsried, Germany			
		This is the 5' sequence of the clone insert			
		Clone from S. Wiemann, Molecular Genome Analysis, German Cancer			
		Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;			
		sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing			
		consortium of the German Genome Project.			
		No sl sequence available.			
		This clone (DKFZp434C044) is available at the RZPD in Berlin.			
		Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059			
		Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.			
FEATURES		Location/Qualifiers			
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		/clone="DKFZp434C044"			
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			/tissue_type="testis"	
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Best Local Similarity	67.1%;	Pred. No. 1.1e-21;		
Matches 188:	Conservative 0;	Mismatches .80;	Indels 12;	Gaps 2;
Oy	99	ctggtttcgtgtaatagtggtccaagcagaatg-----aacctgaaggataccaaac	149	
Dd	1	CTGCTTTCCTCGCATATGCCTTCACAGAACCTGGAGCCCTGTGACTCGAACAAGGAAGAAG	60	
Oy	150	ttagcgagtggcaagaacaactatataagaaglaaca---ttaagaacaacagcgttgtc	206	
Dd	61	GCTGAAGCTGGGAGAGCATTACCAAGAAATACATCTTGTAATAACATGGCATCGTCTC	120	
Oy	207	caagcagctgaagccccgcaccacaaagactatcacgaatgcatcacaagaagcaacagat	266	
Dd	121	CCGGCAGACCAAGCCAGCCACCACCAAGCCTCATAAAGSGCTGCATCAGCAAGCACCTGAT	180	
Oy	267	cggcccgcatatgtttgaccagagcaccagaccagatatccagcagtgatgggaaaatgc	326	
Dd	161	CGATCTTCGCATGTTTGACACAGGCCCAACCAACCAATNACAGGCCACATATGAGAAACAC	240	
Oy	327	ctaccagtggtctctgacctctgcattcattaccatgaatat	366	
Dd	241	CTATCCCTCCCTTCAAGTCGTGATATTATTATTTGSAATAT	280	
RESULT 15				
LOCUS	BF559312/c			
DEFINITION	BF559312	217 bp mRNA	EST	12-DEC-2000
VERSION	UI-R-E1-fa-e-06-0-UI.r1	UI-R-E1 Rattus norvegicus		cdna clone
KEYWORDS	UI-R-E1-fa-e-06-0-UI 5'	mRNA sequence.		
SOURCE	BF559312.1	GI:11669042		
ORGANISM				
	Norway rat.			
	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
REFERENCE	1 (bases 1 to 217)			
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.			
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery			
JOURNAL MEDLINE COMMENT	Genome Res. 6 (9), 791-806 (1996) 9704447			
	Contact: Soares, MB			
	Program for Rat Gene Discovery and Mapping			
	University of Iowa			
	451 Eckstein Medical Research Building Iowa City, IA 52242, USA			
	Tel: 319 335 8250			
	Fax: 319 335 9565			
	Email: msoares@blue.weeg.uiowa.edu			
	cdna Library Preparation: M.B. Soares Lab Clone distribution:			
	This clone is also available through Research Genetics (www.resgen.com)			
	LNUU (info@image.llnl.gov). IMAGE ID= 1779287			
	Seq primer: M13 forward.			
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	/dev_stage="adult"			
	/lab_host="DHI0B (Life Technologies)"			

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-E1 library is a subtracted library derived from the UI-R-E0 library. The UI-R-E0 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dt track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-E1) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-E0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-E0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-E1 library. This procedure has been previously described (Ronald, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 47 a 70 c 42 g 58 t
ORIGIN

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Best Local Similarity 90.2%; Pred. No. 2.5e-20;

Matches 11; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db	217	ggcatcaagaagacacagatcggtcgtatgtttgaccagcacagaccgagatcag	158
QY	307	gcagtgatgaggaagaaatgcctaccaggtgtcttgactctgacatttaccctgaaat	366
Db	157	gcagtgatgaggaagaaatgcctaccaggtgtcttgactctgacatttaccctgaaat	98
QY	367	gttg 369	
Db	97	gttg 95	

Search completed: June 6, 2001, 23:00:43
Job time: 13527 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:35:26 ; Search time 4956.99 Seconds

(without alignments)
481.977 Million cell updates/sec

Title: us-09-587-574-8

Perfect score: 162

Sequence: 1 gcccaatggccaagtctctc.....gtctgagagagcgctgcag 162

Scoring table: IDENTITY-MUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

GenEmbl: *
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2: gb_ba2:*
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4: gb_in1:*
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7: gb_com:*
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13: gb_pl2:*
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19: em_htgo_hum:*
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31: em_htg_inv2:*
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37: em_hum4:*
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87: gb_pr3:*
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89: gb_pr5:*
90: gb_pr6:*
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93: gb_pr9:*
94: gb_rod1:*
95: gb_rod2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	162	9	A98523 Sequence 8
2	162	100.0	2825	9	A98521 Sequence 6
3	162	100.0	2825	94	AF073788 Mus muscu
4	162	100.0	3016	94	AF205889 Mus muscu
5	147.6	91.1	3216	94	AF017757 Rattus no
6	133.4	82.3	191041	69	AC024114 Mus muscu
7	131.6	81.2	2104	89	AK025718 Homo sapi
8	131.6	81.2	3072	88	AF078165 Homo sapi
9	128.4	79.3	2538	88	AF205888 Homo sapi
10	82.8	51.1	3485	8	AB032263 Dantio rer
11	56.4	34.8	3411	88	AF009674 Homo sapi

12 54.8 33.8 2121 8 AF140243 Xenopus 1
13 51.8 32.0 3066 8 AB032262 Danio rer
14 42.8 26.4 3156 8 AF009012 Gallus ga
15 39.8 24.6 23029 91 HS419C1
16 39.8 24.6 36418 85 AC004652
17 39.8 24.6 133065 70 AC026836
18 39.8 24.6 187272 74 AC069076
19 39.8 24.6 278229 76 AC074322
20 38.8 24.0 3460 94 AF017756
21 38.8 24.0 3761 94 AF009011
22 35.2 21.7 154278 68 AC025531
23 35.2 21.7 178343 68 AC024049
24 35.2 21.7 223358 72 AC040933
25 34.8 21.5 2529 8 AF097313
26 34.8 21.5 346294 2 AF002999
27 34.4 21.2 179138 78 AF276758
28 33.8 20.9 1781 1 AB030253
29 33.6 20.7 5027 86 AF032387
30 33.4 20.6 10288 94 MM001103
31 33.4 20.6 131007 92 HS998C11
32 33.4 20.6 215742 61 AC009412
33 33 20.4 127590 85 AC002554
34 33 20.4 131198 78 AL139096
35 33 20.4 209094 80 AL359643
36 32.8 20.2 144798 12 AC026758
37 32.8 20.2 207636 66 AC019122
38 32.4 20.0 1513 94 AF064873
39 32.4 20.0 3102 94 MMJ225122
40 32.4 20.0 190492 75 AC073957
41 32.4 20.0 314146 75 AC073759
42 32.2 19.9 156794 81 AL450307
43 32.2 19.9 214147 71 AC034122
44 32 19.8 36235 6 LMEL7836
45 31.8 19.6 2243 95 RNCROW2

ALIGNMENTS

RESULT 1
LOCUS A98523 162 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 8 from Patent WO9911780.
ACCESSION A98523
VERSION A98523.1 GI:6781609
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 162)
AUTHORS Birchmeier,W. and Behrens,J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 8 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source 1..162
location/Qualifiers
BASE COUNT 36 a 51 c 46 g 29 t
ORIGIN

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Best Local Similarity 100.0%; Pred. NO.1,1e-31;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 acgcctgtggaacacctgtccttcgcgcgcgagatcattccaaagcttgagaagaatgaa 120
Db 61 acgcctgtggaacacctgtccttcgcgcgcgagatcattccaaagcttgagaagaatgaa 120

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Db 121 CTGAGCTGGAAAGCCGCCATAGTCTGGAGAGAGCGGCTGCAG 162

RESULT 2
LOCUS A98521 2825 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 6 from Patent WO9911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier,W. and Behrens,J.
TITLE CONDUCTIVE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source 1..2825
location/Qualifiers

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Db 1241 gccaatggccaagtgtctctacatcatttcgcgagaaacccacgcgtgcgcaagaagatg 1300
OY 61 acgcctgtggaacacctgtccttcgcgcgcgagatcattccaaagcttgagaagaatgaa 120
Db 1301 acgcctgtggaacacctgtccttcgcgcgcgagatcattccaaagcttgagaagaatgaa 1360
OY 121 ctgagctggaagaacgcgcacatagcttgaggagcgctgcag 162
Db 1361 CTGAGCTGGAAAGCCGCCATAGTCTGGAGAGAGCGGCTGCAG 1402

RESULT 3
LOCUS AF073788 2825 bp mRNA ROD 13-JUL-1998
DEFINITION Mus musculus conductin mRNA, complete cds.
ACCESSION AF073788
VERSION AF073788.1 GI:3309246
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 2825)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Behrens,J., Jerchow,B.-A., Wurttele,M., Grimm,J., Asbrand,C.,
Wirtz,R., Kuhl,M., Wedlich,D. and Birchmeier,W.
TITLE Functional interaction of an axin homolog, conductin, with
beta-catenin, APC, and GSK3beta
JOURNAL Science 280 (5363), 596-599 (1998)
MEDLINE 96221239
REFERENCE 2 (bases 1 to 2825)
AUTHORS Behrens,J., Jerchow,B.-A. and Birchmeier,W.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany

FEATURES
source 1..2825
location/Qualifiers

CDs

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BASE COUNT 703 a 815 c 813 g 494 t

ORIGIN

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Oy 61 acgcctgtggaacgtgcgtccttcgcccgcgaagctcatctccaggcttgagaactgaaa 120
Db 1301 acgcctgtggaacgtgcgtccttcgcccgcgaagctcatctccaggcttgagaactgaaa 1360

Oy 121 ctggaagctggaagacgcgcatagtcttgagaagagcgagctcgag 162
Db 1361 ctggaagctggaagacgcgcatagtcttgagaagagcgagctcgag 1402

RESULT 4
AF205889 LOCUS 3016 bp mRNA ROD 03-JAN-2000
DEFINITION Mus musculus Axln2 (Axln2) mRNA, complete cds.
ACCESSION AF205889
VERSION AF205889.1 GI:6653585
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3016)
Zheng,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Jenkins,N.A., Warburton,D. and Costantini,F.
Properties of mouse Axln2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
Unpublished
2 (bases 1 to 3016)
Zheng,T. and Costantini,F.
Direct Submission
Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. H5SC 1416, New York, NY 10032, USA
Location/Qualifiers
1..3016
/organism="Mus musculus"
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/map="between Wnt3 and Pkca"

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55. .2577
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6,2e-32;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1081 gccatggcgaagtgctctctacatttgcgaagaccacacgcctgcgcgaagagatg 1140
    |||||

QY 61 acgcctgtggaaacctgcctgccttcgcgcgcgcgaagctcattccgaagcttgagaactgaaa 120
    |||||
Db 1141 acgcctgtggaaacctgcctgccttcgcgcgcgcgaagctcattccgaagcttgagaactgaaa 1200
    |||||

QY 121 ctggagctggaaagcgcgcattgcttgagagagcgcgctgcag 162
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Db 1201 ctggagctggaaagcgcgcattgcttgagagagcgcgctgcag 1242
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RESULT 5
AF017757 3216 bp mRNA ROD 24-APR-1998
LOCUS AF017757 Rattus norvegicus GSK-3beta Interacting protein Axil mRNA, complete cds.
ACCESSION AF017757
VERSION AF017757.1 GI:3080758
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eutheria; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3216)
AUTHORS Yamamoto,H., Kishida,S., Dochi,T., Ikeda,S., Koyama,S., Asashima,M.
and Kikuchi,A.
TITLE Axil, a member of the Axin family, interacts with both glycogen
synthase kinase 3beta and beta-catenin and inhibits axis formation
of Xenopus embryos
JOURNAL Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
MEDLINE 98226558
REFERENCE 2 (bases 1 to 3216)
AUTHORS Yamamoto,H., Ikeda,S., Murai,H., Kishida,S. and Kikuchi,A.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,
Japan
FEATURES
source
1. .3216
Location/Qualifiers

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* 161171 161270: gap of unknown length
* 164321 164311: contig of 3041 bp in length
* 164312 164411: gap of unknown length
* 164412 167354: contig of 2943 bp in length
* 167355 167454: gap of unknown length
* 167455 171291: contig of 3837 bp in length
* 171292 171391: gap of unknown length
* 171392 174233: contig of 2842 bp in length
* 174234 174333: gap of unknown length
* 174334 177744: contig of 3411 bp in length
* 177745 177844: gap of unknown length
* 177845 179402: contig of 1558 bp in length
* 179403 179502: gap of unknown length
* 179503 182420: contig of 2918 bp in length
* 182421 182520: gap of unknown length
* 182521 184923: contig of 2403 bp in length
* 184924 185023: gap of unknown length
* 185024 187054: contig of 2031 bp in length
* 187055 187154: gap of unknown length
* 187155 188272: contig of 1118 bp in length
* 188273 188372: gap of unknown length
* 188373 189634: contig of 1262 bp in length
* 189635 189734: gap of unknown length
* 189735 191041: contig of 1307 bp in length.

FEATURES
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        1. 191041
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            /db_xref="taxon:10090"
            /chromosome="11"
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BASE COUNT  49790 a 43523 c 42989 g 51816 t 2923 others
ORIGIN

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Query Match
Best Local Similarity 95.8% Pred. No. 6,7e-25;
Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 20 tacctcaatttcgagaaaccacgcgcctgcgcaagagatgagcctgtggaacctgctg 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30765 TCCACACCCTCAGAGAAACCCACCCCTGCCAAGAGATGAGCGCTGTGGAACCTGCTG 30824

OY 80 ccttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30825 CCTTGGCGCCGCGAGCTCATCTCAGCGTGAGAACTGGAACCTGAGCGGAAAGCCGCC 30884

OY 140 atagctcgagagcgcgctgcag 162
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DB 30885 ATAGCTCGAGAGCGCGCTGCAG 30907

RESULT 7
LOCUS AK025718 2104 bp mRNA PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ22065 fis, clone HEP10566, highly similar to
ACCESSION AK025718
VERSION AK025718.1 GI:10438327
KEYWORDS oligo capping: fis (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:hepg2 cDNA to mRNA, clone_11b:HEP
    Clone:HEP10566.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
    1 (sites)
        Kanabara, A., Hijiya, T., Kobatake, N., Inagaki, H., Ikema, Y.,
        Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
        Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
        NEDO human cDNA sequencing project
        Unpublished (2000)
        2 (bases 1 to 2104)
            Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
            Shibahara, T., Tanaka, T. and Nakamura, Y.

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TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'-6 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
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        1. 2104
            /organism="Homo sapiens"
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            /cell_line="hepg2"
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            /clone_11b="HEP"
            /note="Cloning vector pME18SFL3"

misc_feature
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        /note="highly similar to AF078165 Homo sapiens conductin
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BASE COUNT  506 a 610 c 619 g 369 t
ORIGIN

Query Match
Best Local Similarity 81.2% Pred. No. 4,4e-24;
Matches 143; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 gccaatgccaagtgtctacatcattccgagaaaccacgcgcctgcgcaagagatg 60
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DB 338 GCCAATGGCAAGTGTCTTACTCTATTTCCGAGAACCCACCGCTGCCAAGAGATG 397

OY 61 agcgcctggaacctgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
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DB 398 ACCCCCGTGGAACCCCGCACCTTTCGACGTGAGCTGATCTCGAGCTGGAAAGCTGAAG 457

OY 121 cggagctggaagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 458 CTGGAGTTGAGAGCGCGCCACAGCCTGAGAGAGCGCTGCAG 499

RESULT 8
LOCUS AF078165 3072 bp mRNA PRI 21-MAR-1999
DEFINITION Homo sapiens conductin mRNA, complete cds.
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
    1 (bases 1 to 3072)
        Mai, M., Qian, C., Yokomizo, A., Smith, D.I. and Liu, W.
        Cloning of the human homolog of conductin (XXIN2), a gene mapping
        to chromosome 17q23-q24
        Genomics 55 (3), 341-344 (1999)
    2 (bases 1 to 3072)
        Mai, M., Qian, C., Smith, D.I. and Liu, W.
        Direct Submission
        Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,
        200 First Street SW, Rochester, MN 55905, USA
        Location/Qualifiers
            1. 3072
                /organism="Homo sapiens"
                /db_xref="taxon:9606"

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FEATURES
source 1. 3485
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/db_xref="taxon:7955"
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297. 2735
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PKYTMADRCSTARDEDGCGEPGASPSPLAKMTSLPFLGDDOGLAFVYL
EKEKVDITDFACNGFRQMDLKTTHRAKATIKRIENNSYAKLAKLPATFTI
RNNIRQIDSMFQDAQMEIQTAMEENAYQMFITSDILEYRTGCEPVSVPNGVL
GGLKLVCGILPTLINEEEMSCNDFAKALATVYSAKTRSPPLRAVVALKGYRSY
RSDGNGNPRFTSGFAFATISANDSESDALTDMSMTDSVDALIPPKLGSKKO
LQREMRNMNMGOVSLPPEPRTTRPKEMTVEPAFAOLILARLERLKRDEETMS
LEERLOOIOEEERDESEMSSSASHSLPLPCTCEPDPAIIDEHLISVLTQPCCO
SFGILRHSPRSRSPDRPLPRGLSTRSSSSMNGYVPAKPTISROSTRHINHTIHH
NAGPKSKEQIEVEATQVOCICHGTECTAPYIHSRLGRDCASPAVALGHSSTL
SKRLCKSEVEMEGLENSLLOLPADSTDRSQNMWLTESDROTGHKPSQNYKKS
HSLPTRTHTMGCGSSGHLRAHQPAHPVQDPAHPPLPNTLAQLEBARRELEVS
KSKQHRSTSLQRDKSHPVYONGSSAPPMDEKDPKKMGSGHSGSEYVTFEC
GGEIYRRMAMKTHSLTGHFKQLKKNYRIFFRASDEFEGAVFEEMWDCIVLP
MEGKILGVDMRD"
BASE COUNT 986 a 839 c 864 g 796 t
ORIGIN

Query Match 51.1%; Score 82.8; DB 8; Length 3485;
Best Local Similarity 70.3%; Pred. No. 1.5e-11;
Matches 111; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

OY 4 aatggccaagtgtctactcatttcgcgagaaaccacccgctgcgccaagagatgag 63
Db 1332 AACGCCAAAGTCTCTGCTGCTCCCTCCCTAGACACCGCGCCACCTTAAGCATGACT 1391
OY 64 cctgtgaacctgtcgtcgtcgcgcgagatcattccagcgttgagaaactgaa 123
Db 1392 CCGGTGAGCAGCAGCAGCTTTCGACGACAGTGTAGCCAGCTGAGCAGTGAAGCGG 1451
OY 124 gacgtgaaagccgcacatgctctgagagagcgctgca 161
Db 1452 GAACAGGAAACATGAGCTCCCTGAGAGAGACTTCA 1489

RESULT 11
AF009674 3411 bp mRNA PRI 15-JUL-1997
LOCUS Homo sapiens axin (AXIN) mRNA, partial cds.
DEFINITION AF009674
ACCESSION AF009674
VERSION AF009674.1 GI:2252819
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3411)
AUTHORS Vasicsek,T.J., Zeng,L., Guan,X.-J., Zhang,T., Costantini,F. and
Tilghman,S.M.
TITLE Two dominant mutations in the mouse Fused gene are the result of
transposon insertions
JOURNAL Genetics (1997) in press
REFERENCE 2 (bases 1 to 3411)
AUTHORS Zeng,L., Fegotto,F., Zhang,T., Hsu,W., Vasicsek,T.J., Perry,W.L.
3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F.
TITLE The mouse Fused locus encodes Axin, an inhibitor of the Wnt
signaling pathway that regulates embryonic axis formation
JOURNAL Cell 90 (1), 181-192 (1997)
MEDLINE 97373830
REFERENCE 3 (bases 1 to 3411)

AUTHORS Vasicsek,T.J., Tilghman,S.M., Costantini,F., Zeng,L., Perry,W.L. III
and Zhang,T.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1997) Biological Technology, Millennium
Pharmaceuticals, Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
FEATURES
source 1. 3411
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/chromosome="16"
/map="16p13.3"
/dev_stage="ubiquitously expressed in development and in
adults"
<1. 3411
/gene="AXIN"
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mutation due to an Iap insertion in the Axin gene"
<1. 2704
/gene="AXIN"
/function="may inhibit embryonic axis formation"
/note="contains RGS domain and Daughterless similarity;
may inhibit embryonic axis formation"
/codon_start=2
/product="axin"
/protein_id="AAC51624.1"
/db_xref="GI:2252820"
/translation="GPGSRHHNARDLIFGCAVSTDVDCSSAGHSLTQSPKNNIOEG
FPLDLCASPTEDAPRPVPGEGELVSTDPRAVSFGCKGVIGETSTPRKSD
LDLGEPEGASPTPYLAKMELSHLDDOGISLFRFLQEOGCADLLDPMFACG
FKLEPCDSNEERKLARAIYRKYILDNNGIVSRQTKATKSGICGMKOLIDPAM
PQAOETQATMEENTYPSFKSDIYETRTGSGSPKYSQSSGSGGKIGISGLP
TLNEDEMKCDQDMDDEDGRDAPPRRLPQKLLLETAARVSSSRYSRGREFRGSW
REPVNYYVNAGYALAPATISANDSEQSSDAVLTLDSSVDGIPTRIKQHRE
MOESAQVNRVPLPHITRTYRVKPEKRVAPORFAELIRLRAYOTRABEKELERL
KRVMEEGEDEDPSGPPGCHKLPPAPAMHFPRLCTWACAGLRABHEPESI
LDENQORVLRTRGROSPGPHRSPPSGHVAKMPVALGAASGKGVPRSGAKLDAAG
LHHNPHVHHVHSTARPKEQVEAETRAQSSFMGLEPHSGARSRGVSGVGAAP
NMSDCIASHGKGVACRNAAKKAESKSASTEYPCASEAENKQKIMOTITGEEKTS
RHRRTHGSSGTRKQPHENSRLPLSEHWAGQULTSVPSHLFIDPTMPHPAPN
PLQLTEARLRLEEKERASRAFSKORYQVEVWRGRACVRACAFVHLHVAVSDME
LSEETRSQKRVGSGAQCDSIVAVYFCGGEIPYRTLVRSRAVLAQGFKEILTQKQ
SYRYPKKVSDEDCGVFEVEDPAVLVPEEKEKIGAEVWD"

BASE COUNT 752 a 1010 c 1066 g 582 t 1 others
ORIGIN

Query Match 34.8%; Score 56.4; DB 88; Length 3411;
Best Local Similarity 63.6%; Pred. No. 9.1e-05;
Matches 103; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

OY 1 gccaatggccaagtgtctactcatttcgcgagaaaccacccgctgcgccaagagatg 60
Db 1196 GTCAATGGCGGGGTGCGCCCTACATTCGCCGCGACGGGGTCCGGAAGAGGT- 1254
OY 61 aacgcctgtgaacctgtcgtcgtcgcgcgagacatcattccagcgttgagaaactgaa 120
Db 1255 -CCGCGTGAAGCCTCGAAGTTGCGGAGAGACTCTCAACCGCCCTGGAGGCTGTGCAAG 1312
OY 121 ctgagactggaagacgcgcacatgctctgagagagcgagctgacg 162
Db 1313 CGCACCGGAGGCGCCGAGGAGAGAGCTGAGAGCGGCTGGAAG 1354

RESULT 12
AF140243 2121 bp mRNA VRT 07-MAR-2000
LOCUS Xenopus laevis axin-related protein mRNA, complete cds.
DEFINITION AF140243
ACCESSION AF140243
VERSION AF140243.1 GI:6652990
KEYWORDS African clawed frog.
SOURCE Xenopus laevis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Ampibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
AUTHORS	Xenopodinae; Xenopus.
TITLE	1 (bases 1 to 2121)
JOURNAL	Itoh,K., Antipova,A., Ratcliffe,M.J. and Sokol,S.
MEDLINE	Interaction of dishevelled and Xenopus axin-related protein is
PUBMED	required for Wnt signal transduction
REFERENCE	Mol. Cell. Biol. 20 (6), 2228-2238 (2000)
AUTHORS	10688669
JOURNAL	2 (bases 1 to 2121)
MEDLINE	Antipova,A., Itoh,K. and Sokol,S.
PUBMED	Direct Submmission
REFERENCE	Submitted (02-APR-1999) Microbiology and Medical Genetics, Harvard
AUTHORS	Medical School, BIDMC, East Campus, RM663, 330 Brookline Avenue,
JOURNAL	Boston, MA 02215, USA
FEATURES	Location/Qualifiers
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	/db_xref="taxon:8355"
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	/product="axin-related protein"
	/protein_id="AAF22574.1"
	/db_xref="GI:6652991.1"
	/translation="MSSAGVLTCLIPDSCPIFRFMSLRPPQGETNNFKPEKFTMDSCG HLHKRFDFNREAECCVAHDSFRFSRWGSLNLILDDOGATLFRNYLEEGGLDLTTFW FACGFPRAMPDLPEPRTSKTAIAIYRVYONSAAVSGRLPTTRVCECVGNHOLINTWK VFDAOQOIEIORAQEAFSTFLSDIDCKEYRGVEDSPTEPSPGGLPTLEDDEFGCGA LHHSSGMGRKLNRFAESFPFNPNNSHRKELOOTQYFAPASINDSEISDALTEDSMK SMDSGVGDIPYRSKKOREIHRSVSNKGYSLPFVRTPPAEMPTSPAERAKITI TLAEKYKQDAEEKLEBKIQRIKEEBIADYDIPSSHETVPAGALDDPOSILDD HVSVLKTNPANLSPRSOSPFOVRGKGFQPARSKGTSTSCHLRKVPOGMEATSTLAS ELRVSQSOLFRRSRKPEGCTQPHRPREGTSAAVLITPLSPDOERNHSVLQWLDS AKLKSHKHRETASVTPCELKKAHRAASPAHLFDLDTSMPLTAPATLDLEEARBR RLVDKDRPKLHKRCGYOSTLTKRKGTAEPSPSGFTLKSFEORTAKRPSGCG OGLAIYVFFCGERIRPYMI RTREPSLTITOEFEKLLSKGSNKTYRKESHHEPCNAVQC EVSEEDAVLPLEEKTIICKVERAC"
BASE COUNT	637 a 501 c 507 g 476 t
ORIGIN	
Query Match	33.8%; Score 54.8; DB 8; Length 2121;
Best Local Similarity	58.6%; Pred. No. 0.00026;
Matches 95; Conservative	0; Mismatches 67; Indels 0; Gaps 0;
OY	1 gccaatgccaaagtcctcctaaccattctccggaagaacccaggcgctgcgaagagatg 60
Db	907 GCCAATGGAAAAGTCTTTTGCCCTTTGTTCCAAAGCACTATGCGCCACCAGCAGAAGAT 966
OY	61 aacctgtggaacactgcgccttcgcgcgcgcgcgcacatctccaggcttgagaagaactgaa 120
Db	967 ATGCCACAGAGTCACGACGAGAGTAGTTGCACGCAAGCTGACAATAGCTTTGGAGAAATAAAG 1026
OY	121 ctgagactggaagaagccgcgcataagtcttgagaagagacggcgctgcag 162
Db	1027 AAGCAGAGGAGCGCTGAAGAGAACCTGGAGAAAAGTTGCAG 1068
RESULT 13	
AB032262	
LOCUS	AB032262 3066 bp mRNA VRT 01-AUG-2000
DEFINITION	Danio rerio mRNA for axin1, complete cds.
ACCESSION	AB032262
VERSION	AB032262.1 GI:7229077
KEYWORDS	
SOURCE	Danio rerio CDNA to mRNA.
ORGANISM	Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;	
Cypriniformes; Cyprinidae; Rasborinae; Danio.	
1 (sites)	

[illegible]

	Archosauria: Aves; Neognathae: Galliformes; Phasianidae:
REFERENCE	Phasianinae: Gallus.
AUTHORS	1 (bases 1 to 3156)
TITLE	Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasicek, T. J., Perry, W. L. Jrd, Lee, J.J., Tilghman, S.M., Gumbler, B.M. and Costantini, F. The mouse Pax6 locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
JOURNAL	9/373830
MEDLINE	2 (bases 1 to 3156)
REFERENCE	Zeng, L., Zhang, T., Perry, W.L. III, Lee, J.J. and Costantini, F. Direct Submission Submitted (13-JUN-1997) Genetics and Development, Columbia University, 701 W. 168th Street, New York, NY 10032, USA
AUTHORS	Location/Organism
JOURNAL	1. .3156
FEATURES	/organism="Gallus gallus" source
gene	/db_xref="taxon:9031"
CDS	1..3156 /gene="Axin" /note="Fused is the classical dominant mouse tail kink mutation due to an 1ap insertion in the Axin gene" 258..2783 /gene="Axin" /function="may inhibit embryonic axis formation" /codon_start=1 /product="Axin" /protein_id="AAC60245.1" /db_xref="GI:2252818" /translation="MTIOGGKFLDLSRFTEDAAPPVPGEEGLVTDPPRVSHGF YSSSCADAVNETSTATRRSDLDLGYREGASAPPYIKAEBSHLLDDODSINFI RTFLKEQCADLDFWFAISGFRLEICSVNEERRLAKITKYILIDNNGIVSRDI KIPAKSPFKDCVMKLQIDPMFDAOETOCIMEDNTNPYLEKSDILEYTRIGESP KIAPDSPSGSGTGKGDLGYLPTELNDEEMKCDDOTPEBASDSAASSRLNQILLFTA TORASTIRRYSEGREPFHRGSWRREPYNFYVNTGVAMA.PATSANSDOOSMDTWS LTDSITGPIPRYLARKORHREMOESAKANGVP.LPHI.PTRYMPKDIIHEPERAAEL INLRLEPOKEREAEKLEBKRRABEEDGADISSPSYSIKMSAOPFHNFARR YSEGACAGMOMRDHNEENPESIIDEHQVRWKTKGCOSPGRHSKP.RPSSEGHRLK LSGTLCTIPCHGKHHTKSQMKLDAANLYHHKHYHN.IIHHSNM.KPKEOIEACTORY ONSAMNVDSHNYATKSRNS.SENLGMA.PVPSDSL.GSKASLKRINKTDSKSDGPS ANYMSGPDEVENRKILWIIEGEKIESHKKTNNSSGVKK.O.HSDVRAPLSTER PVNAHPVSAQLRNVNOPSHP.EIODPPMPRAP.NPRLTOLEARARREEEKRGKTL LKOLKAPKRSKSGASPOCSENTHVAIFTCGEPTIRYLKVGRVTV.DFOKFELLTKGN YRIYKAFVSDEFDGVVEEVREDTTLPEEKLIKXVERID."
BASE COUNT	875 a 825 c 858 g 598 t
ORIGIN	
Query Match	26.4% Score 42.8; DB 8; Length 3156;
Best Local Similarity	58.9%; Pred. No. 0.29;
Matches	93; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
Oy	1 gccaatggccaaagtctcctaactatttcgcagaaccacaggcgctgcccaaggaatg 60 Db 1341 GAATAATGAACGTGTGCCACTACTACATTCTCGTAATATCATCAATCAAGAATGATAT- 1399
Oy	61 acgccttgtagaacctgcgtcgcttgcgcgcgcagcatctcacagcttgagaagaatgaaa 120 Db 1400 --CACGCTTTGAACAACGAAAGATTCTCTCAGAACATGATCAATCGTTTGGAAACATATACAG 1457
Oy	121 ctgagactggaagacgcgcatagtcttgagaagaagcgct 158 Db 1458 AAGGAACCTGAAGCAGAGAGCAAATTGGAGAGCGCCCT 1495
RESULT 15	
LOCUS	HS419CL1 22039 bp DNA PRI 23-NOV-1999
DEFINITION	Human DNA sequence from cosmid 419CL1 from a contig from the tip of the short arm of chromosome 16, spanning 2mb of 16p13.3.
ACCESSION	Z99754.1 GI:3036781
VERSION	16p13.3.
KEYWORDS	

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SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 22029)
AUTHORS       Smey,R.
TITLE         Direct Submission
JOURNAL       Submitted (27-OCT-1997) Chromosome 16 Project Group
              (http://www.sanger.ac.uk/HGP/chr16/) Sanger Centre, Wellcome Trust
              Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail
              enquiries: humquerry@sanger.ac.uk Clone requests:
              clonerequests@sanger.ac.uk
COMMENT        On Apr 8, 1998 this sequence version replaced gi:2465054.
              IMPORTANT: This sequence is not the entire insert of clone 419C1.
              It may be shorter because we only sequenced overlapping sections
              once, or longer because we arranged for a small overlap between
              neighbouring submissions.
              The true left end of clone 419C1 is at 1 in this sequence. The true
              right end of clone 314G4 is at 104.
              The true left end of clone 33B10 is at 21926.
              419C1 is from a 400kb clone contig on 16p.
              Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit,
              Institute of Molecular Medicine, Oxford.
              419C1 came from the Los Alamos, flow sorted human chromosome 16
              libraries constructed by Norman Doggett (unpublished).

FEATURES             Location/Qualifiers
     source           1..22029
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                     /db_xref="taxon:9606"
                     /map="16p13.3"
                     /clone="LA16-419C1"
                     /clone_id="LA16"
                     43..327
repeat_region       /note="AlusX repeat: matches 1..302 of consensus"
                    345..627
repeat_region       /note="Alusq repeat: matches 21..303 of consensus;
                    incomplete repeat"
                    644..922
repeat_region       /note="Alusq repeat: matches 25..303 of consensus;
                    incomplete repeat"
                    928..1228
repeat_region       /note="Aluv repeat: matches 1..299 of consensus"
                    1244..1529
repeat_region       /note="Alusq repeat: matches 302..28 of consensus;
                    incomplete repeat"
                    1596..1714
repeat_region       /note="Aludv repeat: matches 184..299 of consensus;
                    incomplete repeat"
                    1827..2124
repeat_region       /note="AlusX repeat: matches 1..293 of consensus"
                    2131..2294
repeat_region       /note="Aludv repeat: matches 1..180 of consensus;
                    incomplete repeat"
                    4653..4914
repeat_region       /note="Aludv repeat: matches 302..44 of consensus;
                    incomplete repeat"
                    4928..5213
repeat_region       /note="Alusq repeat: matches 286..1 of consensus"
                    5508..5801
repeat_region       /note="Alusx repeat: matches 294..1 of consensus"
                    5804..6101
repeat_region       /note="Aluv repeat: matches 298..1 of consensus"
                    6106..6383
repeat_region       /note="Alusq repeat: matches 303..6 of consensus"
                    6389..6642
repeat_region       /note="Aludv repeat: matches 247..5 of consensus;
                    incomplete repeat"
                    7150..7437
repeat_region       /note="Aluv repeat: matches 15..301 of consensus"
                    7656..7779
repeat_region       /note="Aludv repeat: matches 1..124 of consensus;
                    incomplete repeat"

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Search completed: June 7, 2001, 00:35:43
Job time: 20957 sec

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repeat_region 9042. .9307
/note="AluDb repeat: matches 267. .1 of consensus;
incomplete repeat"
repeat_region 9532. .9828
/note="AluSg repeat: matches 297. .1 of consensus"
prln_transcript 9967. .10175
/note="match: 5' EST AA085320"
prln_transcript 10450. .>16291
/note="match: mouse 5' EST AA238939"
repeat_region 10683. 10981
/note="AluSx repeat: matches 299. .1 of consensus"
repeat_region 11335. .1635
/note="AluDb repeat: matches 1. .295 of consensus"
unsure 11604
unsure 11609
unsure 11627
repeat_region 11689. 11990
/note="AluY repeat: matches 301. .1 of consensus"
repeat_region 12003. .12110
/note="AluSg repeat: matches 123. .1 of consensus;
incomplete repeat"
repeat_region 12132. 12248
/note="MER42c repeat: matches 1536. .1414 of consensus"
repeat_region 12361. .12508
/note="MER42c repeat: matches 1335. .1186 of consensus"
repeat_region 12672. .12743
/note="MIR repeat: matches 111. .181 of consensus"
repeat_region 13651. 13844
/note="MER1B repeat: matches 333. .139 of consensus"
repeat_region 14879. .14912
/note="17 copies of 2 mer 82 & conserved"
repeat_region 15202. .15422
/note="AluY repeat: matches 7. .227 of consensus;
incomplete repeat"
repeat_region 16542. .16847
/note="AluY repeat: matches 301. .1 of consensus"
repeat_region 17178. .17476
/note="AluY repeat: matches 301. .1 of consensus"
repeat_region 17637. .17936
/note="AluY repeat: matches 1. .300 of consensus"
repeat_region 19054. .19163
/note="AluDb repeat: matches 2. .124 of consensus;
incomplete repeat"
repeat_region 19179. .19468
/note="AluDb repeat: matches 2. .302 of consensus"
repeat_region 20549. .20724
/note="4 copies of 44 mer 88 & conserved"
repeat_region 21693. 21994
/note="AluY repeat: matches 1. .301 of consensus"
repeat_region 21999. .22028
/note="AluSx/g repeat: matches 82. .111 of consensus;
incomplete repeat"
BASE COUNT 5145 a 6217 c 5887 g 4780 t
ORIGIN

Query Match 24.6%; Score 39.8; DB 91; Length 22029;
Best Local Similarity 60.4%; Pred. No. 1.2;
Matches 84; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

OY 24 tcatttcgcgaagccacgcgcctgcgaagagatgaagcctgtgaaactgtgcctt 83
Db 10598 TCCCTCGAGCGCACGCTACGGGCTCCGACAGAGT--CCGCGTGAAGCCTCAGAGTT 10542

OY 84 cgcgcgcgagtcattccagagctggaagaaactgaactgagctggaagcgcgcataag 143
Db 10541 CGCGGAGAGAGCTATCCACCGCTGAGAGGCTGTGCACGCGGAGGCGCGAGAGAA 10482

OY 144 tctgagagagcgcgtgcag 162
Db 10481 GCTGGAGAGAGCGGCTGAAG 10463
```


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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:31:47 ; Search time 276.75 Seconds

(without alignments)
341.726 Million cell updates/sec

Title: US-09-587-574-8

Perfect score: 162

Sequence: 1 gccacatggcacaagtgctctc.....gtctggagggcgctgcag 162

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues 1356552

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_0401:*

1: /SID2/gcgdata/geneseq/geneseq/NA1980.DAT:*

2: /SID2/gcgdata/geneseq/geneseq/NA1981.DAT:*

3: /SID2/gcgdata/geneseq/geneseq/NA1982.DAT:*

4: /SID2/gcgdata/geneseq/geneseq/NA1983.DAT:*

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22: /SID2/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	2523	20	Human conductin CN
2	162	100.0	2825	20	Human conductin CD
3	56.4	34.8	3411	20	Human axin gene.
4	38.8	24.0	3761	20	Murine axin gene.
5	32.4	20.0	1584	20	Mouse brain CNG-2
6	31.2	19.3	1342	20	Human Ih ion channel
7	31.2	19.3	2029	20	Human heart tissue
8	31.2	19.3	2886	20	Human Ih ion channel
9	31.2	19.3	38186	20	Human MERT1 relate
10	31.2	19.3	38186	22	AC004449 cDNA clone
11	30.8	19.0	794	20	Rat olfactory Ih 1

12	30.8	19.0	1247	14	041354	Human GDF-1 coding
13	30.8	19.0	1247	15	038862	Morphogen GDF-1 co
14	30.8	19.0	1247	15	058055	Human morphogenic
15	30.8	19.0	1247	15	067315	Human GDF-1 (fx) mo
16	30.8	19.0	1247	15	045120	Human GDF-1 (fx) mo
17	30.8	19.0	1247	15	067402	Human GDF-1 (fx) mo
18	30.8	19.0	1247	18	V10351	Human GDF-1 cDNA.
19	30.8	19.0	1247	18	T97883	CDNA sequence enco
20	30.8	19.0	1247	19	V25888	Human GDF-1 cDNA.
21	30.8	19.0	1247	19	V19538	Human GDF-1 (fx) p
22	30.8	19.0	1247	19	V19538	Mouse GDF-1 encodi
23	30.8	19.0	2510	13	Q20690	hGDF-1 and hOG-1
24	30.4	18.8	1553	21	Z58953	Human MIF1 protein
25	30.4	18.8	1553	21	Z58958	Human MIF1 protein
26	30.2	18.6	533	21	A42312	Human secreted exp
27	29.8	18.4	537	21	C56489	Eucalyptus grandis
28	29.6	18.3	372	21	C00205	Human secreted pro
29	29.6	18.3	1034	20	X87634	Human porphobilino
30	29.6	18.3	1246	22	F33247	Human porphobilino
31	29.6	18.3	1307	20	X25488	Human cyclic nucle
32	29.6	18.3	1307	20	X84446	Mouse brain CNG-3
33	29.6	18.3	1790	20	X84445	Human brain CNG-2
34	29.6	18.3	1820	20	Z09488	Bovine retina Ih 1
35	29.6	18.3	4751	20	Z09496	Human heart tissue
36	29.2	18.0	3531	21	C58366	Human PRO290 nucle
37	29.2	18.0	3531	21	Z64954	Membrane-bound pro
38	28.8	17.8	550	20	Z07225	Human lung tumour
39	28.8	17.8	751	21	C79115	Human lung tumour
40	28.8	17.8	1034	20	X40107	Gastric cancer ass
41	28.8	17.8	1035	20	X87637	Human porphobilino
42	28.8	17.8	1035	20	X87638	Human porphobilino
43	28.8	17.8	1035	20	X87630	Human porphobilino
44	28.8	17.8	1035	20	X87632	Human porphobilino
45	28.8	17.8	1035	20	X87633	Human porphobilino

ALIGNMENTS

RESULT 1	
ID X23370	standard; cDNA: 2523 BP.
AC X23370;	
DT 17-JUN-1999	(first entry)
XX	
DE Human conductin cDNA.	
KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW Wingless signalling pathway; Adenomatous Polyposis Coll; APC;	
KW tumour suppressor; ss.	
XX	
OS Homo sapiens.	
XX	
PN W09911780-A2.	
XX	
PD 11-MAR-1999.	
XX	
PF 01-SEP-1998; 98MO-DE02621.	
XX	
PR 02-SEP-1997; 97DE-1038205.	
XX	
PA (DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.	
XX	
PI Behrens J, Birchmeier W;	
XX	
XX WPI; 1999-214706/18.	
DR P-PSDB; W93570.	
XX	
PT Tumor-suppressing protein conductin - used for treatment and	
PT diagnosis of tumors	

XX 10-JUL-1997; 97US-0890865.
PR
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Constantini F, Zeng L;
DR WPI: 1999-120510/10.
XX P-PSDB; W96264.
PT
XX Newly isolated nucleic acid encoding "axis inhibition" protein
PS (Axin) - useful for detecting, diagnosing and treating cancer
XX
XX Disclosure; Figure 10A-10B; 95pp; English.

CC Nucleic acids encoding mutant and wild type Axin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axin and homologues of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.

XQ Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;

Query Match	34.88;	Score 56.4;	DB 20;	Length 3411;
Best Local Similarity	63.68;	Pred. No. 1.6e-07;		
Matches 103;	Conservative 0;	Mismatches 56;	Indels 3;	Gaps 1;
Db	1	gccaatgccaagatgtctctacatcttcctcgagaacccacggcctgcgccaaagagatg 60		
Oy	1196	gtcaatggcggtgccccctaccctacatctcccgacgtaacggtgcgcgaaggagatg- 1254		
Db	61	acgcctgttggaacatctgcctctcgcccgccagatccatctccaggcttggaanaactgaa 120		
Oy	1255	--ccgcgtgagagcctcagaagattcgcgagagagagctcaccacacgccttgaggctgtgcag 1312		
Db	121	ctggaagctggaagaagccgcacatagctctggagagagcggtctgacg 162		
Oy	1313	cgacagcgagagccgagaggaagctggaagagcggtctgacg 1354		
RESULT 4				
ID	X09013			
standard:	DNA; 3761 BP.			
AC	X09013;			
DT	14-JUN-1999 (first entry)			
DE	Murine axln gene.			
KW	axln; cancer; breast cancer; colorectal cancer;			
KW	gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;			
KW	diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;			
KW	beta-catenin, os.			
OS	Mus musculus.			
FT	Key	Location/Qualifiers		
FT	CDS	1..2981		
FT	FT -	/*tag= a		
FT	FT -	/product= Axln		
XX	W0902179-A1			

XX 21-JAN-1999.
PD
XX
XX 09-JUL-1998; 98WO-US14414.
PF
XX
XX 10-JUL-1997; 97US-0890865.
PR
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Constantini F, Zeng L;
PI
XX WPI: 1999-120510/10.
XX
XX DR P-PSDB: W96265.
XX
XX Newly isolated nucleic acid encoding "axis inhibition" protein
PT (Axin) - useful for detecting, diagnosing and treating cancer
XX
XX
XX Claim 7; Figure 9A-9B; 95pp; English.
PS
XX
XX Nucleic acids encoding mutant and wild type Axin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axin and homologues of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-actin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
XX Sequence 3761BP; 890 A; 1012 C; 1088 G; 771 T; 0 other;
XX

Query Match	24.0%	Score 38.8	DB 20	Length 3761
Best Local Similarity	56.8%	Pred. No. 0.026		
Matches 92	Conservative 0	Mismatches 67	Indels 3	Gaps
OY	1	gccaatgccaagtctctaccattcttcgcgaagccacccgcgcctgcccagaagatg	60	
Db	1473	gtcaatggcggggtacccttaccattacattcctctgcattaccgaatgtccaaaggagatc	1532	
OY	61	acgcctctggaacactgctgccttcgcgcgcgcagctcattccaggcttgagaactgaaa	120	
Db	1533	--cggttagagagccacagaatattctgaagagcttattaccgcgtcagaagctctccag	1589	
OY	121	ctggaagctggaaaagccgcacatgattctggaagggcgcgctcgag	162	
Db	1590	cgcactcgagagagctgaaagaattgtgaggaagcaagctgaag	1631	
RESULT	5			
ID	X84444/C			
	X84444 standard; cDNA; 1584 bp.			
XX	X84444;			
XX				
DT	10-SEP-1999	(first entry)		
XX				
DE	Mouse brain CNG-2 coding sequence.			
XX				
XX	BCNG; brain cyclic nucleotide gated ion channel; epilepsy; hyperalgesia;			
KW	Alzheimer's Disease; Parkinson's Disease; long QT syndrome; dyslexia;			
KW	sick sinus syndrome; age-related memory loss; cystic fibrosis;			
KW	sudden death syndrome; pacemaker rhythm dysfunction; sensory disorder;			
KW	auditory disorder; respiratory disorder; attention deficit disorder;			
XX	learning disability; drug addiction; therapy; mBCNG-2; ss.			
XX				
OS	Mus sp.			
XX				

XX 26-AUG-1999.
PD 12-FEB-1999: 99WO-EP00942.
XX 17-FEB-1998: 98DE-1006581.
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX Baumann A, Boenigk W, Gauss R, Kaupp B, Scholten A:
PI Seifert R;
XX WPI: 1999-527472/44.
XX
XX New nucleic acid encoding an Ih ion channel, used to identify
PT specific modulators, and for treatment, prevention and diagnosis of
PT e.g. cardiac disease
XX
XX Disclosure: Page 68-69; 82pp; German.
XX
XX This invention describes a novel Ih ion channel, isolated from human,
CC sea urchin, bovine, rat, and fruitfly. The ion channels of the invention
CC have analgesic and cardioactive activity. The Ih ion channel participates
CC in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
CC acid and its encoding protein is used to identify substances (A) that
CC modulate activity of ion channels; to treat and/or diagnose ion
CC channel-related diseases, particularly cardiac or circulatory disorders
CC and to prevent and/or treat cardiac/circulatory disorders (especially
CC faulty regulation of the sinus ganglion), sleep disorders (particularly
CC abnormal function of cortico-thalamic neurons) and/or pain. Fragments of
CC the Ih ion channel nucleic acid are used to detect mutations e.g. for
CC differential diagnosis. This sequence encodes a human Ih channel
CC fragment isolated from heart tissue.
XX
SQ Sequence 2029 BP: 338 A; 774 C; 509 G; 356 T; 52 other:
XX
Query Match 19.3%; Score 31.2; DB 20; Length 2029;
Best Local Similarity 58.7%; Pred. No. 3.9;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
OY 39 ccaccgcctgcccaaggagatgacgcctgtggaacctgctgctgcgcgcgagccat 98
DB 166 CCACGCCATGCTGATGATGACATCTCTTCCCATGTGCTGCCGATGATGATGAT 107
OY 99 ctccaggctggagaagaactgagactgagctg 130
DB 106 CCCACGGCTGGAGACCTCAAAACGACGCTTG 75
RESULT 8
209491/C
ID 209491 standard; DNA: 2886 BP.
XX
AC 209491;
XX
DT 02-NOV-1999 (first entry)
XX
DE Human Ih ion channel DNA fragment #2.
XX
XX Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;
KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;
KW treatment; diagnosis; ion channel-related disease; cardiac disease;
KW circulatory disorder; sinus ganglion regulation; sleep disorder;
KW cortico-thalamic neuron; pain; detection; mutation; ss.
XX
XX Homo sapiens.
XX
XX MO9942574-A1.
XX
XX 26-AUG-1999.
XX
XX 12-FEB-1999: 99WO-EP00942.

XX 17-FEB-1998: 98DE-1006581.
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX Baumann A, Boenigk W, Gauss R, Kaupp B, Scholten A:
PI Seifert R;
XX WPI: 1999-527472/44.
XX
XX New nucleic acid encoding an Ih ion channel, used to identify
PT specific modulators, and for treatment, prevention and diagnosis of
PT e.g. cardiac disease
XX
XX Disclosure: Page 67-68; 82pp; German.
XX
XX This invention describes a novel Ih ion channel, isolated from human,
CC sea urchin, bovine, rat, and fruitfly. The ion channels of the invention
CC have analgesic and cardioactive activity. The Ih ion channel participates
CC in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
CC acid and its encoding protein is used to identify substances (A) that
CC modulate activity of ion channels; to treat and/or diagnose ion
CC channel-related diseases, particularly cardiac or circulatory disorders
CC and to prevent and/or treat cardiac/circulatory disorders (especially
CC faulty regulation of the sinus ganglion), sleep disorders (particularly
CC abnormal function of cortico-thalamic neurons) and/or pain. Fragments of
CC the Ih ion channel nucleic acid are used to detect mutations e.g. for
CC differential diagnosis. This sequence encodes a human Ih channel
CC fragment isolated from human thalamus tissue.
XX
SQ Sequence 2886 BP: 605 A; 774 C; 940 G; 558 T; 9 other:
XX
Query Match 19.3%; Score 31.2; DB 20; Length 2886;
Best Local Similarity 58.7%; Pred. No. 4.2;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
OY 39 ccaccgcctgcccaaggagatgacgcctgtggaacctgctgctgcgcgcgagccat 98
DB 1309 CCACGCCGCTGCTGATGATGACATCTCTTCCCGATGTGCTGCCGATGATGATGAT 1250
OY 99 ctccaggctggagaagaactgagactgagctg 130
DB 1249 CACCCGGCTGGAGACCTCAAACTTGAGCTTG 1218
RESULT 9
232028/C
ID 232028 standard; DNA: 38186 BP.
XX
AC 232028;
XX
DT 10-JAN-2000 (first entry)
XX
DE Human METH1 related EST AC004449.
XX
XX Human; METH1; METH2; anti-angiogenic; metalloproteinase thrombospondin;
KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
KW angiogenesis inhibitor; abnormal wound healing; inflammation;
KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
KW diabetic retinopathy; macula degeneration; hemangioma; detection;
KW arterial-venous malformation; immune deficiency; ss.
XX
XX Homo sapiens.
XX
XX MO9937660-A1.
XX
XX 29-JUL-1999.
XX
XX 22-JAN-1999: 99WO-US01313.
XX
XX 23-JAN-1998: 98US-0072298.
XX
XX 28-AUG-1998: 98US-0098539.

XX (IRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
XX
XX IrueLA-Arispe L, Hastings GA, Ruben SM;
DR WPI, 1999-590684/50.
XX
XX New isolated metalloproteinase thrombospondin polypeptides, useful for
PT treating hyperproliferative disorders, cancers or autoimmune disorders
XX
XX
XX Disclosure; Page 363-387; 457pp; English.
XX
XX Z32000 and Z32001 encode, and Y49501 and Y49502 represent, human
CC metalloproteinase thrombospondin (METH) proteins METH1 and METH2
CC respectively. METH1 and METH2 have been found to be potent inhibitors of
CC angiogenesis both in vitro and in vivo. They can be used for treating
CC cancer and other disorders related to angiogenesis including abnormal
CC wound healing, inflammation, rheumatoid arthritis, psoriasis,
CC endometrial bleeding disorders, diabetic retinopathy, some forms of
CC macula degeneration, haemangiomas, and arterial-venous malformations.
CC They may be useful in treating deficiencies or disorders of the immune
CC system, by activating or inhibiting the proliferation, differentiation,
CC or mobilisation (chemotaxis) of immune cells. The etiology of these
CC immune deficiencies or disorders may be genetic, somatic, such as
CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
CC toxins), or infectious. They can also be used to treat inflammatory or
CC conditions, both chronic and acute conditions. The products can also be
CC used for detection and diagnosis. Z32002 to Z32080, and Y49503 to Y49511
CC represent sequences given in the exemplification of the present
CC invention.
XX
XX Sequence 38186 BP; 7571 A; 11503 C; 12193 G; 6919 T; 0 other:
SQ

Query Match 19.3%; Score 31.2; DB 20; Length 38186;
Best Local Similarity 58.7%; Pred. No. 7.7;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 39 ccaccgctgccaagagatgacgcctgtggaacctgctgctccgcgcgagctcat 98
DB 2492 CCACGCCGCTGGATGAAGTACATCTTCTCCCGATGCTGCGGATGATGACT 2433
OY 99 ctcagctgtggaagaactggaactgtgagcttg 130
DB 2432 CACCCGCTGGGAAGACCTCGAAGCTTGAGCTTG 2401

RESULT 10
C90085/c
ID C90085 standard; DNA; 38186 BP.
XX
XX C90085;
XX
XX 19-MAR-2001 (first entry)
XX
XX AC004449 cDNA clone.
XX
XX METH: metalloproteinase; thrombospondin; angiogenesis inhibition;
KW cancer therapy; benign tumour; ocular angiogenic disease;
KW rheumatoid arthritis; psoriasis; wound healing; endometriosis;
KW vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
KW scleroderma, trachoma; vascular adhesion; myocardial angiogenesis;
KW coronary collateral; cerebral collateral; arteriovenous malformation;
KW ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;
KW plaque neovascularisation; telangiectasia; haemophilic joint; EST;
KW angiofibroma; fibromuscular dysplasia; expressed sequence tag;
KW Croun's disease; atherosclerosis; birth control; ss.
XX
XX Unidentified.

PN W0200071577-A1.
XX
XX 30-NOV-2000.
XX
XX 25-MAY-2000; 2000WO-US14462.
XX
XX 25-MAY-1999; 99US-0318208.
XX 20-JUL-1999; 99US-0144882.
XX 10-AUG-1999; 99US-0147823.
XX 13-AUG-1999; 99US-0373658.
XX 22-DEC-1999; 99US-0171503.
XX 22-FEB-2000; 2000US-0183792.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (SMK) SMTKLIN BECHAM CORP.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA (IRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
PA (JONAK/) JONAK Z L.
PA (TRULL/) TRULLI S H.
PA (FORN/) FORNWALD J A.
PA (TERR/) TERRITT J A.
XX
XX IrueLA-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulll SH;
PI Fornwald JA, Territt JA;
XX WPI: 2001-025136/03.
XX
XX METH1 and METH2 polynucleotides and encoded polypeptides, used to
PT inhibit angiogenesis in the treatment of disorders such as cancer,
PT rheumatoid arthritis and psoriasis -
XX
XX Claim 7; Pages 663-687; 768pp; English.
XX
XX The present invention relates to human METH1 and METH2, (ME for
CC metalloproteinase and TH for thrombospondin; see B50002 and B50003). The
CC present sequence is an expressed sequence tag (EST) for METH. METH can be
CC used for inhibiting angiogenesis in an individual, and for treating
CC cancer, benign tumours, an ocular angiogenic disease, rheumatoid
CC arthritis, psoriasis, delayed wound healing, endometriosis,
CC vasculogenesis, granulations, hypertrophic scars, nonunion fractures,
CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
CC coronary collaterals, cerebral collaterals, arteriovenous malformations,
CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC fibromuscular dysplasia, wound granulation, Croun's disease or
CC atherosclerosis. METH can also be used in birth control. METH can also be
CC used in diagnostic methods for the prognosis of cancer.
XX
XX Sequence 38186 BP; 7571 A; 11502 C; 12194 G; 6919 T; 0 other:
SQ

Query Match 19.3%; Score 31.2; DB 22; Length 38186;
Best Local Similarity 58.7%; Pred. No. 7.7;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 39 ccaccgctgccaagagatgacgcctgtggaacctgctgctccgcgcgagctcat 98
DB 2492 CCACGCCGCTGGATGAAGTACATCTTCTCCCGATGCTGCGGATGATGACT 2433
OY 99 ctcagctgtggaagaactggaactgtgagcttg 130
DB 2432 CACCCGCTGGGAAGACCTCGAAGCTTGAGCTTG 2401

RESULT 11
Z09494/c
ID Z09494 standard; DNA; 794 BP.
XX
XX Z09494;
XX
XX 02-NOV-1999 (first entry)
XX

XX	Morphogen; homodimer; stimulate; proliferation; progenitor cell;
KW	differentiation; growth; redifferentiation; transformation; human;
KM	mouse; Drosophila; Xenopus; committed cells; hippocampus;
KV	growth/differentiation factor 1; GDF-1; ss.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	CDS 84..1202
ET	/tag= a
XX	
PX	MO9305172-A.
PD	18-MAR-1993.
PF	28-AUG-1992; 92WO-US07359.
PR	30-AUG-1991; 91US-0752861.
PA	(CREA-) CREATIVE BIOMOLECULES INC.
PI	Cohen CN, Kuberampath T, Oppermann H, Ozkaynak E, Pang RHL,
PT	Rueger DC, Smart JE;
PS	WPt: 1993-100993/12. P-PsDB: R33942.
PP	Screening cpds. to determine ability to modulate effective concn.
PT	of a morphogen - by assaying test tissue type cells for parameter
PR	indicative of a prodn. level change of morphogen
PS	Disclosure: Page 116-118; 132pp; English.
XX	This sequence encodes the morphogen growth/differentiation factor 1 (GDF-1). Isolated from human brain. This morphogen is inactive when reduced but is active as an oxidised homodimer and when oxidised in combination with other morphogens. These morphogens are capable of stimulating proliferation of progenitor cell, stimulating the differentiation of progenitor cells, stimulating the proliferation of differentiated cells and supporting the growth and maintenance of differentiated cells, including the redifferentiation of transcribed cells. These morphogens may also be capable of inducing rediffer-
CC	entiation of committed cells under appropriate environmental
CO	conditions.
SQ	Sequence 1247 BP: 127 A; 497 C; 448 G; 175 T; 0 other:
Query Match	19.0%; Score 30.8; DB 14; Length 1247;
Best Local Similarity	52.3%; Pred.No. 4.5;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps	0;
OY	3l cggaaacccaccgctgcccaagagtgaagcctgttgagaactgcgtcgacctgcgcgc 90
Dd	
OY	71l ccgcgcaggccccttcgctgtgcgtgcctaagcccccgcccgccgtgcgcgcgcgc 770
Dd	
OY	91 gagcacatcccaagcctgagaaactgaaaactgtaaacctgcggaagccgatgctgag 150
Dd	
OY	77l ctgcgcggagcgtcgtcgtcgtgltgacacctggaacccgcgcgttgtgcacccctggcc 830
Dd	
OY	15l gagegcgtgc 160
Dd	
OY	83l cgccgcgcgcgc 840
Dd	
RESULT 14	
ID O58055 standard; cdna; 1247 BP.	
AC Q58055;	
XX 25-AUG-1994 (first entry)	

XX		Human morphogenic protein GDF-1(fx) cDNA.	
DE			
KM		Human morphogenic protein; GDF-1(fx); morphogen;	
KW		infant food formulation; tissue morphogenesis; tissue development;	
RN		bone growth; morphogen-enriched nutritional product; ss.	
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	84..1202	
FT		/*tag= a	
FT		//function= morphogenic_protein	
FT		/note= "GDF-1(fx) cDNA"	
PN	MO9403075-A.		
XX			
PD	17-FEB-1994.		
XX			
PF	29-JUL-1993;	93WO-US07190.	
XX			
PR	31-JUL-1992;	92US-0923780.	
PR	04-MAR-1993;	93US-0029335.	
PR	31-MAR-1993;	93US-0040510.	
PR	31-JUL-1992;	92US-0922813.	
PR	16-SEP-1992;	92US-0946235.	
PA	(CREA-) CREATIVE BIOMOLECULES INC.		
XX			
PI	Jones WK, Kuberasampath T, Oppermann H, Ozkaynak E;		
PI	Rueger DC, Tucker RF, Cohen CM, Pang RHL;		
XX			
DR	WI: 1994-065304/08.		
DR	P-PSDB: RA6750.		
XX			
PT	Morphogen enriched dietary compositions and infant formula -		
PT	capable of enhancing tissue morphogenesis, development and		
PT	viability, e.g. in infants, aged individuals and metabolic		
PT	disorders, e.g. anorexia nervosa, etc		
XX			
PS	Disclosure and Claims 25-26; Page 139-141; 160pp; English.		
XX			
CC	Human GDF-1 (fx) morphogen and proteins having at least 70%		
CC	homology with it are preferred morphogens for inclusion in new		
CC	morphogen-enriched nutritional formulations. The formulations		
CC	are dietary compositions suitable for people at risk for tissue		
CC	damage due to protein energy malnutrition or to altered metabolism		
CC	function and infant formulations to enhance tissue development in		
CC	an infant or juvenile.		
SX			
SO	Sequence 1247 BP; 127 A; 494 C; 451 G; 175 T; 0 other;		
QY	Query Match	19.0%; Score 30.8; DB 15; Length 1247;	
	Best Local Similarity	52.3%; Pred. NO. 4.5;	
	Matches 68; Conservative	0; Mismatches 62; Indels 0; Gaps	0;
Dd	711 ccgaaaccccccgcctcgtcccaagaagatgaacgctggaacctcgcttcggcgcc	90	
	711 ccgcgcagactccgcctcgtcgctgctgaagcccccgggccctcgccgcgcgcgc	770	
QY	91 gactcatctccaggctggaanaactggaactggaagctggaagcccatagtctgag	150	
Dd	771 ctggcgcggagcctcgtcgtctgttgacctcgaccgcgcgcgtgtgccacccttggcc	830	
QY	151 gagcgagctgc	160	
Dd	831 cggcgcgcgcgc	840	
RESULT	15		
ID1	Q67315 standard; DNA; 1247 BP.		
	067315		

Job time: 8632 sec

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XX 067315;
AC
DT 11-OCT-1994 (first entry)
DE Human GDF-1(fx) morphogen.
XX
XX OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx);
KM GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx);
KM tooth socket; alveolus; osteogenic protein; morphogen;
KM morphogenic protein; periodontal tissue; regeneration;
KM tooth implant; integration; inhibition; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 84..1202
XX /*tag=
XX /label= GDF-1
XX
XX MO9406399-A.
XX
XX 31-MAR-1994.
XX
XX 15-SEP-1993; 93MO-US08742.
XX
XX 15-SEP-1992; 92US-0945285.
XX PR 04-MAR-1993; 93US-0029335.
XX PR 31-MAR-1993; 93US-0040510.
XX
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Cohen CM, Kuberanampath T, Oppermann H, Ozkaynak E;
XX Pang RHL, Rueger DC, Smart JE;
XX
XX WPI: 1994-118107/14.
XX
XX P-PSDB; R57980.
XX
XX Morphogen-induced periodontal tissue regeneration - used in
XX integrating as implanted tooth in tooth socket or to inhibit
XX tissue loss associated with periodontal disease or injury
XX
XX Claim 28-29; Page 114-116; 132pp; English.
XX
XX Morphogens comprising an amino acid sequence sharing at least
XX 70% homology with OP-1, OP-2, CBMP2, Vgl(fx), Vgr(fx),
XX GDF-1(fx), 60A(fx) and at least 80% homology with BMP3(fx),
XX BMP5(fx) and BMP6(fx) are useful for integrating an implanted
XX tooth in a tooth socket and for inhibiting tissue loss associated
XX with periodontal disease or injury.
XX
XX Sequence 1247 BP: 127 A; 494 C; 451 G; 175 T; 0 other;
SQ

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Query Match 19.0%; Score 30.8; DB 15; Length 1247;
 Best Local Similarity 52.3%; Pred. No. 4.5;
 Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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OY 31 ccgagaccacccgctgcccagagagatgagcctgtggaactgtgcttcgcccgc 90
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DB 711 ccgagcagctcgcctgagcgtgctgagcgtgagcccccgcgctcgcgtcgcgcg 770
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OY 91 gagctcattccagagctggaagaaactggaactggaagccgcaatgctgag 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 771 ctggccgagcgcctcgtcgtgagccctgaccccgctgagcccccctgagc 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 151 gagcgagctgc 160
    ||| ||| |||
DB 831 ccgcccgcgcgc 840

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Query Match 19.0%; Score 30.8; DB 1; Length 1247;
Best Local Similarity 52.3%; Pred. No. 0.82; Mismatches 62; Indels 0; Gaps 0;
Matches 68; Conservative 0;

QY 31 ccgagaccacgcgcctgcgaagagatgacgctgtggaacctgtgcttgcgcgcgc 90
DB 711 cccgcgacgctccgctgcgcgcctgaccccccgcgcgccttgcgcgcgcgc 770
QY 91 gagctatctccagctgcggaacctgaacctgagctggaagccgcatagtctgag 150
DB 771 ctgcccagagccttgcgtgctgctgacccctgacccgcttgcaccccttgcgc 830
QY 151 gagcgctgc 160
DB 831 cggccgcccgc 840

RESULT 2

US-08-155-343A-32
Sequence 32, Application US/08155343A
Patent No. 5656593

GENERAL INFORMATION:

APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
TITLE OF INVENTION: REGENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155.343A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION: /product= "GDF-1"

US-08-155-343A-32

Query Match 19.0%; Score 30.8; DB 1; Length 1247;
Best Local Similarity 52.3%; Pred. No. 0.82; Mismatches 62; Indels 0; Gaps 0;
Matches 68; Conservative 0;

QY 31 ccgagaccacgcgcctgcgaagagatgacgctgtggaacctgtgcttgcgcgcgc 90

DB 711 cccgcgacgctccgcttgcgcgcctgaccccccgcgcgccttgcgcgcgcgc 770
QY 91 gagctatctccagctgcggaacctgaacctgagctggaagccgcatagtctgag 150
DB 771 ctgcccagagccttgcgtgctgctgacccctgacccgcttgcaccccttgcgc 830
QY 151 gagcgctgc 160
DB 831 cggccgcccgc 840

RESULT 3

US-08-406-672-32
Sequence 32, Application US/08406672
Patent No. 567484

GENERAL INFORMATION:

APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406.672
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: PENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-060CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION: /product= "GDF-1"

US-08-406-672-32

Query Match 19.0%; Score 30.8; DB 1; Length 1247;
Best Local Similarity 52.3%; Pred. No. 0.82; Mismatches 62; Indels 0; Gaps 0;
Matches 68; Conservative 0;


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; Patent No. 5849686
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: PANG, ROY H. L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,468A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-072FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
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; Query Match          19.0%; Score 30.8; DB 2; Length 1247;
; Best Local Similarity 52.3%; Pred. No. 0.82;
; Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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; QY 31 ccgagaaccacgcctgcacgaagatgagcgtgtggaacctgtccttcgcgcgc 90
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; RESULT 9
; US-08-461-397A-32
; Sequence 32, Application US/08461397A
; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
```

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; APPLICANT: PANG, ROY H. L.
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
;
; US-08-461-397A-32
;
; Query Match          19.0%; Score 30.8; DB 2; Length 1247;
; Best Local Similarity 52.3%; Pred. No. 0.82;
; Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
;
; QY 31 ccgagaaccacgcctgcacgaagatgagcgtgtggaacctgtccttcgcgcgc 90
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; DB 711 ccgagcagccttcgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 770
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; QY 151 gagcgctgc 160
;      || || ||
; DB 831 cggccgcgcgc 840
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; RESULT 10
; US-08-912-088-32
; Sequence 32, Application US/08912088
; Patent No. 5994131
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07190
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: BRAIN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
; OTHER INFORMATION: /note= "GDF-1 cDNA"
; PCT-US93-07190-32

Query Match
Best Local Similarity 19.0%; Score 30.8; DB 5; Length 1247;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 31 ccgaagaccacgcctcctcccaagagatgacgctgtggaactgtgcttgcgcgc 90
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 771 CTGGCCGAGGCGCTGCTGCTGTGACCTGACCGCCGCGCTGTGACCCCTGGCC 830
QY 151 gagcgagctgc 160
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DB 831 CGGCCGCGGC 840

RESULT 15
PCT-US93-07231-32
; Sequence 32, Application PC/TUS9307231
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
; TITLE OF INVENTION: REPAIR
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07231
; FILING DATE: 19930729
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
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```

; NAME: KELLEY, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: BRAIN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
; OTHER INFORMATION: /note= "GDF-1 cDNA"
; PCT-US93-07231-32

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Search completed: June 7, 2001, 00:26:34
Job time: 19737 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:43 ; Search time 3054.04 Seconds
(without alignments)
463.402 Million cell updates/sec

Title: US-09-587-574-8
Perfect score: 162
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues
Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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191:	em_gss_pin2:	459	18	A1272864	A1272864 q143h03.x
192:	em_gss_pro:	487	18	A1307112	A1307112 q189f01.x
193:	em_gss_rod1:	409	8	AA489644	AA489644 aa43d02.s
194:	em_gss_rod2:	460	20	A1419942	A1419942 tg40d01.x
195:	em_gss_rod3:	543	17	A1220032	A1220032 q978h02.x
196:	em_gss_rod4:	591	102	A1818109	A1818109 w427c05.x
197:	em_gss_rod5:	418	103	A1858567	A1858567 w164d08.x
198:	em_gss_vrt1:	391	13	AA884421	AA884421 am16b12.s
199:	em_gss_vrt2:	508	119	AW762829	AW762829 ur66f04.y
200:	em_gss_vrt3:	413	19	A1336613	A1336613 q062c07.x
201:	gb_gss1:	399	8	AA489748	AA489748 aa43d02.r
202:	gb_gss2:	551	13	AA915999	AA915999 oh86g11.s
203:	gb_gss3:	546	23	A1660139	A1660139 web1a09.x
204:	gb_gss4:	408	23	R33823	R33823 yh76f12.r1
205:	gb_gss5:	361	155	AW207598	AW207598 ui-h-B11-
206:	gb_gss6:	285	117	AW566657	AW566657 fk03a11.y
207:	gb_gss7:	345	24	A1742962	A1742962 w976d09.x
208:	gb_gss8:				
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Db	409	CCAAATGCCCAAGTGTCTCTACCTCATTTCCCGAGAACCCACCGCTGCGCAAGAGATGA	350
Oy	62	cgcccttggaacacgtgcttccttcgcgcgcgcagctcaatcctcaggcttgagaactgaac	121
Db	349	CCCCCTGCAACCCGCCACCTTTCAGCTGAGCTGATCTCGACGCTCGAAAAGCTGAAGC	290
Oy	122	tggagcttgaaagccgcacatagctcggagggagcgagctcag	162
Db	289	TGGAGTTGGAGAGCCGCCACAGCTTGGAGAGAGCGCTCGAG	249
RESULT	5		
LOCUS	AI119942/c		
DEFINITION	AI119942	EST	30-MAR-1999
ACCESSION	AI119942	sequence.	
VERSION	AI119942		
KEYWORDS	AI119942.1	GI:4265873	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (Info@image.lln.gov) for further information.		
	Insert Length: 740 Std Error: 0.00		
	Seq primer: -40UP from GIDCO		
	High quality sequence stop: 421.		
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	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NBHL19W, testis NHT, and B-cell		
	NCI-GARP GCBI) were mixed, and ss circles were made in		
	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The diver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I.M.A.G.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bernaldo.		
BASE COUNT	67 a 124 c 162 g 107 t		
ORIGIN			
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Oy	61	acgccttggaacacgtgcttccttcgcgcgcgcagctcaccatcctcaggcttgagaactga	120
Db	361	ACCCCTTGGAACCCGCCACCTTTCAGCTGAGCTGATCTCGAGCTCGAAAAGCTGAAG	302

Oy	121	ctggaagctggaaagccgcacatgcttctgaggagcgtcgag	162
Dd	301	CTGGAGTTGGAGAGCCGCCACACGCTTGAGAGAGCGCCTGCAG	260
RESULT	6		
	A122003/c		
DEFINITION	A1220032	543 bp mRNA	EST 30-NOV-1998
LOCUS	gg78H02.x1 Soares_NFL_T_GBC_SI Homo sapiens cDNA clone		
	IMAGE:1841331 3' similar to Tr:O42400 O42400 AXIN.; ; mRNA		
	sequence.		
ACCESSION	A1220032		
VERSION	A1220032.1	GI:3802235	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CCAP),		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert_Strausberg@nih.gov		
	This clone is available royalty-free through LINT; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Insert length: 752 Std Error: 0.00		
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	a modified polylinker; Site_1: Not I; Site_2: Eco RI;		
	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NBHL19W, testis NHT, and B-cell		
	NCL-CGAP-GCB1) were mixed, and ss circles were made in		
	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The diver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I.M.A.C.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo."		
BASE COUNT	87 a 149 c 176 g 130 t	1 others	
ORIGIN			
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	Best Local Similarity 87.0%; Pred. No. 1.2e-26;		
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Dd	348	ACCACCGTGAAGACCGCCACACCTTTGCACGTAGCTGATCTGCAGAGCTGGAAGAAAGCTGAAG	289
Oy	121	ctggaagctggaaagccgcacatgcttctgaggagcgtcgag	162
Dd	288	CTGGAGTTGGAGAGCGGCCACACAGCCTTGAGAGAGCGCCTGCAG	247
RESULT	7		
	A1818109/c		

LOCUS	A1818109	591 bp	mRNA		EST	21-DEC-1999
DEFINITION	wk27c05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413544	3'				
ACCESSION	A1818109					
VERSION	A1818109.1	GI:5437188				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index Unpublished (1998) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.linnl.gov/dbtpr/image/Image.html Insert Length: 700 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 465. Location/Qualifiers 1..591 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2413544" /clone_lib="NCI CGAP_Brn25" /tissue.type="anaplastic oligodendroglioma" /lab_host="DH10B" /note="Organ: brain; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5' TGTTAACCAATCTGAAGTGGAGCGCCGCAGTAGGTCTTTTTTTTTTTTTTTT T 3']: double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."					
BASE COUNT	102 a	159 c	192 g	138 t		
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Gaps	0;					
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QY	61 acgcctgtgaacctgcgtccttcgccgcgcgagagcatctccagcttgagagaactgaaa	120				
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DEFINITION	w164d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429679	3'				

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Similar to TR:088566 088566 CONDUCTIN..	..	mRNA sequence.		
AT85867	AT85867.1	GI:5512183		
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
SOURCE				
BASE COUNT				
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Best Local Similarity	83.6%;	Pred. No. 1.7e-23;		
Matches 133; Conservative	0;	Mismatches 26; Indels 0; Gaps 0		
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Db	418	AAGGGCGAAATGTCTACTCACTCAATTCGCCGAGAACCCACGCGCTGCCAAGTGAAGTGACC	359	
Y	64	ccttggaacctgctgctgcgcgcgcgcgcacatctccagctggaagaactgaaatg	123	
Db	358	CCCGTGAATTCGCCACACTTTCAGAGCTGAGTCACTTCGAGGCTGGAAAAGCTGAAGCTG	299	
Y	124	gaagctggaagccgcacatagctctgagagagcgagctgacg	162	
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DEFINITION	AA884421	391 bp	mRNA	27-MAR-1998
	am16b12.s1 Soares.NFL.T.GBC.S1 Homo sapiens cDNA clone			
	IMAG:146675 3' similar to TR:042400 042400 AXIN..			
	sequence.			

[illegible]

REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Other ESTs: ur66f04.x1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LNL at:
image.llnl.gov/image/html/lresources.shtml
MGI:1058019
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Glbco
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
library constructed by Life Technologies. Investigators
providing samples: lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgene model: Xu et al., Nature Genetics
22, 37-43 (1999)."
BASE COUNT 118 a 154 c 108 g 128 t
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Query Match 62.3%; Score 101; DB 119; Length 508;
Best Local Similarity 100.0%; Pred. No. 8,4e-19;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 43 gccgcgcgaagagatgacgcctgtgaacatgtctgcctgcgcgcgagctatctcc 102
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Db 101 GCGCTGCCCAAGAGATACGCGCTGTGAACTGCTGCTTCGCCGCCGAGCTCATCTCC 42
Oy 103 aggcctgagaacttgaacttgaagcttgaagacgcgcataag 143
|||||
Db 41 AGGCTGGAGAAACTGAACCTGGAGCTGGAAGAGCCGCATAG 1
RESULT 11
LOCUS A1336613/c EST 13-FEB-1999
DEFINITION similar to TR:042400 042400 AXIN.; mRNA sequence.
ACCESSION A1336613
VERSION A1336613.1 GI:4073540
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 761 Std Error: 0.00
 Seq primer: -400P from Gibco.

FEATURES

SOURCE

1. 413
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1913100"
 /clone_1lb="NCI-CGAP_C08"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"

/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

56 a 116 c 156 g 85 t

ORIGIN

Query Match Best Local Similarity 60.6%; Score 98.2; DB 19; Length 413;

Matches 109; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 36 aaccacgcgtgcacccaagatgacgctgtggaacctgtccttcgcccgagct 95

Db 413 AACCCACGCGCTGCCAAGAGATGACCCCGCTGGACCCGCTTGACGCGAGCT 354

OY 96 catctccagcgtcggaagaactgaactgagctgtgaaagccgacatgtctgagagagcg 155

Db 353 GATCTCGAGGCTGGAAGCTGACGTGGAGAGCCGCCACAGCCTTGAGAGAGCG 294

OY 156 gctcgag 162

Db 293 CCTGCAG 287

RESULT 12

AA489748 399 bp mRNA EST 11-AUG-1997

LOCUS aa43d02.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:823683

ACCESSION AA489748

VERSION AA489748.1 GI:2219350

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 399)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kuebb, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, T., Wylie, T., Waterston, R. and Wilson, R.
 Contact: Wilton RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

FEATURES

SOURCE

1. 399
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:823683"
 /clone_1lb="Soares_NHMPu_S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_host="DH10B"

/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus 2NbHM, and fetal heart 2NbHM) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT

97 a 106 c 110 g 86 t

ORIGIN

Query Match Best Local Similarity 55.1%; Score 89.2; DB 8; Length 399;

Matches 97; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 gccaatgccaagatgctctctacatttccgagaccacgcctgcacgaagatg 60

Db 290 GCCAATGCGCAGAGTGTCTTACCTCATTTCCCGAACCACCGCTCCGACGAGATG 349

OY 61 acgcctgtggaacctgtcgtccttcgacgagctcattcctcagagctga 110

Db 350 ACCCCGTGGACCCGCCACCTTTCAGCTGAGTGTGAGGCTGGA 399

RESULT 13

AA915999/c 546 bp mRNA EST 29-APR-1998

LOCUS oh86g11.s1 NCI-CGAP_C08 Homo sapiens cDNA clone IMAGE:1473956 3'

ACCESSION AA915999

VERSION AA915999.1 GI:3055391

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 546)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 524 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 73.
 Location/Qualifiers

1. 546

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1473956"
/clone_11d="NCI_CGAP_C08"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo (dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Benito Soares and M. Fatima Bonaldo."

BASE COUNT 95 a 133 c 186 g 131 t 1 others

ORIGIN

Query Match 52.2%; Score 84.6; DB 13; Length 546;
Best Local Similarity 74.8%; Pred. No. 4,1e-14;
Mismatch 119; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

0y 3 caatgagcaagtgtctcaactcatttcgcgaagaacacacgcgcctgcgaagagatgac 62
|||||
Db 447 CAATTGCCAAGGTATTCATCA-TTCCCGGAACCCACCGCTTGCAGAGAGATGAC 389
|||||

0y 63 gcctgagcaagctgtcgtccttcgcgcgcgcagctccacagctcgagaaactgaaact 122
|||||
Db 388 CCCCATGAAACCGCTACTTTTGCAGCTGAGACTGATCTCGACCTTGGAAGAGCTAAAGCT 329
|||||

0y 123 ggaagctgaaagcgcgcatagtctgagagagcgcgctga 161
|||||
Db 328 GGAGTTGGAGAGCCCGACGCTGAGGAGAGATCCTGCA 290
|||||

RESULT 14
LOCUS A1660139/c
DEFINITION
A1660139 408 bp mRNA EST 18-DEC-1999
w61ja09.x1 Soares_thymus.NHFT Homo sapiens cDNA clone
IMAGE:2345560 3' similar to TR:088566 088566 CONDUCTIN. ; mRNA
sequence.
A1660139
A1660139.1 GI:4763709
EST.
human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 408)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 788 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 333.
Location/Qualifiers
1. 408
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2345560"
/clone_11d="Soares_thymus_NHFT"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
/note="Organ: thymus; pooled; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

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	Best Local Similarity	76.5%;	Pred. No. 1.5e-13;			
	Matches 114;	Conservative	0;	Mismatches 34;	Indels 1;	Gaps 1;
Oy	14	tgtctactcatttccgagaacccccgcgccttcaccaagatgatgacctgttgaaac	73			
Db	407	TTCCTTTCCAGCCTGCTGTAGAGAACCACGCCCGTCCCAAGAGATGAC -CCCGTGAAAC	349			
Oy	74	ctgtgctcttcgccgcgaagtcatctccaggctggagaaactgaactgtagctcgaaa	133			
Db	348	CCGCACCTTCGCAAGCTGAGCTGACTGCTGAGAGCTGGAAAACCTGAAGCTGAGTTGGACA	289			
Oy	134	gcccaccatgctcagagagagcgcgctcgag	162			
Db	288	GCCGCCACAGCCTGGAGAGCGCCTGACG	260			
RESULT	15					
LOCUS	R33823					
DEFINITION	R33823	361 bp	mRNA	EST	28-Apr-1995	
ACCESSION	R33823	y/h8f12.r1 Soares placenta ND2HP	Homo sapiens	cdna clone		
VERSION	R33823	IMAGE:135887.5,	mRNA sequence.			
KEYWORDS	R33823.1	GI:789681				
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
	1 (bases 1 to 361)					
	Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,					
	Chissee,S., Dietrich,N., Dubugue,T., Favellio,A., Gish,W., Hawkins					
	,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore					
	,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,					
	Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E.,					
	Underwood,K., Wohlmann,P., Waterston,R., Wilson.R. and Marra,M.					
	Generation and analysis of 280,000 human expressed sequence tags					
	Genome Res. 6 (9), 807-828 (1996)					
TITLE	97044478					
JOURNAL	Contact: Wilson RK					
MEDLINE	Washington University School of Medicine					
COMMENT	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108					
	Tel: 314 286 1800					
	Fax: 314 286 1810					
	Email: est@watson.wustl.edu					
	Insert Size: 445					
	High quality sequence stops: 235					
	Source: IMAGE Consortium, LLNL					
	This clone is available royalty-free through LLNL ; contact the					
	IMAGE Consortium (info@image.llnl.gov) for further information..					
	Seq primer: M13RP1					
	High quality sequence stop: 235.					
FEATURES	location/Qualifiers					
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	/db_xref="taxon:9606"					
	/clone="IMAGE:135887"					
	/clone_lib="Soares placenta ND2HP"					
	/sex="Female"					
	/der_stage="placenta obtained at birth (full term)"					

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/lab host="DH10B (ampicillin resistant)"
/Note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer [5'
AACTGGAAGAATTCGGCGCCGAGGAAATTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaudo. "

```

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BASE COUNT      69 a      109 c      111 g      66 t      6 others
ORIGIN

```

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Query Match      48.9%; Score 79.2; DB 155; Length 361;
Best Local Similarity 82.6%; Pred. No. 1.3e-12;
Matches 90; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 54 ggagatgacgacctgtggaacctgtgaccttcgcccgaagctcatctccaggctgagaa 113
DB 11 GGAGATGACCCCCCGTGGACCCCGCCACCTTTGCACTGAGCTGNTCTCGAGGCTGGAAGA 70
QY 114 acctgaactggagcttgaagagccgcacatagcttgaagagcgagctgcag 162
DB 71 GCTGAAGCTGGAGTGGAGAGCGCCACAGCCTGAGAGAGAGCGCCTGCAG 119

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Search completed: June 6, 2001, 23:00:46
Job time: 15530 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:35:43 ; Search time 4956.99 Seconds
(without alignments)
615.859 Million cell updates/sec

Title: US-09-587-574-9
Perfect score: 207
Sequence: 1 cagatccggagagatgaaga.....gtcaagccacggtccgcg 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
6: gb_in3: *
7: gb_cm: *
8: gb_ov: *
9: gb_pat1: *
10: gb_pat2: *
11: gb_ph: *
12: gb_pl1: *
13: gb_pl2: *
14: gb_pl3: *
15: gb_pl4: *
16: em_ba1: *
17: em_ba2: *
18: em_fun: *
19: em_htgo_hum: *
20: em_htgo_inv: *
21: em_htgo_rtd: *
22: em_htg_hum1: *
23: em_htg_hum2: *
24: em_htg_hum3: *
25: em_htg_hum4: *
26: em_htg_hum5: *
27: em_htg_hum6: *
28: em_htg_hum7: *
29: em_htg_hum8: *
30: em_htg_inv1: *
31: em_htg_inv2: *
32: em_htg_other: *
33: em_htg_rtd: *
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69: gb_htg10: *
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71: gb_htg12: *
72: gb_htg13: *
73: gb_htg14: *
74: gb_htg15: *
75: gb_htg16: *
76: gb_htg17: *
77: gb_htg18: *
78: gb_htg19: *
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82: gb_htg23: *
83: gb_htg24: *
84: gb_htg25: *
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86: gb_pr2: *
87: gb_pr3: *
88: gb_pr4: *
89: gb_pr5: *
90: gb_pr6: *
91: gb_pr7: *
92: gb_pr8: *
93: gb_pr9: *
94: gb_ro1: *
95: gb_ro2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	100.0	207	9 A98524	A98524 Sequence 9
2	207	100.0	2825	9 A98521	A98521 Sequence 6
3	207	100.0	2825	94 AF073788	AF073788 Mus muscu
4	207	100.0	3016	94 AF205889	AF205889 Mus muscu
5	195.4	94.4	191041	69 AC024114	AC024114 Mus muscu
6	192.6	93.0	3216	94 AF017757	AF017757 Rattus no
7	133.4	64.4	2104	89 AK025718	AK025718 Homo sapi
8	133.4	64.4	2538	88 AF205888	AF205888 Homo sapi
9	133.4	64.4	3072	88 AF078165	AF078165 Homo sapi
10	72.6	35.1	3485	8 AB032263	AB032263 Danto rer
11	44.8	21.6	3066	8 AB032262	AB032262 Danto rer

12 43.8 21.2 3156 8 AF009012 AF009012 Gallus ga
13 42 20.3 2529 8 AF097313 AF097313 Xenopus l
14 38.4 18.6 3761 9 AF009011 AF009011 Mus muscu
15 37.2 18.0 171415 62 AC011505 AC011505 Homo sapi
16 37.2 18.0 229061 86 AC007786 AC007786 Homo sapi
17 37 17.9 227243 86 AC008569 AC008569 Homo sapi
18 36.8 17.8 3460 94 AF017756 AF017756 Rattus no
19 36.2 17.5 132830 62 AC011051 AC011051 Homo sapi
20 36 17.4 453 12 AF057337 AF057337 Aspergill
21 35.4 17.1 151132 79 AL353052 AL353052 Homo sapi
22 35 16.9 2416 8 CHK3ACOL M83179 Gallus gall
23 35 16.9 2801 8 GGCOLA3IX X64712 G. gallus mr
24 34.8 16.8 22029 91 HS419C1 299754 Human DNA s
25 34.8 16.8 133069 70 AC026836 AC026836 Homo sapi
26 34.8 16.8 133019 80 AL355574 AL355574 Homo sapi
27 34.8 16.8 187272 74 AC069076 AC069076 Homo sapi
28 34.8 16.8 278229 96 AC074322 AC074322 Homo sapi
29 34.4 16.6 21718 94 MMU04056 U04056 Mus musculu
30 34.2 16.5 39203 90 AP001066 AP001066 Homo sapi
31 34.2 16.5 86742 68 AC023223 AC023223 Homo sapi
32 34.2 16.5 110000 60 AC003656 AC003656 Continuation (5 of
33 34.2 16.5 148845 90 AP001067 AP001067 Homo sapi
34 34.2 16.5 162738 71 AC021291 AC021291 Homo sapi
35 34.2 16.5 183000 69 AC025134 AC025134 Homo sapi
36 34.2 16.5 187114 71 AC026998 AC026998 Homo sapi
37 34.2 16.5 214561 65 AC016713 AC016713 Homo sapi
38 34.2 16.5 340000 90 AP001754 AP001754 Homo sapi
39 34 16.4 4036 85 AB037776 AB037776 Homo sapi
40 34 16.4 146393 70 AC026791 AC026791 Homo sapi
41 34 16.4 154101 80 AL357565 AL357565 Homo sapi
42 34 16.4 167725 82 AL513485 AL513485 Homo sapi
43 34 16.4 176422 66 AC019138 AC019138 Homo sapi
44 34 16.4 177826 65 AC016852 AC016852 Homo sapi
45 34 16.4 186797 67 AC021965 AC021965 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS A98524 207 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 9 from Patent WO9911780.
ACCESSION A98524
VERSION A98524.1 GI:6781610
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 207)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 9 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source Location/Qualifiers
1..207
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 44 a 73 c 59 g 31 t
ORIGIN

Query Match 100.0%; Score 207; DB 9; Length 207;
Best Local Similarity 100.0%; Pred. No. 5, 3e-42;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagatccggagagatgaagaagaaggaggtctagcagagccctgagctcagggatgga 60
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Db 1 CAGATCCGGAGGAGATGAAGAAAGAGGGGTCTGAGCAGCCCTGAGCTCAGGGATGGA 60
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QY 61 gcaccggtccagagccccctcgccctctaccctccgagcagctatgaagagaccacaa 120
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Db 61 GCACCGGTCCAGCACACCCCTGGCCCTCTACCCCTCCGCGAGCTATGAAGAGACCCACAA 120
QY 121 accatttggagacacacacctctcagggctcctcaagaccaccccggtctcaatccccgt 180
|||||
Db 121 ACCATTTTGGAGACACACCTCTCCAGGGGTCTCAAGACCCCGGCTGTCAATCCCCCTGT 180
QY 181 gtgggtcgctacagccacaggtcccg 207
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Db 181 GTGGGTCTGCTACAGCCACGAGTCCCGC 207

RESULT 2
LOCUS A98521 2825 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 6 from Patent WO9911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TUMOR ILLNESSES
JOURNAL Patent: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

Query Match 100.0%; Score 207; DB 9; Length 2825;
Best Local Similarity 100.0%; Pred. No. 3e-42;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1403 CAGATCCGGAGGAGATGAAGAAAGAGGGGTCTGAGCAGCCCTGAGCTCAGGGATGGA 1462
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QY 61 gcaccggtccagagccccctcgccctctaccctccgagcagctatgaagagaccacaa 120
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Db 1463 GCACCGGTCCAGCACACCCCTGGCCCTCTACCCCTCCGCGAGCTATGAAGAGACCCACAA 1522
|||||
QY 121 accatttggagacacacacctctcagggctcctcaagaccaccccggtctcaatccccgt 180
|||||
Db 1523 ACCATTTTGGAGACACACCTCTCCAGGGGTCTCAAGACCCCGGCTGTCAATCCCCCTGT 1582
QY 181 gtgggtcgctacagccacaggtcccg 207
|||||
Db 1583 GTGGGTCTGCTACAGCCACGAGTCCCGC 1609

RESULT 3
LOCUS AF073788 2825 bp mRNA ROD 13-JUL-1998
DEFINITION Mus musculus conductin mRNA, complete cds.
ACCESSION AF073788
VERSION AF073788.1 GI:3309246
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 2825)
AUTHORS Behrens, J., Jerchow, B.-A., Wurtz, M., Grimm, J., Asbrand, C., Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W.
TITLE Functional interaction of an axlin homology, conductin, with beta-catenin, APC, and GSK3beta
JOURNAL Science 280 (5363), 596-599 (1998)

MEDLINE 9821239
REFERENCE 2 (bases 1 to 2825)
AUTHORS Behrens,J., Jerchow,B.-A. and Birchmeier,W.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany
FEATURES
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1..2825
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215..2737
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IKKQOIGSYMFDOAQTEIOAYMEENAYOVFLTDYILEVRSRGENTAYMSGIGSL
KVLGCLPTLNEEBMTCADLKCKISPTVVGISLTTLATASVSTETARENGFRSK
SDPNPVHVGSGVFPAPATSSANDSLSDALTDDSMSTSDVDVPPYRMGSKQLO
REHNSVANGQVSLPHFPRTRRLPKEMTPVEPAFAELISRLKLELESRLSLE
ERLQOIREDEKESGEQALSRDGAPOVHPALLPSSYEEDPOTLDDHLSRLVLT
GCOSGVGRYSRPSRPHNHQHHOQCHTLLSTGKLPYACPLGKSLTKOT
TKVHHNHYNHNAVPKTEKEIEAETORVRCPCGCTDYCYCSKSHPKAPEPLGE
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PPLTPNLTQLEACRLAEYSKPOKORCVASQORDRNHNSAAGACASPPANSLA
PEDHKEPKLASVHALQSELVYTFEGEELIPYRMKLAOSLTGLGHKEQLSKNGY
RYFFKASDEFACGAVFEIWDDEVLPYMEGRILGKVERID"

BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3e-42;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgaatccggaggatgaagaaggagggtctgagcagccctgagctcagcgatga 60
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DB 1403 CAGATCCGGAGATGAAGAAAAGAGGGGTCTGACGACGCCCTGAGTCACGGATGA 1462
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QY 61 gcaaccggtccagacaccccttgccctcctacccctcggaagctataaagagaccacaa 120
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DB 1463 GCACCGGTCCACACCCCTTGCCCTCCACCTCCGCGACGATGAAAGAGCCACCA 1522
|||
QY 121 accatttgaagacacactctcgaaggtctcgaagaccctcggtctgaatccctggt 180
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DB 1523 ACCATTTTGAGACGACACCTCTCCAGGTCCTCAAGACCCCGCGCTGTCAATCCCTGCT 1582
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QY 181 gtgggtcgctacagaccagctccgcg 207
|||
DB 1583 GTGGGTCTGCTACAGCCACGCTCCGC 1609
|||

RESULT 4
LOCUS AF205889 3016 bp mRNA ROD 03-JAN-2000
DEFINITION Mus musculus Axlin2 (Axlin2) mRNA, complete cds.
ACCESSION AF205889
VERSION AF205889.1 GI:6653585
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3016)
Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Jenkins,N.A., Waburton,D. and Costantini,F.
Properties of mouse Axlin2 and human Axlin1: Chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3016)
AUTHORS Zhang,T. and Costantini,F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 M168th St. HSC 1416, New York, NY 10032, USA
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55..2577
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IKKQOIGSYMFDOAQTEIOAYMEENAYOVFLTDYILEVRSRGENTAYMSGIGSL
KVLGCLPTLNEEBMTCADLKCKISPTVVGISLTTLATASVSTETARENGFRSK
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REHNSVANGQVSLPHFPRTRRLPKEMTPVEPAFAELISRLKLELESRLSLE
ERLQOIREDEKESGEQALSRDGAPOVHPALLPSSYEEDPOTLDDHLSRLVLT
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TKVHHNHYNHNAVPKTEKEIEAETORVRCPCGCTDYCYCSKSHPKAPEPLGE
EQOSKSRPHSAQSIKSYPLESARAAPGERVSRHHLGASGHSVARAHPTOPAM
PPLTPNLTQLEACRLAEYSKPOKORCVASQORDRNHNSAAGACASPPANSLA
PEDHKEPKLASVHALQSELVYTFEGEELIPYRMKLAOSLTGLGHKEQLSKNGY
RYFFKASDEFACGAVFEIWDDEVLPYMEGRILGKVERID"

BASE COUNT 766 a 858 c 837 g 555 t
ORIGIN

Query Match 100.0%; Score 207; DB 94; Length 3016;
Best Local Similarity 100.0%; Pred. No. 3e-42;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1243 CAGATCCGGAGATGAAGAAAAGAGGGGTCTGACGACGCCCTGAGTCACGGATGA 1302
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QY 61 gcaaccggtccagacaccccttgccctcctacccctcggaagctataaagagaccacaa 120
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DB 1303 GCACCGGTCCACACCCCTTGCCCTCCACCTCCGCGACGATGAAAGAGCCACCA 1362
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QY 121 accatttgaagacacactctcgaaggtctcgaagaccctcggtctgaatccctggt 180
|||
DB 1363 ACCATTTTGAGACGACACCTCTCCAGGTCCTCAAGACCCCGCGCTGTCAATCCCTGCT 1422
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QY 181 gtgggtcgctacagaccagctccgcg 207
|||
DB 1423 GTGGGTCTGCTACAGCCACGCTCCGC 1449
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RESULT 5
LOCUS AC024114 191041 bp DNA HTG 06-NOV-2000
DEFINITION Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
ACCESSION AC024114
VERSION AC024114.8 GI:11094615
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191041)

AUTHORS
 Metzker, M. L., Lewis, L. R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hoges, M., Hosok, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kover, C., Liu, J., Liu, W., Louised, H., Lozado, R. T., Martin, R., Massey, E., McLeod, M. P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, R., Muzny, D. M., Rives, R., Scherer, S., Sodergren, E., Weinstein, G., Worley, K. and Glbbs, R.

TITLE
 Direct Submission

REFERENCE
 Unpublished
 2 (bases 1 to 191041)

AUTHORS
 Worley, K. C.

JOURNAL
 Direct Submission
 Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Nov 4, 2000 this sequence version replaced g1:9929587.

COMMENT
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: MACA
 Center clone name: RP23-278J12
 ----- Summary Statistics
 Sequencing vector: M13: 108821
 Chemistry: Dye-primer Bodypy: 95% of reads
 Assembly: Dye-terminator Big Dye: 5% of reads
 Assembly program: Phrap: version 0.990329
 Consensus quality: 158769 bases at least Q40
 Consensus quality: 172780 bases at least Q30
 Consensus quality: 179030 bases at least Q20
 Estimated insert size: 180377; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-gel estimation
 Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html).
 NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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 19344: contig of 19344 bp in length
 19345 19444: gap of unknown length
 19445 33763: contig of 14319 bp in length
 33764 33863: gap of unknown length
 33864 47738: contig of 13875 bp in length
 47739 47838: gap of unknown length
 47839 59611: contig of 11773 bp in length
 59612 59711: gap of unknown length
 59712 67897: contig of 8186 bp in length
 67898 67997: gap of unknown length
 67998 77929: contig of 9932 bp in length
 77930 78029: gap of unknown length
 78030 86605: contig of 8576 bp in length
 86606 86705: gap of unknown length
 86706 93904: contig of 7199 bp in length
 93905 94004: gap of unknown length
 94005 104236: contig of 10232 bp in length
 104237 104336: gap of unknown length
 104337 113241: contig of 8905 bp in length

113242 113341: gap of unknown length
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 * 120172 120271: gap of unknown length
 * 120272 125989: contig of 5718 bp in length
 * 125990 126089: gap of unknown length
 * 126090 131869: contig of 5780 bp in length
 * 131870 131970: gap of unknown length
 * 131970 132994: contig of 7325 bp in length
 * 132995 133295: gap of unknown length
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 * 146007 146106: gap of unknown length
 * 146107 150788: contig of 4682 bp in length
 * 150789 150888: gap of unknown length
 * 150889 156925: contig of 6037 bp in length
 * 156926 157025: gap of unknown length
 * 157026 161170: contig of 4145 bp in length
 * 161171 161270: gap of unknown length
 * 161271 164311: contig of 3041 bp in length
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 * 167355 167454: gap of unknown length
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 * 171392 174233: contig of 2842 bp in length
 * 174234 174333: gap of unknown length
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 * 179403 179502: gap of unknown length
 * 179503 182420: contig of 2918 bp in length
 * 182421 182520: gap of unknown length
 * 182521 184923: contig of 2403 bp in length
 * 184924 185023: gap of unknown length
 * 185024 187054: contig of 2031 bp in length
 * 187055 187154: gap of unknown length
 * 187155 188272: contig of 1118 bp in length
 * 188273 189634: gap of unknown length
 * 189635 189734: contig of 1262 bp in length
 * 189735 191041: contig of 1307 bp in length.

FEATURES
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BASE COUNT 49790 a 43523 c 42989 g 51816 t 2923 others

ORIGIN

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 Best Local Similarity 99.5% Pred. No. 9.6e-40;
 Matches 196; Conservative 0; Mismatches 1; Indels 0;

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 Db 31065 AGGATGAAGAAAGAGAGGGGCTGAGCAGCGCCCTGAGCTCAGCGATGAGACACCGGTCC 31124

QY 71 agcaccctcgcctcctcctacccctcgcgcagctatgaagagagaccacaacccatttgg 130
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 Db 31125 AGCACCCTCGCCCTCTACCTCCGCGACCTGTAAGAGAGACCCACCAACCATTTTGG 31184

QY 131 acgaccactctcagagctcctcagagaccccgctgtcaatccctcgtgtgtgtgct 190
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 Db 31185 ACGACCACTCTCAAGAGGCTCTCAAGACCCCGCTGTCAATCCCTGTGTGGTGGCT 31244

QY 191 acagccacggtccgcg 207
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 Db 31245 ATAGCCACGCTCCCGC 31261

RESULT 6
 AF017757

LOCUS AF017757 3216 bp mRNA ROD 24-APR-1998
 DEFINITION Rattus norvegicus GSK-3beta interacting protein Axin mRNA, complete cds.
 ACCESSION AF017757
 VERSION AF017757.1 GI:3080758
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 3216)
 Yamamoto, H., Kishida, S., Uochi, T., Ikeda, S., Koyama, S., Asashima, M. and Kikuchi, A.
 Axin, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos
 Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
 98226558
 2 (bases 1 to 3216)
 Yamamoto, H., Ikeda, S., Mural, H., Kishida, S. and Kikuchi, A.
 Direct Submission
 Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734, Japan
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 BASE COUNT 860 a 914 c 872 g 570 t
 ORIGIN
 Query Match 93.0%; Score 192.6; DB 94; Length 3216;
 Best Local Similarity 95.7%; Pred. No. 1.2e-38;
 Matches 198; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 7
 LOCUS AK025718
 DEFINITION Homo sapiens cDNA: FLJ22065 fis, clone HEP10566, highly similar to AF078165 Homo sapiens conductin mRNA.
 ACCESSION AK025718
 VERSION AK025718.1 GI:10438327
 KEYWORDS Oligo capping: fis (full insert sequence).
 SOURCE Homo sapiens hepatoma cell_line:HEPG2 cDNA to mRNA, clone_1b:HEP clone:HEP10566.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (sites)
 Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
 MEDO human cDNA sequencing project
 Unpublished (2000)
 2 (bases 1 to 2104)
 Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
 Direct Submission
 Submitted (29-AUG-2000) to the DDBJ/EMBL/Genbank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
 MEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
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 Best Local Similarity 77.8%; Pred. No. 9.3e-24;
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RESULT 8
AF205888 2538 bp mRNA PRI 03-JAN-2000
LOCUS Homo sapiens AXIN2 (AXIN2) mRNA, complete cds.
DEFINITION AF205888
ACCESSION AF205888.1 GI:6653583
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2538)
AUTHORS Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
Tenkins,N.A., Warburton,D. and Costantini,F.
TITLE Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2538)
AUTHORS Zhang,T. and Costantini,F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HSC 1416, New York, NY 10032, USA
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BASE COUNT 617 a 724 c 724 g 473 t
ORIGIN
Query Match 64.4%; Score 133.4; DB 88; Length 2538;
Best Local Similarity 77.8%; Pred. No. 8.9e-24;
Matches 161; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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Db 1415 ACGTACTGACATCATCCCTGTCACAGGTCCTCAAGACCCCTGCTGCCAGTCTCCGGGC 1474
QY 181 gTgggtcgtctacagccacaggtccgcg 207
Db 1475 GTAGCCCGCTATAGCCCTCGCTCCGC 1501
RESULT 9
AF078165 3072 bp mRNA PRI 21-MAR-1999
LOCUS Homo sapiens conductin mRNA, complete cds.
DEFINITION AF078165
ACCESSION AF078165.1 GI:4454790
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3072)
AUTHORS Mal,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.
TITLE Cloning of the human homolog of conductin (AXIN2), a gene mapping
to chromosome 17q23-q24
JOURNAL Genomics 55 (3), 341-344 (1999)
REFERENCE 2 (bases 1 to 3072)
AUTHORS Mal,M., Qian,C., Smith,D.I. and Liu,W.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic,
200 First Street SW, Rochester, MN 55905, USA
FEATURES
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VYCGYLPITNEEEMTCADFKCKLSPTVVGSSKTLRAFSYRSTETVDSGRKRS
DPVNPYHIGSVFAPATISANDSEISSALDDSMSTDSVDGIPIYRVGSKQLOK
EMHRSVKANGRYSLPFRTHRLPKEMTPVEPATFAELLISLEKLELSRHLSE
RLOQIREDEBERGSELTINSREGAPTOHPLSLPGSYEDPOTLIDHLSRYLTPG
COSPGVGRYSRPSRSDPHNNHSHQYHSLPPGKLPALASPGACPLGGGKGYTKO
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BOFGQSTKKAAPLESARSSPGRARHNMCGSHRPTPRALPTPODAMPSELTP
POTLAHLEACGRILAEVSKPRQRCVVASOORDRHSHTVTCGATPESNPSTLAPRDK
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BASE COUNT 769 a 838 c 883 g 582 t
ORIGIN
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Query Match 64.4%; Score 133.4; DB 88; Length 3072;
Best Local Similarity 77.8%; Pred. No. 8.6e-24;
Matches 161; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 cagatccggaagatgaagaagaaggaggtctgagcagccctgagctcagggatgga 60
Db 1278 CAGATCCGAGAGATGAGAAGAGAGGGGCTCCGAGCTCACACTCAATTCGGGAGGGG 1337
QY 61 gcaaccggtcagacacccccctgacctctaccctccggcagctatgaaagagaccaca 120
Db 1338 GCGCCACAGACACCCCTCTCCCTACTGCTCCGACCTACGAGGAGAACCCCGAG 1397
QY 121 acaatttggagcacacctctcagggtctcctcaagaccccccggtctgaatccctgt 180
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[illegible]

	RESULT	13
Locus	AF097313	Xenopus laevis axin mRNA, complete cds.
DEFINITION	Xenopus laevis axin mRNA, complete cds.	VRT
ACCESSION	AF097313	16-MAR-1999
VERSION	AF097313.1	GI:3834642
SOURCE	African clawed frog.	
ORGANISM	Xenopus laevis	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;	
TITLE	Xenopodinae; Xenopus.	
JOURNAL	1 (bases 1 to 2529)	
MEDLINE	Hedgepeth,C.M., Deardorff,M.A. and Klein,P.S.	
REFERENCE	Xenopus axin interacts with glycogen synthase kinase-3 beta and is	
AUTHORS	expressed in the anterior midbrain	
TITLE	Mech. Dev. 80 (2), 147-151 (1999)	
JOURNAL	2 (bases 1 to 2529)	
MEDLINE	Hedgepeth,C.M., Deardorff,M.A. and Klein,P.S.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (06-OCT-1998) Medicine, University of Pennsylvania	
TITLE	Medical School, 415 Curie Blvd., Philadelphia, PA 19104, USA	
JOURNAL	Location/Qualifiers	
FEATURES	1..2529	
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	1..2529	
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	/product="axin"	
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	KNYDSNDSGTGKGPSTLPFLNDEEMRCDDGGEHERERKCIPSSLFSOKLADSS	
	SHCAGSNRRILDGREFRPTWEVNPYPVTGYAGAATVANDSEQSSMSDAJTM	
	LTDSEVDGIPIPYRLKHFRREMEOESANGSPRIPIRTYHMPEVDIVDEKEFAELE	
	IISLEGVLDRDEADKLLEERLKVRYAEVGWDGVSSPVYSHLPGSRPHNHNS	
	YSEHGVMGOIRAHNEEPESILDEHYEAVRGDDTCOSPGVGHSPKRSRDPDHLSKT	
	LGSLGITMGCHGHSKSKTAQVDSGNHHNKHYNNHNHNGCYPKQIDGESQR	
	OTNPVYNESHNTAKTSRNVAESMGMARNPDLSLTSEKVSMLKRNRKADLDGASE	
	ASHMPVVPEDSERHKQLIOWIMGEKEI IIRKKSNSHSSSAKKOPELARPLSIEE	
	PGAHVWPWSAQLRWVPOSHPIIDPTMPNPAPNPLQLVSKGARLEEEREKNAKK	
	POKORLKPORKNVASQPQNDNIIVAYVFCEGDIPIYRTMVAGRVTTLGQFEELLTKK	
	NYRYFPKVSDEFFCGVVEEVREDMTLPIYEERIIGOVEKID"	
BASE COUNT	761 a 602 c 635 g 531 t	
ORIGIN		
Query Match	20.3%; Score 42; DB 8; Length 2529;	
Best Local Similarity	62.3%; Pred. No. 0.76;	
Matches	66; Conservative 0; Mismatches 40; Indels 0; Gaps 0;	
Oy	102 ctatgaagagaaccacaacatttggagaccacctctcagggtccctaagaagccc	161
Db	1392 CCACAGAGAAAATTCGGGATCATTTCTGGATGAAACAGTGACGCTGTATTGAAAAACC	1451
Oy	162 cgagctcaatccccggtgttggtgcgtctaaagccacagttcccg	207
Db	1452 GGCGTCCAGTCCCTGGGACTGAGACGTCAITCCCCCAAATATCCC	1497
RESULT	14	


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* 72481 72580: gap of unknown length
* 72581 88457: contig of 15877 bp in length
* 88458 88557: gap of unknown length
* 88558 101414: contig of 12857 bp in length
* 101415 101514: gap of unknown length
* 101515 115884: contig of 14370 bp in length
* 115885 115984: gap of unknown length
* 115985 133510: contig of 17526 bp in length
* 133511 133610: gap of unknown length
* 133611 151017: contig of 17407 bp in length
* 151018 151117: gap of unknown length
* 151118 171415: contig of 20298 bp in length.

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/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2081K17"
/clone_lib="Caltech human BAC library D"

BASE COUNT 43300 a 41368 c 40333 g 44601 t 1813 others
ORIGIN

Query Match 18.0%; Score 37.2; DB 62; Length 171415;
Best Local Similarity 51.9%; Pred. No. 4.8;
Matches 84; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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OY 9 ggaagatgaagaagaaggaggggtctgagcagggcctgaagtcacgggatgagcacccggt 68
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4476 GGAGAGGCGCACAGATGAGTGTATCCATACAGAGAGAGTGGAGAGAGTGGCGCACCACT 4417
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 69 ccagcaccccccctggccctctaccctcgcgcagctatgaagaggaaccacaacattt 128
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4416 CCAGTGGCCCCACCAAGTCCCGTAACCTACACTAGCACTGAAGAGCCCTGCACCTACACCATG 4357
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 129 ggaagacacacctctccagggtctcctaagaagccccggcgtgtca 170
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4356 GGATCTGCACATCACCAAGCCTCCAGGCCATACAGACCTCCA 4315
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Search completed: June 7, 2001, 00:36:12
Job time: 20986 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:31:54 ; Search time 276.75 Seconds
(without alignments)
436.649 Million cell updates/sec

Title: US-09-587-574-9

Perfect score: 207

Sequence: 1 cagctccgggggagatgaaga.....gtctacagccacggtccgcg 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : N_Geneseq_0401:*

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2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	207	100.0	2523	20	X23370
2	207	100.0	2825	20	X23369
3	38.4	18.6	3761	20	X09013
4	35.2	17.0	402	21	C75493
5	33.2	16.0	3411	20	X09012
6	32.8	15.8	15202	20	X28371
7	31.4	15.2	438	21	F11514
8	31.2	15.1	2326	20	X86273
9	30.6	14.8	10384	21	X236256
10	30.4	14.7	849	13	O32483
11	30.4	14.7	849	13	O32482

C	12	30.4	14.7	1280	13	O32494
C	13	30.4	14.7	1280	13	O32495
C	14	30.4	14.7	1518	21	Z46454
C	15	30.4	14.7	3564	13	O32501
C	16	30.4	14.7	4447	20	C76436
C	17	30.4	14.7	5535	21	Z32057
C	18	30.4	14.7	5535	20	X21355
C	19	30.4	14.7	5535	22	C90314
C	20	30.4	14.7	7911	13	O32436
C	21	30.2	14.6	421	20	V87645
C	22	30.2	14.6	720	21	Z53528
C	23	30.2	14.6	720	21	Z53530
C	24	30.2	14.6	957	21	Z53533
C	25	30.2	14.6	960	21	Z53531
C	26	30.2	14.6	1212	20	Z28297
C	27	30.2	14.6	1520	21	Z90525
C	28	30.2	14.6	3362	21	C77294
C	29	30.2	14.6	3852	20	Z20298
C	30	30	14.5	849	13	O32472
C	31	30	14.5	1280	13	O32479
C	32	30	14.5	3564	13	O32442
C	33	29.8	14.4	1340	21	Z45317
C	34	29.8	14.4	1352	20	X85693
C	35	29.8	14.4	2045	14	O43374
C	36	29.8	14.4	10097	13	O24802
C	37	29.8	14.4	10279	13	O22487
C	38	29.8	14.4	10279	20	V81865
C	39	29.6	14.3	498	21	C99118
C	40	29.6	14.3	4024	20	X84595
C	41	29.6	14.3	4226	20	X84594
C	42	29.6	14.3	5828	20	X84592
C	43	29.6	14.3	6056	20	X84593
C	44	29.6	14.3	29879	14	O46806
C	45	29.4	14.2	705	20	Z15831

ALIGNMENTS

RESULT	ID	1	ALIGNMENTS
X23370	X23370	standard; cDNA; 2523 BP.	
XX	XX	X23370;	
XX	XX	17-JUN-1999 (first entry)	
XX	XX	Human conductin cDNA.	
DE	DE	Human conductin cDNA.	
XX	XX	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;	
KW	KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;	
KW	KW	Wingless signalling pathway; Adenomatous Polyposis Coll; APC;	
KW	KW	tumour suppressor; ss.	
XX	XX	Homo sapiens.	
OS	OS	Homo sapiens.	
XX	XX	WO911780-A2.	
PN	PN	WO911780-A2.	
XX	XX	11-MAR-1999.	
PD	PD	11-MAR-1999.	
XX	XX	01-SEP-1998; 98WO-DE02621.	
PF	PF	01-SEP-1998; 98WO-DE02621.	
XX	XX	02-SEP-1997; 97DE-1038205.	
PR	PR	02-SEP-1997; 97DE-1038205.	
XX	XX	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
PA	PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX	XX	Behrens J, Birchmeier W;	
PI	PI	Behrens J, Birchmeier W;	
XX	XX	WPI; 1999-214706/18.	
DR	DR	P-PSDB; W93570.	
XX	XX	Tumor-suppressing protein conductin - used for treatment and	
PT	PT	diagnosis of tumors	

XX PS Claim 18; Fig 3; 22pp; German.
XX CC This invention describes a novel human conductin protein which has
XX CC anti-tumour activity. Detecting the presence or amount of conductin,
XX CC at protein or nucleic acid levels, is used to diagnose tumours, while
XX CC agents that (re)activate conductin are used for tumour therapy.
XX CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
XX CC resulting in blockade of the Wnt/Wingless signalling pathway in
XX CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
XX CC fragments and, in conjunction with APC, acts as a tumour suppressor.
SQ Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;

Query Match 100.0%; Score 207; DB 20; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1,7e-48;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1189 cagatccggagagatgaagaaagaggggtctgagcagcgccctgagctcacggatga 1248
QY 61 gaacgggtccagacacccctggcctctaccctccggcagctatgaagagaccacaa 120
DB 1249 gaacgggtccagacacccctggcctctaccctccggcagctatgaagagaccacaa 1308
QY 121 accatttggagcagacactctccagggtctccaaagaccccgctgtcaatccctgt 180
DB 1309 accatttggagcagacactctccagggtctccaaagaccccgctgtcaatccctgt 1368
QY 181 gtgggtcgctacagccacggtccgc 207
DB 1369 gtgggtcgctacagccacggtccgc 1395

RESULT 2
X23369 ID X23369 standard; CDNA; 2825 BP.
XX AC X23369;
XX DT 17-JUN-1999 (first entry)
XX DE Human conductin DNA.
XX KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
XX KW Tumour suppressor; ss.
XX OS Homo sapiens.
XX PS Key
FH CDS 215..2737
FT /tag= a
FT /product= "Conductin"
FT 446..814
FT /tag= b
FT /note= "regulator of G-protein signalling region as
FT 1241..1402 described in Claim 19"
FT /tag= c
FT /bound_molety= GSK-3beta
FT /note= "as described in Claim 20"
FT 1403..1609
FT /tag= d
FT /bound_molety= beta-catenin
FT /note= "as described in Claim 21"
FT 2561..2713
FT /tag= e
FT /note= "Disvelled homology region as described in
FT Claim 22"

XX PN W09911780-A2.
XX PD 11-MAR-1999.
XX PF 01-SEP-1998; 98WO-DE02621.
XX PR 02-SEP-1997; 97DE-1038205.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Behrens J, Birchemer W;
XX DR WPI: 1999-214706/18.
XX DR P-PSDB: W93569.
XX PT Tumor-suppressing protein conductin - used for treatment and
XX PT diagnosis of tumors
XX PS Claim 18; Fig 2; 22pp; German.
XX CC This invention describes a novel human conductin protein which has
XX CC anti-tumour activity. Detecting the presence or amount of conductin,
XX CC at protein or nucleic acid levels, is used to diagnose tumours, while
XX CC agents that (re)activate conductin are used for tumour therapy.
XX CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
XX CC resulting in blockade of the Wnt/Wingless signalling pathway in
XX CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
XX CC fragments and, in conjunction with APC, acts as a tumour suppressor.
SQ Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;

Query Match 100.0%; Score 207; DB 20; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1,8e-48;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagatccggagagatgaagaaagaggggtctgagcagcgccctgagctcacggatga 60
DB 1403 cagatccggagagatgaagaaagaggggtctgagcagcgccctgagctcacggatga 1462
QY 61 gaacgggtccagacacccctggcctctaccctccggcagctatgaagagaccacaa 120
DB 1463 gaacgggtccagacacccctggcctctaccctccggcagctatgaagagaccacaa 1522
QY 121 accatttggagcagacactctccagggtctccaaagaccccgctgtcaatccctgt 180
DB 1523 accatttggagcagacactctccagggtctccaaagaccccgctgtcaatccctgt 1582
QY 181 gtgggtcgctacagccacggtccgc 207
DB 1583 gtgggtcgctacagccacggtccgc 1609

RESULT 3
X09013 ID X09013 standard; DNA; 3761 BP.
XX AC X09013;
XX DT 14-JUN-1999 (first entry)
XX DE Murine axin gene.
XX KW Axin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
XX KW beta-catenin; ss.
XX OS Mus musculus.
XX PS Key
FH CDS Location/Qualifiers
FT 1..2981

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FM      /*tag= a
FT      /product= Axlin
FN
PN
PD      MO9902179-A1.
XX
XX      21-JAN-1999.
XX
PD      09-JUL-1998; 98MO-US14414.
XX
XX      10-JUL-1997; 97US-0890865.
XX
XX      (UYCO ) UNIV COLUMBIA NEW YORK.
PA
XX      Constantini F, Zeng L;
PI
XX      WPI: 1999-120510/10.
DR      P-PSDB; W96265.
XX
PT      Newly isolated nucleic acid encoding "axis inhibition" protein
PT      (Axlin) - useful for detecting, diagnosing and treating cancer
PS
XX      Claim 7; Figure 9A-9B; 95pp; English.
CC
CC      Nucleic acids encoding mutant and wild type Axlin and
CC      oligonucleotides derived from them are useful for detecting
CC      mutations in the Axlin gene and for determining whether a subject is
CC      likely to develop cancer (including breast, colorectal,
CC      gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC      type Axlin and homologues of Axlin are useful for treating subjects
CC      who are likely to develop cancer (thyroid carcinomas). The nucleic
CC      acids are also useful for diagnosing cancer and for detecting
CC      mutations in cancerous cells. Wild type Axlin, its antisense
CC      molecule and identified compounds form pharmaceutical compositions
CC      in the treatment of cancer. The compositions are also useful for
CC      treating cancer by inhibiting tumorigenesis (by inducing degradation
CC      of beta-catenin). The nucleic acid encoding Axlin acts through
CC      negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
SQ      Sequence 3761 BP: 890 A; 1012 C; 1088 G; 771 T; 0 other;
XX
Query Match      18.6%; Score 38.4; DB 20; Length 3761;
Best Local Similarity      62.5%; Pred. NO. 0.1;
Matches      60; Conservative      0; Mismatches      36; Indels      0; Gaps      0;
OY      102 ctatgaagaggaccacacacacattttggaagaccactctccagggtccctaagacc 161
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1772 ccatgagggaggaacccctggagacatctctggatcagagcagtgcaaaaggtatgagacacc 1831
OY      162 cggctgcacatccctctgctcggtcgtgtacagcc 197
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1832 tgcgtccagtcacactctgcccagagccacgcgtctcc 1867
XX
RESULT      4
ID      C75493
XX      C75493 standard; cDNA; 402 BP.
AC      C75493;
XX
XX      08-FEB-2001 (first entry)
DE      Human ORF1048 polynucleotide sequence SEQ ID NO:2095.
XX
XX      Human; open reading frame; ORF; detection; cyostatic; hepatotropic;
KW      vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW      anticonvulsant; osteoporotic; antiarthritic; immunosuppressant; cardiant;
KW      immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW      hypotensive; dermatological; immunosuppressive; antinflamatory;
KW      antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW      antinaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW      neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW      cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW

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[illegible]

[illegible][illegible]

KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; Identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
XX Aspergillus niger.
OS
XX
PN WO200056762-A2.
FD
XX 28-SEP-2000.
XX
PF 22-MAR-2000; 2000WO-US07781.
XX
PR 22-MAR-1999; 99US-0273623.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
XX (NOVO) NOVO NORDISK AS.
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IC, Olsen PB;
XX WPI: 2000-594572/56.
DR
XX
PT Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 87; Page 1782; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. F07478 to P11247 represents ESTs from Venenatum; P11248 to P11831 represents ESTs from Aspergillus niger; P11834 to P14878 represents ESTs from Aspergillus oryzae; and P14879 to P15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.

Sequence 438 BP; 84 A; 92 C; 91 G; 170 T; 1 other;

Query Match	15.2%	Score 31.4;	DB 21;	Length 438;
Best Local Similarity	56.2%;	Pred. No. 5.8;		
Matches	59;	Conservative	0;	Mismatches 46; Indels 0; Gaps 0;
OY 100 agcatatgaagaggaccacaacattcttgacagcaccccttcacaggtcctaagaacc				
Dd 160 AGGAAGAAAGAAAGATTAAAGAAGCATTTTGAACCTAACAATTCACACCGCTTCCTTC				
OY 160 ccggcgctgcataatcccctggtgtgtgtgtgcctacagaagccaaggtcc				
Dd 100 TCCGCATAAATAGCCTCTAATTTCCGGATGTGCACTGCCAAGACC				

RESULT 8
X86273 standard: DNA: 2326 BP.
ID X86273 standard: DNA: 2326 BP.
XX

AC	X86273.
XX	
DT	22-SEP-1999 (first entry)
XX	
DE	DNA encoding a human PIG protein.
XX	
KW	p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
KM	neoplastic; PIG; ss.
XX	
OS	Homo sapiens.
XX	
PN	M09914356-A2.
XX	
PD	25-MAR-1999.
XX	
PF	17-SEP-1998; 98WO-US19300.
XX	
PR	30-MAR-1998; 98US-0079817.
PR	17-SEP-1997; 97US-0059153.
XX	
PA	(UYSJO) UNIV JOHNS HOPKINS.
XX	
PI	Kinzler KW, Polyak K, Vogelstein B:
XX	
DR	WPI; 1999-443793/37.
PT	Use of p53 transcription tags to determine p53 status in, e.g,
XX	cancer diagnosis
PS	Disclosure: Page 64-65; 73pp; English.
XX	
CC	The specification describes the use of p53 transcription tags for
CC	developing products to determine p53 status, to diagnose cancer
CC	and to evaluate cytotoxicity or carcinogenicity of a test agent.
CC	A method for diagnosing cancer or determining p53 status in a sample
CC	suspected for being neoplastic comprises comparing the level of
CC	transcription of an RNA transcript in a first sample (s1) of a first
CC	tissue (t1) to the level of transcription of the transcript in a second
CC	sample (s2) of a second tissue (s2), where s1 is suspected of being
CC	neoplastic and s2 is a normal human tissue (of the same type) and the
CC	transcript is identified by a tag; and categorizing s1 as neoplastic
CC	or as having a mutant p53 when transcription is found to be the same
CC	or lower in the first, than in s2. The methods and products can be used
CC	to determine p53 status, to diagnose cancer and to evaluate cytotoxicity
CC	or carcinogenicity of a test agent. X86265-75 encode human PIG proteins.
SQ	Sequence 2326 BP: 544 A; 635 C; 637 G; 510 T; 0 other;
Query Match	15.1%; Score 31.2; DB 20; Length 2326;
Best Local Similarity	48.8%; Pred. No. 9.2;
Matches	84; Conservative 0; Mismatches 88; Indels 0; Gaps 0
OY	23 aggaagggtctgagcagcgccctgagtcaacggatgtagcacgcggtccagaaccgcccttg 82 Db 1 aggccggagagaggtgctgtgcggcgltggtcgtgtgcgagaccggttcacagacctgtg 60 OY 83 cccctcatccccctccgcgaagctaataagaaaggaccaacaaccattttggacgacaccctct 142 Db 61 gccgcgcgcacacaaggcgcttcttaagctcccctcccgcagcgaacgcgcgcctcttc 120 OY 143 ccaggctcctcaagaccgcccgctgtccaactccctgtgttgtgctgcacag 194 Db 121 cgcggcctcgaatgtgacaggaatgtcctctgacctaacgtgacgcgtlccgg 172
RESULT	9
ID	236256/c
XX	Z36256 standard; DNA: 10384 BP.
AC	Z36256;
DT	22-FEB-2000 (first entry)

XX DNA sequence of the human longevity assurance gene 1 (LAG1).
DE
XX
XX
XX Human: longevity assurance gene 1; LAG1; LAG1HS; cell longevity;
KM cell tolerance; cellular stress; starvation; acidic pH;
KM cell reproductive capacity; ss.
OS
XX Homo sapiens.
XX
XX WO958671-A2.
XX
XX 18-NOV-1999.
XX
XX 10-MAY-1999; 99WO-US10160.
XX
XX 08-MAY-1998; 98US-0075014.
XX
XX (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX
XX Jazwinski SM, Kirchner P, Jiang J;
XX
XX WPI; 2000-053098/04.
XX
XX Novel human homologue for increasing longevity, tolerance and
PT reproductive capacity of a cell -
XX
XX Example 7; Page 92-99; 98pp; English.
XX
XX The present sequence represents the human longevity assurance gene 1
CC (LAG1), designated LAG1HS. The LAG1HS cDNA was isolated from total brain
CC mRNA. The LAG1 protein, or proteins with at least 25-30% homology to the
CC LAG1HS protein, is administered to increase the longevity of a human
CC cell. Expression of these polypeptides is used to increase tolerance of
CC human cells to cellular stresses, such as starvation or acidic pH
CC (5-5.5). The LAG1 proteins are also used for increasing reproductive
CC capacity of human cells. LAG1 polynucleotides can be used as probes for
CC detecting LAG1 from different species, as the LAG1 gene is highly
CC conserved across the spectrum of eukaryotes.
XX
XX Sequence 10384 BP; 2135 A; 2839 C; 3598 G; 1812 T; 0 other;
SQ

Query Match 14.8%; Score 30.6; DB 21; Length 10384;
Best Local Similarity 51.9%; Pred. No. 18;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 73 caccctccgagcctctaccctccgagcgtatgaagagagaccacaacatttgac 132
DB 2032 CTCACCCAGCCGCGCCACACCCCGCATCTACCGGTTCCCGCCAGCACCTGTGTA 1973
QY 133 gaccactctcagaggtctcaagacccccggctgtaatccctgggtgtggtgctac 192
DB 1972 AGGGGGCGCGCGCGCGCGAGAGACCTTATCTGTGGGCTCCAAGCTCTGCGCTCTCC 1913
QY 193 agcccaaggtccc 205
DB 1912 AGCCCGAGGCCCC 1900

RESULT 10
Q32483/c
ID Q32483 standard; DNA; 849 BP.
XX
XX Q32483;
XX
XX 26-APR-1993 (first entry)
XX
XX HCV NS2-NS4 clone MX25-2.
XX
XX Clone: polypeptide; NS2-NS4; Hepatitis C; virus; HCV; serum; HC;
KM transcriptase; cDNA; primer; allele; ss.
XX
XX Hepatitis C virus.
OS

XX
XX EP518313-A.
XX
XX 16-DEC-1992.
XX
XX 11-JUN-1992; 92EP-0109812.
XX
XX 11-JUN-1991; 91JP-0139268.
XX 12-JUL-1991; 91JP-0172794.
XX 07-OCT-1991; 91JP-0287008.
XX 16-DEC-1991; 91JP-0332329.
XX 20-APR-1992; 92JP-0099957.
XX
XX (MITU) MITSUBISHI KASEI CORP.
XX
XX Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
PI Teranishi Y;
XX
XX WPI; 1992-417213/51.
XX P-PSDB; R29852.
XX
XX New hepatitis C virus gene and its encoded protein - used for
PT diagnosing and vaccinating against hepatitis C virus infections
XX
XX Disclosure; Page 147-49; 305pp; English.
XX
XX The sequences given in Q32483-501 are various clones which were used
CC in the isolation of the NS2-NS4 regions of the Hepatitis C virus
CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
CC sequences were isolated from the serum of a patient suffering from
CC hepatitis C (HC). The isolated RNA sequences were converted into
CC cDNA using transcriptase in the presence of one of the primer
CC sequences given in Q32578-79. The sequences were then amplified
CC using primer pairs. The cDNA sequences isolated represent different
CC alleles of the same region of the HCV gene. Sequence comparisons of
CC these clones showed that it is possible for a patient to carry more
CC than one HCV strain at one time. See also Q32436.
XX
XX Sequence 849 BP; 150 A; 250 C; 247 G; 202 T; 0 other;
SQ

Query Match 14.7%; Score 30.4; DB 13; Length 849;
Best Local Similarity 59.1%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 16 gaagaagaaggaggtctgagcagccttgagctcaaggatggagacagctcagcac 75
DB 123 GAAGAACAACAAGAAAGAGAGATGCCATGCCCTCCCGCATGATGCTGATGAGGAC 64
QY 76 ccctcgccctctaccctccgagcagct 103
DB 63 CACGAGTTCTCCAAAGCGCGCTCAGCT 36

RESULT 11
Q32482/c
ID Q32482 standard; DNA; 849 BP.
XX
XX Q32482;
XX
XX 26-APR-1993 (first entry)
XX
XX HCV NS2-NS4 clone MX25-1.
XX
XX Clone: polypeptide; NS2-NS4; Hepatitis C; virus; HCV; serum; HC;
KM transcriptase; cDNA; primer; allele; ss.
XX
XX Hepatitis C virus.
XX
XX EP518313-A.
XX
XX 16-DEC-1992.
XX

PF 11-JUN-1992: 92EP-0109812.
XX
PR 11-JUN-1991: 91JP-0139268.
PR 12-JUL-1991: 91JP-0172794.
PR 07-OCT-1991: 91JP-0287008.
PR 16-DEC-1991: 91JP-0332329.
PR 20-APR-1992: 92JP-0099957.
XX
PA (MITU) MITSUBISHI KASEI CORP.
XX
PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
PI Teranishi Y;
XX
DR WPI: 1992-417213/51.
DR P-PSDB: R29851.
XX
PT New hepatitis C virus gene and its encoded protein - used for
PT diagnosing and vaccinating against hepatitis C virus infections
XX
PS Disclosure: Page 146-47; 305pp; English.
XX
CC The sequences given in Q32472-82 and Q32442 are various clones which
CC encode the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of
CC the invention. These sequences were isolated from the serum of a
CC patient suffering from hepatitis C (HC). The isolated RNA sequences
CC were converted into cDNA using transcriptase in the presence of one
CC of the primer sequences given in Q32553-64. The sequences were
CC then amplified using primer pairs. The cDNA sequences isolated
CC represent different alleles of the same region of the HCV gene.
CC Sequence comparisons of these clones showed that it is possible for a
CC patient to carry more than one HCV strain at one time. See also
CC Q32436.
XX
SQ Sequence 849 BP; 146 A; 245 C; 249 G; 209 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 849;
Best Local Similarity 59.1%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 16 gaagaaagaggggtcagcagccctgagctcagggatgagcaccggtccagcac 75
DB 123 GAAGAACACAAAGAGAGAGATGCCATCGCTCCCGCATGGATGCTCATTTGAGGAC 64
QY 76 cccctggcctcctaccctccgagcact 103
DB 63 CACCAAGTCTCCAAAGCGCCCTCAGCT 36

RESULT 12
Q32494/C
ID Q32494 standard; DNA: 1280 BP.
XX
AC Q32494;
XX
DT 26-APR-1993 (first entry)
XX
DE HCV NS2-NS4 clone MX25026A-1.
XX
KM Clone: polypeptide: NS2-NS4; Hepatitis C; Virus; HCV; serum; HC;
KM transcriptase: cDNA; primer: allele; ss.
XX
OS Hepatitis C virus.
XX
FH Key 1.1278 Location/Qualifiers
FH CDS 1..1278 /*tag- a
FT
FT
XX
PN EP518313-A.
XX
PD 16-DEC-1992.
XX
PF 11-JUN-1992: 92EP-0109812.

XX
PR 11-JUN-1991: 91JP-0139268.
PR 12-JUL-1991: 91JP-0172794.
PR 07-OCT-1991: 91JP-0287008.
PR 16-DEC-1991: 91JP-0332329.
PR 20-APR-1992: 92JP-0099957.
XX
PA (MITU) MITSUBISHI KASEI CORP.
XX
PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
PI Teranishi Y;
XX
DR WPI: 1992-417213/51.
DR P-PSDB: R29863.
XX
PT New hepatitis C virus gene and its encoded protein - used for
PT diagnosing and vaccinating against hepatitis C virus infections
XX
PS Disclosure: Page 165-67; 305pp; English.
XX
CC The sequences given in Q32483-501 are various clones which were used
CC in the isolation of the NS2-NS4 regions of the Hepatitis C Virus
CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
CC sequences were isolated from the serum of a patient suffering from
CC hepatitis C (HC). The isolated RNA sequences were converted into
CC cDNA using transcriptase in the presence of one of the primer
CC sequences given in Q32578-79. The sequences were then amplified
CC using primer pairs. The cDNA sequences isolated represent different
CC alleles of the same region of the HCV gene. Sequence comparisons of
CC these clones showed that it is possible for a patient to carry more
CC than one HCV strain at one time. See also Q32436.
XX
SQ Sequence 1280 BP; 222 A; 385 C; 376 G; 297 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 1280;
Best Local Similarity 59.1%; Pred. No. 14;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 16 gaagaaagaggggtcagcagccctgagctcagggatgagcaccggtccagcac 75
DB 123 GAAGAACACAAAGAGAGAGATGCCATCGCTCCCGCATGGATGCTCATTTGAGGAC 64
QY 76 cccctggcctcctaccctccgagcact 103
DB 63 CACCAAGTCTCCAAAGCGCCGATCAGCT 36

RESULT 13
Q32495/C
ID Q32495 standard; DNA: 1280 BP.
XX
AC Q32495;
XX
DT 26-APR-1993 (first entry)
XX
DE HCV NS2-NS4 clone MX25026B-1.
XX
KM Clone: polypeptide: NS2-NS4; Hepatitis C; Virus; HCV; serum; HC;
KM transcriptase: cDNA; primer: allele; ss.
XX
OS Hepatitis C virus.
XX
FH Key 1.1278 Location/Qualifiers
FH CDS 1..1278 /*tag- a
FT
FT
XX
PN EP518313-A.
XX
PD 16-DEC-1992.
XX
PF 11-JUN-1992: 92EP-0109812.

PR 11-JUN-1991; 91JP-0139268.
 PR 12-JUL-1991; 91JP-0172794.
 PR 07-OCT-1991; 91JP-0287008.
 PR 16-DEC-1991; 91JP-0332329.
 PR 20-APR-1992; 92JP-0099957.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
 PI Teranishi Y;
 XX
 DR WPI: 1992-417213/51.
 DR P-PSDB; R29864.
 XX
 PT New hepatitis C virus gene and its encoded protein - used for
 PT diagnosing and vaccinating against hepatitis C virus infections
 PS Disclosure; Page 167-69; 305pp; English.
 XX
 CC The sequences given in Q32483-501 are various clones which were used
 CC in the isolation of the NS2-NS4 regions of the Hepatitis C virus
 CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
 CC sequences were isolated from the serum of a patient suffering from
 CC hepatitis C (HC). The isolated RNA sequences were converted into
 CC cDNA using transcriptase in the presence of one of the primer
 CC sequences given in Q32578-79. The sequences were then amplified
 CC using primer pairs. The cDNA sequences isolated represent different
 CC alleles of the same region of the HCV gene. Sequence comparisons of
 CC these clones showed that it is possible for a patient to carry more
 CC than one HCV strain at one time. See also Q32436.
 XX
 SQ Sequence 1280 BP; 222 A; 385 C; 376 G; 297 T; 0 other;
 OY Query Match 14.7%; Score 30.4; DB 13; Length 1280;
 DB Best Local Similarity 59.1%; Pred. No. 14;
 Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 OY 16 gaagaaagagggtctgacagagccctgagctcagcgatgagacacggctccagcac 75
 DB 123 GAAAGAACACAAAGAAAGAGAGATGCGATCGCTCCGCCATGAGATGCTGCAITGAGGAC 64
 OY 76 cccctgagccctcctaccctcgcgacgt 103
 DB 63 CACCAAGTTCTCCAGGCGGCGATCAGCT 36
 XX
 RESULT 14
 ID 249454
 AC 249454; standard; DNA; 1518 BP.
 XX
 DT 04-APR-2000 (first entry)
 DE Mouse Voltage-gated Potassium channel monomer, Kv6.2 gene.
 XX
 KW Voltage gated potassium channel; Kv6.2; mouse; excitability; ion flux;
 KW resting potential; alpha subunit; modulator; hearing/vision problem;
 KW migraine; central nervous system; CNS; seizure; neuroprotective agent;
 KW psychotic disorder; reporter; treatment; detection; antibody; probe;
 KW primer; ds.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..1518
 FT /*tag= a
 FT /label= Mouse_Kv6.2_polypeptide
 FT /note= "Voltage gated potassium channel subunit"
 FT 1381..1389
 FT /*tag= b
 FT /note= "This region encodes the amino acid sequence

FT ELK, which is represented in the specification
 FT as the typographical error Kv6.2 (an insertion
 FT of the protein name)"
 XX
 PN WO200001811-A1.
 XX
 PD 13-JAN-2000.
 XX
 PF 30-JUN-1999; 99WO-US14945.
 XX
 PR 01-JUL-1998; 98US-0091466.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 DR WPI: 2000-126937/11.
 DR P-PSDB; Y44564.
 XX
 PT New voltage-gated potassium channel alpha subunit, useful for
 PT identifying modulators of voltage-gated channel activity useful for
 PT treating central nervous system disorders e.g. migraines and as
 PT neuroprotective agents -
 PS Claim 5; Page 65-66; 80pp; English.
 XX
 CC The present sequence is the gene encoding the mouse Kv6.2 monomer, which
 CC is an alpha subunit of heteromeric voltage-gated potassium channel. It
 CC is isolated from brain tissue and maintains the resting potential and
 CC controls the excitability of a cell. Kv6.2 polypeptide can be used to
 CC identify compounds, that modulate the ion flux through heteromeric
 CC voltage-gated potassium channels. Such modulators are used as
 CC neuroprotective agents and for treating CNS disorders, such as migraines,
 CC hearing and vision problems and for treating CNS disorders and seizures. It can
 CC also be used as reporter molecules in assays and to produce antibodies.
 CC Kv6.2 DNA sequence can be used to produce specific primers or probes
 CC for detection purposes.
 XX
 SQ Sequence 1518 BP; 271 A; 467 C; 470 G; 310 T; 0 other;
 OY Query Match 14.7%; Score 30.4; DB 21; Length 1518;
 DB Best Local Similarity 51.5%; Pred. No. 14;
 Matches 70; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 OY 2 agatccggagatgaagaaaggaggtcgtgacgagccctgagctacggatgag 61
 DB 176 agatccctagtgatgtggtggtgcccagcggtacctgctgcccggagcacccggatgct 235
 OY 62 caacggtccagcaccctcctaccctcgcgacgtatgaagagacccacaaa 121
 DB 236 tcccgctgagccgcctcgcgacgactccggctgtgcccagcagcatgagggatcacgcagc 295
 OY 122 ccatttggagacaca 137
 DB 296 tctgcatgactaca 311
 XX
 RESULT 15
 ID Q32501/c
 AC Q32501; standard; DNA; 3564 BP.
 XX
 DT 26-APR-1993 (first entry)
 DE HCV NS2-NS4 clone N25N15-1.
 XX
 KW Clone; polypeptide; NS2-NS4; Hepatitis C; Virus; HCV; serum; HC;
 KW transcriptase; cDNA; primer; allele; ss.
 XX
 OS Hepatitis C virus.
 XX

PN EP518313-A.
 XX
 PD 16-DEC-1992.
 XX
 PF 11-JUN-1992; 92EP-0109812.
 XX
 PR 11-JUN-1991; 91JP-0139268.
 PR 12-JUL-1991; 91JP-0172794.
 PR 07-OCT-1991; 91JP-0287008.
 PR 16-DEC-1991; 91JP-0332329.
 PR 20-APR-1992; 92JP-0099957.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 PI Hayashi N, Honda Y, Murakami T, Seki M, Takahashi K;
 PI Teranishi Y;
 XX
 DR WPI: 1992-417213/51.
 XX P-PSDB: R29870.
 PT New hepatitis C virus gene and its encoded protein - used for
 PT diagnosing and vaccinating against hepatitis C virus infections
 XX
 PS Disclosure; Page 186-92; 305pp; English.
 XX
 CC The sequences given in Q32483-501 are various clones which were used
 CC in the isolation of the NS2-NS4 regions of the Hepatitis C Virus
 CC (HCV) gene of the invention (see also Q32442 and Q32472-82). These
 CC sequences were isolated from the serum of a patient suffering from
 CC hepatitis C (HC). The isolated RNA sequences were converted into
 CC cDNA using transcriptase in the presence of one of the primer
 CC sequences given in Q32578-79. The sequences were then amplified
 CC using primer pairs. The cDNA sequences isolated represent different
 CC alleles of the same region of the HCV gene. Sequence comparisons of
 CC these clones showed that it is possible for a patient to carry more
 CC than one HCV strain at one time. See also Q32436.
 XX
 SQ Sequence 3564 BP; 668 A; 1064 C; 1046 G; 786 T; 0 other;

Query Match 14.7%; Score 30.4; DB 13; Length 3564;
 Best Local Similarity 59.1%; Pred. No. 17;
 Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 OY 16 gaagaaaggagggtcgtgagcagccctgagctcaaggagtgagcaaccgctcagcac 75
 DB 123 GAAGAACACACAGAGAGAGAGATGCCATGCCCTCCGCTATGATGCTCATTTAGAGAC 64
 OY 76 cccctggccctcctaccctccggcagct 103
 DB 63 CACCAGGTTCTCCAGGCGGCTCAGCT 36

Search completed: June 7, 2001, 00:31:59
 Job time: 8637 sec

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STREET: Abbott Laboratories D377/APd-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952.US..01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
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NAME/KEY: CDS
LOCATION: 19..10722
OTHER INFORMATION: /codon_start=19
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OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 4171..4428
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OTHER INFORMATION: acyl carrier domain of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4471..10722
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: module 4"
FEATURE:
NAME/KEY: misc_feature
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LOCATION: 4471..5847
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OTHER INFORMATION: beta-ketoacylACPSynthase domain of module "
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7165..9216
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OTHER INFORMATION: dehydratase and enoylreductase domains m"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9433..9984
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OTHER INFORMATION: beta-ketoreductase of module 4"
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NAME/KEY: misc_feature
LOCATION: 10225..10483
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OTHER INFORMATION: acyl carrier domain of module 4"
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NAME/KEY: CDS
LOCATION: 10723..20235
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OTHER INFORMATION: /product- "orf3 encoding modules 5 & 6
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
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NAME/KEY: misc_feature
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OTHER INFORMATION: module 5"
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NAME/KEY: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12375..13350
OTHER INFORMATION: /function- "approximatr span of
OTHER INFORMATION: acyltransferase domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14062..14610
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15166..20235
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..15696
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18379..18921

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OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: thioesterase domain of module 6"
US-07-642-734C-3

Query Match 14.3%; Score 29.6; DB 1; Length 20235;
Best Local Similarity 57.6%; Pred. No. 13;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Oy 55 gatgagacacgggtccagacacccctgagcctctacacctccggagcgtatgaagagac 114
    |||||
Db 3262 GACGCGGGGGGGCTCGCTGCTCTGTCGACGTCGCGGGGGGCGGCGCTGCCGAGGAC 3321
    |||||

Oy 115 ccacacaccatttggacgacacccctccacg 146
    |||||
Db 3322 CACCTCGCGGTCCGGGACGCGCCCTCCACGG 3353
    |||||

RESULT 4
US-08-439-009A-3
; Sequence 3, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; NUMBER OF INVENTION: Specific Polypeptides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstein
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 4952.US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharopolyspora erythraea

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STRAIN: NRRL 238
FEATURE:
NAME/KEY: CDS
LOCATION: 19..10722
OTHER INFORMATION: /codon_start=19
OTHER INFORMATION: /function="gene eryA"
OTHER INFORMATION: /product="eryA ORF2 encoding modules 3 & 4 for
OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19..4470
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 97..1482
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1693..2670
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4471..10722
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4471..5847
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of module"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: dehydratase and enoylreductase domains m"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9433..9984
OTHER INFORMATION: /function="approximate span
OTHER INFORMATION: beta-ketoreductase of module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10225..10483
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
FEATURE:
NAME/KEY: CDS
LOCATION: 10723..20235
OTHER INFORMATION: /codon_start=10723
OTHER INFORMATION: /function="gene -eryA"
OTHER INFORMATION: /product="orf3 encoding modules 5 & 6
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10723..15165

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OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12379..13350
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyltransferase domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14062..14610
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15166..20235
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..16569
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18379..18921
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: thioesterase domain of module 6"
US-08-439-009A-3

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Query Match 14.3%; Score 29.6; DB 3; Length 20235;
Best Local Similarity 57.6%; Pred. No. 13;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
OY 55 gatgagcaccggtccagaccaccttgagcctcctacccctcgagcagctatgaagagac 114
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3262 GAGCAGCGGGGGCGCTCTGCTGCGACGTCTGCGCGCGCGCGCGCGCGAGAC 3321
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 115 ccacaaccatttggagcagcaccctctccag 146
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3322 CACCTCGCGGTCGCGGACGCGCGCTCCACGG 3353
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 5
US-08-356-060A-42/c
; Sequence 42; Application US/08356060A
; Patent No. 5844079
; GENERAL INFORMATION:

```

```

APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tablin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMT-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 3900 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3897
US-08-356-060A-42

Query Match 14.1% Score 29.2; DB 2; Length 3900;
Best Local Similarity 56.1% Pred. No.12;
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0

OY 64 ccggttcagacacccctctccctctacccctcggcagctatgaaagagaccacaacc 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 CTGATCGAGCGCCACCTTGCGGCGTGCACCCACAGCTGCGTATGTAAGATCCGAGAAATA 61

OY 124 attttgacagcacccctctccaggtctctcaagacc 161
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Db 60 TTTCATCGACACACATCGCCGTGTGTGTCGGAGCG 23

RESULT 6
US-08-460-900C-42/c
Sequence 42, Application US/08460900C
Patent No. 6165747
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tablin, Clifford J.
APPLICANT: Bumcrot, David A.
APPLICANT: Marti-Gorosita, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP

```

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STREET One Post Office Square
City: Boston
STATE MA
COUNTRY USA
ZIP 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,900C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 3900 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3897
US-08-460-900C-42

Query Match 14.1%; Score 29.2; DB 4; Length 3900;
Best Local Similarity 56.1%; Pred.No. 12;
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Oy 64 ccgttcacagaccctccctcactacctccgcggcgcaagtatgaaggagaccaaaccc 123
Db 120 CTGATCGAGCCCACTTGTGGGTCACACCACACTGGTGCGTAGTAAGAATCGAGAAATAA 61

Oy 124 atttgagacaacaccttccaagggtcctaagaacccc 161
|| ||||||| | | | | | | | | | | | | | |
Db 60 TTTCTCATCGAACACAATGCCGTGTGTCTCGGAACGC 23

RESULT 7
US-08-540-406-5/C
Sequence 5, Application US/08540406
Patent No. 5837538
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched genes and their use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
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DB 321 CTGATGAGCGCCACTTGGGCGTCCACCCAGCTGTCGTATGTAAGATCCGAGATAA 262
QY 124 atttggacgacacacccctccagggtccctcaagacccc 161
DB 261 TTTCTCATGACACCATCGCGCTGTGTCTCCGGAACGC 224

RESULT 10

PCT-US95-13233-5/C

Sequence 5, Application PC/TUS9513233

GENERAL INFORMATION:

APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY

TITLE OF INVENTION: Patched Genes and their use

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13233

FILING DATE: 06-OCT-1990

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Berttram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60190-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 4434 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

PCT-US95-13233-5

Query Match 14.1%; Score 29.2; DB 5; Length 4434;
Best Local Similarity 56.1%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 64 ccggtccgacacccctcgccctccaccctccgagacatagaagagaccccaaac 123
DB 321 CTGATGAGCGCCACTTGGGCGTCCACCCAGCTGTCGTATGTAAGATCCGAGATAA 262
QY 124 atttggacgacacacccctccagggtccctcaagacccc 161
DB 261 TTTCTCATGACACCATCGCGCTGTGTCTCCGGAACGC 224

RESULT 11

US-07-953-230A-2

Sequence 2, Application US/07953230A

Patent No. 5476779

GENERAL INFORMATION:

APPLICANT: CHEN, Thomas T

APPLICANT: SHAMLOTT, Michael J

TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTORS ISOLATED

TITLE OF INVENTION: FROM RAINBOW TROUT

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/953,230A

FILING DATE: 30-SEP-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Crane-Feary, Sharon E

REGISTRATION NUMBER: 36,113

REFERENCE/DOCKET NUMBER: 028755-010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 732 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-953-230A-2

Query Match 13.9%; Score 28.8; DB 1; Length 722;
Best Local Similarity 52.5%; Pred. No. 10;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 cagatccgagagatgaagaagaggggtctgagcagagccctgagctcagcgagatga 60
DB 594 CAGGGCCCGGAAGTTCGAGGCGGCGTGAAGATCAAGCCCAAGACGAGCGATGT 653
QY 61 gaacggtccagacacccctcgccctccaccctccgagacatgaagagaccccaac 120
DB 654 CCACGGCCCTGTGATCATCCTGCCACGACGATTCGCCCGCCACGAGCA 713

RESULT 12

US-09-036-987A-1/C

Sequence 1, Application US/09036987A

Patent No. 6143526

GENERAL INFORMATION:

APPLICANT: Baltz, Richard H.

APPLICANT: Broughton, Mary C.

APPLICANT: Crawford, Kathryn P.

APPLICANT: Madduri, Krishnamurthy

APPLICANT: Merlo, Donald J.

APPLICANT: Treadway, Patti J.

APPLICANT: Turner, Jan R.

APPLICANT: Waldron, Clive

TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

TITLE OF INVENTION: Production

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dow Agrosciences LLC Patent Department

STREET: 9330 Zionsville Road

CITY: Indianapolis

STATE: Indiana

COUNTRY: USA

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/036,987A

FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

Query Match 13.9%; Score 28.8; DB 4; Length 80161;
Best Local Similarity 52.5%; Pred. No. 29;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 43 ctgaactcagggatggagaccggtccagaccctctgacctctaccctccggcagc 102
DB 78772 CTCACCGGACACGACGCGGCGACGCTGACACCGCTCTCAACTCCAGCGGGGCGGAC 78713
OY 103 tatgaagagaccacacacatttggagaccacctctccagggtctcctaaagacccc 162
DB 78712 GCCGCTACACCGGACCAACCGCTGAGCGCGGCTGCTGCTGCTGACGAGCGGCTCC 78653

RESULT 13
US-09-010-928B-3/c

Sequence 3, Application US/09010928B

Patent No. 5994099

GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V

APPLICANT: Hayashi, Cheryl Y

TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA

TITLE OF INVENTION: CODING THEREFOR

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 8110 GATEHOUSE RD. SUITE 500E

CITY: FALLS CHURCH

STATE: VIRGINIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,928B

FILING DATE: 22-JAN-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M

REGISTRATION NUMBER: 28977

REFERENCE/DOCKET NUMBER: 1447-109P

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2824 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: -

LOCATION: 1..2824

OTHER INFORMATION: /note="Flagelliform DNA sequence
OTHER INFORMATION: taken from 3' region. Stop codon begins at position 2722.
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2724
US-09-010-928B-3

Query Match 13.8%; Score 28.6; DB 2; Length 2824;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 64 ccggctcagacacccctctgacctctaccctccggcagctatgaagagaccacaaacc 123
DB 883 CTGGTCACACACTCCAGGCTCTACACCTCTGTCGAGCCACACAGCCTACACCTC 824
OY 124 atttggacacacacctctccagggtctcctaaagacccc 162
DB 823 CTGGTCACACACACCGGGGTCGGAACCTCCAGCACAC 785

RESULT 14
US-08-403-852D-14

Sequence 14, Application US/08403852D

Patent No. 5891695

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique

APPLICANT: Bianche, Francis

APPLICANT: Crouzet, Joel

APPLICANT: Jacques, Nathalie

APPLICANT: Lacroix, Patricia

APPLICANT: Thibaut, Denis

APPLICANT: Zagorec, Monique

APPLICANT: Debussche, Laurent

APPLICANT: De Crey-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The

TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences

TITLE OF INVENTION: Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,852D

FILING DATE: 10-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR 93/00923

FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441

FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806.0054-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4400

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 474 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:46 ; Search time 3054.04 Seconds
(without alignments)
592.125 Million cell updates/sec

Title: US-09-587-574-9

Perfect score:

207

Sequence: 1 cagatccggggagatgaaga.....gtctacagccacaggtccgc 207

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	133.4	64.4	345	24	A1742962	A1742962 wg76d09.x
C 2	133.4	64.4	408	23	A1660139	A1660139 we61a09.x
C 3	133.4	64.4	543	17	A1220032	A1220032 q978b02.x
C 4	133.4	64.4	591	102	A1818109	A1818109 wk27c05.x
C 5	131.8	63.7	460	20	A1419942	A1419942 c940d11.x
C 6	130.4	63.0	418	103	A1858567	A1858567 w164d08.x
C 7	122	58.9	383	112	AW207598	AW207598 UI-H-B11-
C 8	121.4	58.6	413	19	A1336613	A1336613 q062c07.x
C 9	121.4	58.6	459	18	A1272864	A1272864 q143b03.x
C 10	121.4	58.6	487	18	A1307112	A1307112 q189f01.x
C 11	117.6	56.8	299	19	A1363868	A1363868 qy60a10.x
C 12	111.6	53.9	346	13	AA915999	AA915999 oh86g11.s
C 13	111	53.6	282	13	AA474251	AA474251 xs23a05.x
C 14	106.8	51.6	449	8	AA489644	AA489644 aa43d02.s
C 15	101.2	48.9	444	13	AA937585	AA937585 of71h02.s
C 16	90.4	43.7	181	111	AW172276	AW172276 xj36f12.x
C 17	82.6	39.9	391	13	AA884421	AA884421 am16b12.s
C 18	81.6	39.4	360	155	R33824	R33824 yh78f12.s1


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2722356"
/clone_1ib="NCI_CGAP_Sud3"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT7S3-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sud3 library is a subtracted library derived from
the NCI_CGAP_Sud1 library, which is a subtracted library
derived from Bi. Bi constitutes a mixture of 21
normalised or subtracted NCI_CGAP libraries:
NCI_CGAP_P122, NCI_CGAP_P128, NCI_CGAP_Co10,
NCI_CGAP_Co16, NCI_CGAP_kid5, NCI_CGAP_kid121,
NCI_CGAP_kid3, NCI_CGAP_kid81, NCI_CGAP_lym2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_GIL1, NCI_CGAP_Ge12
NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Lu19, NCI_CGAP_Gc6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a

```

Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center


```

/db_xref="taxon:9606"
/clone="IMAGE:1435827"
/clone_lib="NCI_CGAP_C08"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pTR73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTR73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bernaldo. "

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	Query Match	Best Local Similarity	48.9%;	Score 101.2;	DB 13;	Length 444;
	Matches 139;	Conservative	0;	Mismatches 43;	Indels 2;	Gaps 1;
QY	1	cgagtcgggaggatgaagaaagaggaggtctgagcagggccctgaagtcacggaatga	60			
Db	224	CAATATCGAGAGAGATGAAGAGAGAGAGGGCTCCGAGCTCAACTCATTAATTCGGCGGAGGG	165			
QY	61	ggacgggtccagcaccacctggccctctaccctccggcagctatgaagagaccacaa	120			
Db	164	GGCCCCAGCAGCACACCCCTCTCCCTACT--GCACCGGCAAGCTACAGGAGAACCCCGCAG	107			
QY	121	accattttggaagcaccctctccaggtgtctcaagaaccccggtcgtcaatcccttgt	180			
Db	106	ACGATCTGTGAGAGATCCACTGTCCAGGGTCTCTCAAGACCCCTGGCTGCACGTCTCCGGAG	47			
QY	181	gtggg	184			
Db	46	TAGG	43			

Search completed: June 6, 2001, 23:00:45
Job time: 15533 sec

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Search completed: June 6, 2001, 23:00:49
Job time: 1553 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:36:12 ; Search time 4956.99 Seconds
(without alignments)
455.200 Million cell updates/sec

Title: US-09-587-574-10
Sequence: 1 ttgacctggccacttcaa.....tgtacgaagcagatctctg 153

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 1283235 segs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	153	9	A98525 Sequence 10
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4	153	100.0	3016	94	AF205889 Mus muscu
5	143.4	93.7	3216	94	AF017757 Rattus no
6	121	79.1	1863	85	AB052751 Homo sapi
7	121	79.1	2104	89	AK025718 Homo sapi
8	121	79.1	2538	88	AF205888 Homo sapi
9	121	79.1	3072	88	AF078165 Homo sapi
10	91.8	60.0	3156	8	AF009012 Gallus ga
11	88.6	57.9	3411	88	AF009674 Homo sapi

12 88.6 57.9 3485 8 AB032263
13 85.6 55.9 2529 8 AF097313
14 83.8 54.8 3460 94 AF017756
15 82.2 53.7 3781 94 AF009011
16 79.7 51.6 3066 8 AB032262
17 68.8 45.0 2121 8 AF140243
18 55.8 36.5 31557 91 HS31464
19 55.8 36.5 133069 70 AC026836
20 55.8 36.5 187272 74 AC069076
21 52 34.0 191041 69 AC024114
22 38.2 25.0 278229 76 AC074322
23 38 24.8 2232 5 AF086811
24 38 24.8 3990 5 AF091813
25 36.2 23.7 2177 93 HS046461
26 36.2 23.7 2889 88 AF006011
27 36.2 23.7 2955 94 AF143545
28 36.2 23.7 2955 94 AF143546
29 36 23.5 3286 94 MM010115
30 33.4 21.8 5596 1 AF026544
31 32.6 21.3 36308 2 D88802
32 32.6 21.3 213190 2 BSUB0004
33 32.4 21.2 79663 12 AC006593
34 32.4 21.2 122557 91 HS22948
35 32.4 21.2 157875 91 HS272116
36 32.2 21.0 145294 61 AC009856
37 32.2 21.0 178518 80 AL357632
38 32 20.9 12217 1 AE004520
39 32 20.9 219785 74 AC069035
40 31.8 20.8 347660 2 AP002994
41 31.6 20.7 130279 92 HSDJ31316
42 31.6 20.7 176277 70 AC025941
43 31.2 20.4 128639 63 AC013527
44 31 20.3 9200 1 AF130422
45 30.8 20.1 135468 64 AC016503

ALIGNMENTS

RESULT 1
A98525 153 bp DNA PAT 26-JAN-2000
LOCUS Sequence 10 from Patent WO9911780.
ACCESSION A98525
VERSION A98525.1 GI:6781611
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 153)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
JOURNAL TUMOR ILLNESSES
PATENT: WO 9911780-A 10 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
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QY 61 aagaagcagagtgaggaatttcctcgagcagcttttgaggaatctggagcagcag 120
DB 61 aagaagcagagtgaggaatttcctcgagcagcttttgaggaatctggagcagcag 120

DB 61 AAGAAGCGCAGTGAGCAATTTGCTCCGCGAGCAGTTTGTGAGAGATCTGGAGCAGCAG 120
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RESULT 2
A98521 2825 bp DNA PAT 26-JAN-2000
LOCUS Sequence 6 from Patent WO9911780.
ACCESSION A98521
VERSION A98521.1 GI:6781607
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SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2825)
AUTHORS Birchmeier, W. and Behrens, J.
TITLE CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
JOURNAL TUMOR ILLNESSES
PATENT: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
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QY 61 aagaagcagagtgaggaatttcctcgagcagcttttgaggaatctggagcagcag 120
DB 2621 AAGAAGCGCAGTGAGCAATTTGCTCCGCGAGCAGTTTGTGAGAGATCTGGAGCAGCAG 2680
QY 121 acagtgctcccatgtacgaagcagagatctg 153
DB 2681 ACAGTGCTCCCATGTACGAGAGCAGAGATCCTG 2713

RESULT 3
AF073788 2825 bp mRNA ROD 13-JUL-1998
LOCUS Mus musculus conductin mRNA, complete cds.
DEFINITION AF073788
ACCESSION AF073788
VERSION AF073788.1 GI:3309246
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2825)
AUTHORS Behrens, J., Jerchow, B.-A., Wurtz, M., Grimm, J., Asbrand, C.,
Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W.
TITLE Functional interaction of an axin homolog, conductin, with
beta-catenin, APC, and GSK3beta
JOURNAL Science 280 (5363), 596-599 (1998)
MEDLINE 98221239
REFERENCE 2 (bases 1 to 2825)
AUTHORS Behrens, J., Jerchow, B.-A. and Birchmeier, W.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center for
Molecular Medicine, Robert-Rössle 10, Berlin 13122, Germany
FEATURES
SOURCE location/Qualifiers
1..2825

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/product="conductin"
/protein_id="AAC26047.1"
/db_xref="GI:3309247"
/translation="MSSAVLVTLDPSSSFREDAPRPVPEEGEETPPCPQSVGKVQ
STKPMVSNARNEDGLPEGRASPDLRTWTKSLHSLGDDGALFRTFLERE
KCVDTLDFWFCNFRGNMLKDTLRVAKYKRIENNSVSKOLKATRTYIDG
IKKOOIGSMFOAOETEIOAVEMNAOYVFLSDIYLEVRSRGENTAAVNSGGSL
KVLCSGLPTLNEEBEWTCDLCKLSPTVYSSKTLRTASVRSSTERNENRSEKR
SDPVNHYVSGVIFAPATSDNSLSDALTDSSMTDSSVDGVPPYRMGSKOLQ
REMRHSVKANGQVSLPFPRTIRLPKEMTPVEPAFAELISRLKLELSRHSLE
ERLQOIREDDEEKEGSEOLASRDGAPVQHPLALPESGYEEDPOTILDHLSRVLT
GCOSPCVGRYSRSPRDHNNHNOCHTLSTGKLPVPAACPLLGKSELTQOT
TKHVNHYIHNHNAVPTKTEIEAATORVRCLPQGTDDYCYSKCKSHKAPEDLGE
OPCSRGCTLPKRNKCTEPGLASARDGMSAAGPOLPEEGDRSDVNMWLES
ERQSKSPHSAQSIKSTIPLESARAPGERSVRRHLLGASGHSRVARAHPTQDPAM
PLTPEPTLAOLEACRLAEVSKPOKRCVAAQOQRNNSAQAQASPRANPSLA
PEDHKEPKLASVHALQASSELVYTFECGEELIPYRMLKAQSLTLGHFEKQLSKGNY
RYVFKASDEPACGAVFEIIMDETVLPMYEGRIILGKVERID"

BASE COUNT 703 a 815 c 813 g 494 t
ORIGIN

Query Match 100.0%; Score 153; DB 94; Length 2825;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttgacctgggccaacttcagaagagcagctcagaacaaaggaataatcaggtattttc 60
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Db 2561 ttgacctgggccaacttcagaagagcagctcagaacaaaggaataatcaggtattttc 2620
|||||

Qy 61 aagaagcgagtgacgaatttcctgcgagagcagttttgaagagatctcggagcagcag 120
|||||
Db 2621 aagaagcgagtgacgaatttcctgcgagagcagttttgaagagatctcggagcagcag 2680
|||||

Qy 121 acagtgctcccatgtacgaagcagagatcctg 153
|||||
Db 2681 acagtgctcccatgtacgaagcagagatcctg 2713
|||||

RESULT 4
AF205889 3016 bp mRNA ROD 03-JAN-2000
LOCUS Mus musculus Axln2 (Axln2) mRNA, complete cds.
DEFINITION AF205889
ACCESSION AF205889.1 GI:6653585
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3016)
AUTHORS Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
Jenkins, N.A., Warburton, D. and Costantini, F.
TITLE Properties of mouse Axln2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
Unpublished
2 (bases 1 to 3016)
AUTHORS Zhang, T. and Costantini, F.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HSC 1416, New York, NY 10032, USA
Location/Qualifiers
1..3016
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/map="between Wnt3 and Pkca"

gene 1..3016
/gene="Axln2"
55..2577
/gene="Axln2"
/codon_start=1
/product="Axln2"
/protein_id="AAF22800.1"
/db_xref="GI:6653586"
/translation="MSSAVLVTLDPSSSFREDAPRPVPEEGEETPPCPQSVGKVQ
STKPMVSNARNEDGLPEGRASPDLRTWTKSLHSLGDDGALFRTFLERE
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IKKOOIGSMFOAOETEIOAVEMNAOYVFLSDIYLEVRSRGENTAAVNSGGSL
KVLCSGLPTLNEEBEWTCDLCKLSPTVYSSKTLRTASVRSSTERNENRSEKR
SDPVNHYVSGVIFAPATSDNSLSDALTDSSMTDSSVDGVPPYRMGSKOLQ
REMRHSVKANGQVSLPFPRTIRLPKEMTPVEPAFAELISRLKLELSRHSLE
ERLQOIREDDEEKEGSEOLASRDGAPVQHPLALPESGYEEDPOTILDHLSRVLT
GCOSPCVGRYSRSPRDHNNHNOCHTLSTGKLPVPAACPLLGKSELTQOT
TKHVNHYIHNHNAVPTKTEIEAATORVRCLPQGTDDYCYSKCKSHKAPEDLGE
OPCSRGCTLPKRNKCTEPGLASARDGMSAAGPOLPEEGDRSDVNMWLES
ERQSKSPHSAQSIKSTIPLESARAPGERSVRRHLLGASGHSRVARAHPTQDPAM
PLTPEPTLAOLEACRLAEVSKPOKRCVAAQOQRNNSAQAQASPRANPSLA
PEDHKEPKLASVHALQASSELVYTFECGEELIPYRMLKAQSLTLGHFEKQLSKGNY
RYVFKASDEPACGAVFEIIMDETVLPMYEGRIILGKVERID"

BASE COUNT 766 a 858 c 837 g 555 t
ORIGIN

Query Match 100.0%; Score 153; DB 94; Length 3016;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttgacctgggccaacttcagaagcagctcagaacaaaggaataatcaggtattttc 60
|||||
Db 2401 ttgacctgggccaacttcagaagcagctcagaacaaaggaataatcaggtattttc 2460
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Qy 61 aagaagcgagtgacgaatttcctgcgagagcagttttgaagagatctcggagcagcag 120
|||||
Db 2461 aagaagcgagtgacgaatttcctgcgagagcagttttgaagagatctcggagcagcag 2520
|||||

Qy 121 acagtgctcccatgtacgaagcagagatcctg 153
|||||
Db 2521 acagtgctcccatgtacgaagcagagatcctg 2553
|||||

RESULT 5
AF017757 3216 bp mRNA ROD 24-APR-1998
LOCUS Rattus norvegicus GSK-3beta interacting protein Axli mRNA, complete
DEFINITION cds.
ACCESSION AF017757
VERSION AF017757.1 GI:3080758
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3216)
AUTHORS Yamamoto, H., Kishida, S., Uochi, T., Ikeda, S., Koyama, S., Asashima, M.
and Kikuchi, A.
TITLE Axli, a member of the Axin family, interacts with both glycogen
synthase kinase 3beta and beta-catenin and inhibits axis formation
of Xenopus embryos
Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
JOURNAL MEDLINE 98226558
REFERENCE 2 (bases 1 to 3216)
AUTHORS Yamamoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1997) Biochemistry, Hiroshima University, School
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,
Japan
Location/Qualifiers
1..3216

CDS

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/db_xref="taxon:10116"
85..2601
/note="GSK-3beta interacting protein; Axin like protein"
/codon_start=1
/product="Axin"
/protein_id="AAC40089.1"
/db_xref="GI:3080759"
/translacion="MSSAVLVTLPLDPSSFRDAPRPVPEEGEPPEPCOPSVKVO
STKPMVSNARNRNEDGPEEGRASPDSPILTRMTKSLHSLIGDDQVAFRTPLRE
KCVDTLDFPACNGSRQNMKDKTLRAKATYRRYIENNSVYSQOLPARKTYTRDC
IKKOQISVMTDQOTEIOAVENNAVIVFTLSDIYLYVSGGENTANGSGSL
KVLGCLPTLNEEEMTCADLCKLSPVTVGLSSTLTATASVRSSTAEANGSFKR
SEPNVHVAGSGVYFAPATNSANDELSDSLDDSMSTDSVDGIPIYRMGSKQLQ
REMRHSVANGQVSLPHPTPTRLPKEMTPVEPAFAELISRLKLELESRSKLE
ERLQOIREDEKEESEGLSSRDGAPVOHPIALLPSGSEEDPOTILLDHLSTYLRTP
GOSPGVRSYRSPRSRPHHHHHCOCALLPTGCKLPPEACPLIGSKSLTYQTK
HVHHHYIHHHVPKTEETLEATDQVRCCLCPGGIDYICYSCKSHSKPPEPLPEOP
CGSRGTLPKNTKGTETPGALIPAREGSMSSAAGAPQLGEGRSQDVWOMLESER
OSKSPHSTOSIRKSYPLESARAPGERVSHHLLGAPRPSARAPHTQDAMP
LTPPTLQLEACRLEAVSKPKQRCVSAQOORHHPATGAGPTSPNSLASE
DHKEPKRLASVHALOASELIYTFECGEETIRYRMLKQSLTLGHFKQSLSKKNYR
YFKASDFACGAVPEEIMDEFTVLPMEGRILGVERID"

BASE COUNT 860 a 914 c 872 g 570 t

ORIGIN

Query Match 93.7% Score 143.4 DB 94 Length 3216;
Best Local Similarity 96.1% Pred. No. 1.2e-34;
Matches 147; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ttgacctggcgccactcaaggagcagctcagcaaaagggaattacaggtatatttc 60
|||||
Db 2425 TTGACCTGGCGCAGCTTCAAGAGCAGCTCAGCAAAAGGAATTACAGTATTACTTC 2484
|||||
Oy 61 aagaagcgagtgaggaattgctctcgagcaggttttgagagatctggagcagcag 120
|||||
Db 2485 AAGAAAGCGCAGTGAGCAATTCCTGTGAGCAGCTTTGAGAGATCTGGGATGATGAG 2544
|||||
Oy 121 acagtgctcccatgtacgaagcagcagctctg 153
|||||
Db 2545 ACGTGTCTCCCATGTACGACGAGCATCTGTG 2577
|||||

RESULT 6
AB052751 1863 bp mRNA PRI 21-DEC-2000
LOCUS Homo sapiens Axin2 mRNA for conductin, partial cds and 3'UTR.
DEFINITION AB052751
ACCESSION AB052751.1 GI:11967903
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Homology: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Takahashi,M. and Furukawa,Y.
TITLE Identification of 3' UTR of Axin2
JOURNAL Published Only in Database (2000) In press
REFERENCE 2 (bases 1 to 1863)
AUTHORS Nakamura,Y., Furukawa,Y. and Takahashi,M.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yotchi
Furukawa, Institute of Medical Science, Human Genome Center, 4-6-1-
Shirokane-dai, Minato-Ku, Tokyo 108-1639, Japan
(E-mail:furukawa@ims.u-tokyo.ac.jp, Tel:81-35449-5373,
Fax:81-35449-5406)

FEATURES
SOURCE 1..1863
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..1863
gene
/gene="Axin2"

CDS

<1..446
/gene="Axin2"
/codon_start=3
/product="conductin"
/protein_id="BAB19762.1"
/db_xref="GI:11967904"
/translacion="LEACRRLAEVSPKQRCVSAQDRHNSATVGTGAPFNSP
SLAPEDKEPKLAGHALOASELIYTFECGEETIRYRMLKQSLTLGHFKQSLSK
KNYRYFKKASDFACGAVPEEIMDEFTVLPMEGRILGVERID"
447..1863
/gene="Axin2"
3'UTR

BASE COUNT 484 a 375 c 452 g 552 t

ORIGIN

Query Match 79.1% Score 121 DB 85 Length 1863;
Best Local Similarity 86.9% Pred. No. 1.3e-27;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ttgacctggcgccactcaaggagcagctcagcaaaagggaattacaggtatatttc 60
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Db 270 TTGACCTGGCGCAGCTTCAAGAGCAGCTCAGCAAAAGGAATTACAGTATTACTTC 329
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Oy 61 aagaagcgagtgaggaattgctctcgagcaggttttgagagatctggagcagcag 120
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Db 330 AAAAAGCAAGCAGATGAGTTCCTGTGAGCAGCTTTGAGAGATCTGGGAGATGAG 389
|||||

Oy 121 acagtgctcccatgtacgaagcagcagctctg 153
|||||
Db 390 ACGTGTCTCCCATGTACGACGAGCATCTGTG 422
|||||

RESULT 7
AK025718 2104 bp mRNA PRI 29-SEP-2000
LOCUS Homo sapiens cDNA: FLN22065 fls, clone HEP10566, highly similar to
DEFINITION AF078165 Homo sapiens conductin mRNA.
ACCESSION AK025718
VERSION AK025718.1 GI:10438327
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:Hepl02 cDNA to mRNA, clone_11b:HEP
clone:HEP10566.
ORGANISM Homo sapiens
Homology: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kawabata,A., Hiki,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Odayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEBO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 2104)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Odayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center,
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEBO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
SOURCE 1..2104
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hepl02"

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/cell_type="hepatoma"
/clone="HEP10566"
/clone_11b="HEP"
/note="cloning vector pHE18SFL3"
misc_feature
1. 2104
/note="highly similar to AF078165 Homo sapiens conductin
mRNA"
BASE COUNT      506 a      610 c      619 g      369 t
ORIGIN

Query Match
Best Local Similarity 86.9%; Pred. No. 1.3e-27;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ttgaccctggccacttcaagagcagctcagcaaaaggaatactagattatc 60
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Db 1667 ttgacctggccactttaaagagcagctcagcaaaaggaatactagattatc 1726
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QY 61 aagaagcgagtgagcaaatctgctcgagagcagcttttgaagagatctggagcagcag 120
|||||
Db 1727 aaaaaagcaagcagatgagcttgccttgagcagcgtgttgagagatctggagagatgag 1786
|||||

QY 121 acagtgctcccatgtacgagcagcagctctg 153
|||||
Db 1787 acggtctcccatgtatgagcagcagctctg 1819
|||||

RESULT 8
AF205888 2538 bp mRNA PRI 03-JAN-2000
LOCUS Homo sapiens AXIN2 (AXIN2) mRNA, complete cds.
DEFINITION AF205888
ACCESSION AF205888.1 GI:6653583
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 2538)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G.,
Jenkins, N.A., Warburton, D. and Costantini, F.
Properties of mouse Axin2 and human AXIN2: chromosomal location,
expression pattern, interaction with Axin and effects on embryonic
axis formation
Unpublished
JOURNAL 2 (bases 1 to 2538)
REFERENCE Zhang, T. and Costantini, F.
AUTHORS Direct Submission
TITLE Submitted (16-NOV-1999) Genetics & Development, Columbia
JOURNAL University, 701 W68th St. HHSC 1416, New York, NY 10032, USA
FEATURES
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1. 2538
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/db_xref="taxon:9606"
/chromosome="17"
/map="17q24"
/tissue_type="Brain; Lymphoblast"
/note="similar to ESTs 823683 and 446378"
1. 2538
/gene="AXIN2"
110. 2443
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/db_xref="GI:6653584"
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CVDITLDFWACNGFROMLKDTLRVAKATKRIENNSIVSKOLPATKTYIRGIGI
KQOIDSIMFDOAGTQEIQSVMEBNAYOMFLTSDIYLEYRSGGENTAYVNSNGIGSLK
VVCGLTPTNEEREEMTCADFCKLSPYVGLSKTLRATVASYRSTETVDSGYSFERS
DVVNYHIGSGIVFAPATISANDSEISSDLTDDSMKMTDSSVDGIPRYVNGSKKOLR
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EMHRSVKANGRVSLPHFPTTHRLPKEMTPVDPATEAELISRLKLELESRHSLEE
RLOOIREDEBERGSELTLSNREGAPLOHLSLPSGSYEDPOTLIDHLSRVLTGPG
COSPGVGRSPRSRSDHNNHNSOYHSLPFGCKLRPAASPGCLGSGFYTKO
TKTHVNHHTIHHNAVPKTELEAETQVHOCPCREGSEYTCYSCKSKSRAPETMPS
EOPGAOSTKRAYPLESARSSPGERRHHLWGNSSGHPTTPRALFTDPPMPSLTP
PMTLALHEACRRLAEVSKRPKORCCVAAQOQDRNHSATVQCATPFSNLAPEDHK
EPKLAGVIALOASLWVTFYFGEIEIPYRMLKQSLTGHFKBOLSKGNVRYFYK
KASDFACAGVFEIEMEDETVLPMVEGRILGVERLD"
BASE COUNT      617 a      724 c      724 g      473 t
ORIGIN

Query Match
Best Local Similarity 86.9%; Pred. No. 1.4e-27;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ttgaccctggccacttcaagagcagctcagcaaaaggaatactagattatc 60
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Db 2267 ttgacctggccactttaaagagcagctcagcaaaaggaatactagattatc 2326
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QY 61 aagaagcgagtgagcaaatctgctcgagagcagcttttgaagagatctggagcagcag 120
|||||
Db 2327 aaaaaagcaagcagatgagcttgccttgagcagcgtgttgagagatctggagagatgag 2386
|||||

QY 121 acagtgctcccatgtacgagcagcagctctg 153
|||||
Db 2387 acggtctcccatgtatgagcagcagctctg 2419
|||||

RESULT 9
AF078165 3072 bp mRNA PRI 21-MAR-1999
LOCUS Homo sapiens conductin mRNA, complete cds.
DEFINITION AF078165
ACCESSION AF078165
VERSION AF078165.1 GI:4454790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 3072)
Mali, M., Qian, C., Yokomizo, A., Smith, D. I. and Liu, W.
Cloning of the human homolog of conductin (AXIN2), a gene mapping
to chromosome 17q23-q24
Genomics 55 (3), 341-344 (1999)
JOURNAL 99168905
MEDLINE
REFERENCE 2 (bases 1 to 3072)
AUTHORS Mali, M., Qian, C., Smith, D. I. and Liu, W.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo Clinic,
200 First Street SW, Rochester, MN 55905, USA
FEATURES
source
1. 3072
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/chromosome="17"
/map="17q23-q24"
90. 2621
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/product="conductin"
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/db_xref="GI:4454791"
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IKQOIDSIMFDOAGTQEIQSVMEBNAYOMFLTSDIYLEYRSGGENTAYVNSNGIGSLK
KYVCGTLPTENEEREEMTCADFCKLSPYVGLSKTLRATVASYRSTETVDSYRSRKR
SDPVNUNHIGSGVGFAPATISANDSEISSDLTDDSMKMTDSSVDGIPRYVNGSKOLR
REMHRSVKANGRVSLPHFPTTHRLPKEMTPVDPATEAELISRLKLELESRHSLEE
ERLOOIREDEBERGSELTLSNREGAPLOHLSLPSGSYEDPOTLIDHLSRVLTGPG
COSPGVGRSPRSRSDHNNHNSOYHSLPFGCKLRPAASPGCLGSGFYTKO
TKTHVNHHTIHHNAVPKTELEAETQVHOCPCREGSEYTCYSCKSKSRAPETMPS
EOPGAOSTKRAYPLESARSSPGERRHHLWGNSSGHPTTPRALFTDPPMPSLTP
PMTLALHEACRRLAEVSKRPKORCCVAAQOQDRNHSATVQCATPFSNLAPEDHK
EPKLAGVIALOASLWVTFYFGEIEIPYRMLKQSLTGHFKBOLSKGNVRYFYK
KASDFACAGVFEIEMEDETVLPMVEGRILGVERLD"
OTTKVNHHTIHHNAVPKTELEAETQVHOCPCREGSEYTCYSCKSKSRAPETMPS
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BASE COUNT 769 a 838 c 883 g 582 t
 BRIGIN

Query Match	79.1%	Score 121	DB 88	Length 3072
Best Local Similarity	86.9%	Pred. 0.14e-27		
Matches 133	Conservative	0	Mismatches 20	Indels 0
			Gaps 0	
QY 1	ttgacctggygcacattcaagagcagctcagcaaaagggaattacaggtattatttc	60		
Db 2445	TTGACCTGGGCGCCACTTTAAAGAGAGCCTCAGCAAAAAGGAATTATAGGATTACTTC	2504		
QY 61	aagaagcgagattgcgaatttcgctcgcgagacagttttttagggagatctgggacgaag	120		
Db 2505	AAAAAAGCAACCGATGATGATTTGGCCGTGTGGACCGGCTGTTGAGGAGATCTGGGAGAGATGAG	2564		
QY 121	acagtgctcccatgtacgaagacagagctgctg	153		
Db 2565	ACGGTCTCTCCGATGTATGAAGGCCCGGATTTCTG	2597		

RESULT	10
LOCUS	AF009012
DEFINITION	AF009012 3156 bp mRNA
ACCESSION	Gallus gallus axin mrna, complete cds.
VERSION	AF009012.1 GI:2252817
KEYWORDS	.
SOURCE	chicken.
ORGANISM	Gallus gallus
VRT	15-JUL-1997

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	(bases 1 to 3156)	Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasicek, T. J., Perry, W. L. 3rd, Lee, J. J., Tillyman, S. M., Gumbiner, B. M. and Costantini, F.	The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation	Cell 90 (1), 181-192 (1997)	2	(bases 1 to 3156)	Zeng, L., Zhang, T., Perry, W. L. III, Lee, J. J. and Costantini, F.	Direct Submission	Submitted (13-JUN-1997) Genetics and Development, Columbia University, 701 W. 168th Street, New York, NY 10032, USA

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gene      /organism="Gallus gallus"
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          /gene="Axin"
          /note="Fused is the classical dominant mouse tail kink
mutation due to an IAP insertion in the Axin gene"
CDS       256..2783

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/function"may inhibit embryonic axis formation"
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/product="Axin"
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ORIGIN
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LOCUS	AF009674	3411 bp	mrna	PRI	15-JUL-1997
DEFINITION	Homo sapiens axin (AXIN) mRNA, partial cds.				
ACCESSION	AF009674				
VERSION	AF009674.1	GI:2252819			
KEYWORDS					
SOURCE	human.				

REFERENCE AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 3411)
Vasicek,T.J., Zeng,L., Guan,X.-J., Zhang,T., Costantini,F. and Tilghman,S.M.

TITLE
Two dominant mutations in the mouse fused gene are the result of transposon insertions

JOURNAL
Genetics (1997) in press

REFERENCE AUTHORS
2 (bases 1 to 3411)
Zeng,L., Fogotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L., 3rd, Lee,J.-J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F.
The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation

TITLE
Cell 90 (1), 181-192 (1997)
97373830

JOURNAL
MEDLINE
3 (bases 1 to 3411)
Vasicek,T.J., Tilghman,S.M., Costantini,F., Zeng,L., Perry,W.L. III and Zhang,T.

TITLE
Direct Submission

JOURNAL
Submitted (22-JUN-1997) Biological Technology, Millennium Pharmaceuticals, Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
Location/Qualifiers

FEATURES

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CDS

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a	1012	c	1088	g	771	t
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ORIGIN

Query match	53.76;	Score 82.2;	DB 94;	Length 3761;
Best local similarity	71.58;	Pred NO 3	5a-15.	

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Db 2866 AGAAGTGAATGACTTTGACTGTGCTGCTA

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Job time: 20991 sec

Job time: 20991 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:31:59 ; Search time 276.75 Seconds
(without alignments)
322.741 Million cell updates/sec

Title: US-09-587-574-10
Perfect score: 153
Sequence: 1 ttgaacctggccacttcaa.....ttgaagaagcagatctctg 153

Scoring table: IDENTITY_NUC
Gapop 10.0, Capext 1.0

Searched: 678276 seqs, 291890651 residues
Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	153	100.0	2523	20	X23370 Human conductin CD
2	153	100.0	2825	20	X23369 Human conductin DN
3	121	79.1	401	21	A77754 cDNA encoding huma
4	121	79.1	1205	21	A77843 cDNA encoding huma
5	88.6	57.9	3411	20	X09012 Human axin gene.
6	82.2	53.7	3761	20	X09013 Murine axin gene.
7	33	21.6	925	12	Q12839 Variable region of
8	30.2	19.7	657	14	Q36130 M4H7 Mab heavy ch
9	29.6	19.3	363	21	C41830 Arabidopsis thalia
10	29.6	19.3	575	21	C33133 Arabidopsis thalia
11	29.6	19.3	623	21	C51167 Arabidopsis thalia

12	29.6	19.3	627	21	C38945 Arabidopsis thalia
13	29.6	19.3	811	21	C51169 Arabidopsis thalia
14	29.6	19.3	825	21	C35517 Arabidopsis thalia
15	29.2	19.1	340	16	T19983 Human gene signatu
16	29.2	19.1	1397	21	A52642 Eosinophil activat
17	29.2	19.1	1484	21	C47412 Arabidopsis thalia
18	29.2	19.1	1487	21	C36225 Arabidopsis thalia
19	28.8	18.8	1815	21	C79811 Human secreted pro
20	28.8	18.8	5503	21	C74570 Human ORX ORF125
21	28.4	18.6	1021	21	C37835 Arabidopsis thalia
22	28.2	18.4	457	21	A67611 Eucalyptus grandis
23	28	18.3	1130	21	C40313 Arabidopsis thalia
24	28	18.3	1130	21	C48750 Arabidopsis thalia
25	27.6	18.0	1404	18	T93777 cDNA encoding Arab
26	27.6	18.0	1890	20	T52940 Human prostate tum
27	27.4	17.9	1041	21	A49788 Arabidopsis wax sy
28	27.4	17.9	1041	21	A38860 Arabidopsis wax sy
29	27.4	17.9	1041	21	A38860 Arabidopsis wax sy
30	27.2	17.8	559	21	C65784 Human lung cancer-
31	27.2	17.8	1289	21	P12525 Aspergillus oryzae
32	27	17.6	6741	21	A10595 Gene encoding a su
33	26.8	17.5	300	20	Z14749 Human gene express
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35	26.8	17.5	8102	20	X13181 Enterococcus faeca
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37	26.6	17.4	1935	20	Z30413 Arabidopsis thalia
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39	26.4	17.3	770	20	Z15585 Human gene express
40	26.4	17.3	1166	20	Z19440 M. tuberculosis an
41	26.4	17.3	1166	20	Z19440 M. tuberculosis re
42	26.4	17.3	1242	21	C35947 Arabidopsis thalia
43	26.4	17.3	1377	21	Z91259 Coa ligase fccf nu
44	26.4	17.3	8648	20	X20550 Polynucleotide seq
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ALIGNMENTS

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ID X23370	X23370 standard; CDNA: 2523 BP.
XX X23370:	
XX	17-JUN-1999 (first entry)
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DE	Human conductin cDNA.
XX	
KW	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW	Wingless signalling pathway; Adenomatous Polyposis Coll; APC;
KW	tumour suppressor; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09911780-A2.
XX	
PD	11-MAR-1999.
XX	
PF	01-SEP-1998: 98WO-DE02621.
XX	
PR	02-SEP-1997: 97DE-1038205.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Behrens J, Birchmeier W;
XX	
DR	WPI: 1999-214706/18.
XX	
DR	P-PSDB: W93570..
XX	
PT	Tumor-suppressing protein conductin - used for treatment and
	diagnosis of tumors

XX
PS Claim 18; Fig 3; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
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SQ Sequence 2523 BP; 620 A; 728 C; 723 G; 452 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 5.1e-41;
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Db 2407 aagaagcgagtgacgaatttgcctcgagcagcttttgaaggagactcgagcagcag 2466
QY 121 acagtgtcccatgtacgaaggcagatcctg 153
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ID X23369 standard; cDNA; 2825 BP.
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AC X23369;
XX
DT 17-JUN-1999 (first entry)
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DE Human conductin DNA.
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KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW tumour suppressor; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS
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FT 446..814
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FT /*tag= e
FT /*note= "Discovered homology region as described in
FT Claim 22"
XX
XX WO9911780-A2.
XX
XX 11-MAR-1999.
XX
PD

XX
PF 01-SEP-1998; 98WO-DE02621.
XX
XX
PR 02-SEP-1997; 97DE-1038205.
XX
XX
PA (DEIB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Behrens J, Birchmeier W;
XX
DR WPI: 1999-214706/18.
DR P-PSDB; W93569.
XX
PT Tumor-suppressing protein conductin - used for treatment and
PT diagnosis of tumors
XX
PS Claim 18; Fig 2; 22pp; German.
XX
CC This invention describes a novel human conductin protein which has
CC anti-tumour activity. Detecting the presence or amount of conductin,
CC at protein or nucleic acid levels, is used to diagnose tumours, while
CC agents that (re)activate conductin are used for tumour therapy.
CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
CC resulting in blockade of the Wnt/Wingless signalling pathway in
CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
CC fragments and, in conjunction with APC, acts as a tumour suppressor.
XX
SQ Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;

Query Match 100.0%; Score 153; DB 20; Length 2825;
Best Local Similarity 100.0%; Pred. No. 5.3e-41;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC A77754;
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DT 14-NOV-2000 (first entry)
XX
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KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
KW immunotherapy; diagnosis; progression; ss.
XX
OS Homo sapiens.
XX
PN WO200037643-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US30909.
XX
XX
PR 23-DEC-1998; 98US-0221298.
PR 02-JUL-1999; 99US-0347496.
PR 22-SEP-1999; 99US-0401064.
PR 19-NOV-1999; 99US-0444242.
PR 02-DEC-1999; 99US-0454150.
XX
XX

PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yugu J;
XX
DR WPI: 2000-442671/38.
XX
XX New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer -
XX
XX
PS Claim 1: Page 96-97; 229pp; English.
XX
XX Sequences A77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumours.
CC The invention also specifically discloses 8 human colon tumour proteins
CC (B11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be
CC cloned and then administered back to the patient to inhibit cancer
CC development. Nucleic acids encoding the polypeptides and antibodies
CC against the polypeptides may be used to determine the expression level
CC of a tumour protein of the invention, and therefore to determine whether
CC cancer cells are present. Such diagnostic methods may also be used to
CC monitor the progression of a cancer by repeating the processes at time
CC intervals, and comparing the current result to previous results. The
CC present sequence represents a cDNA encoding a human colon tumour
CC polypeptide.
CC
XX Sequence 401 BP; 105 A; 88 C; 123 G; 85 T; 0 other;
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Query Match 79.1%; Score 121; DB 21; Length 401;
Best Local Similarity 86.9%; Pred. No. 1e-30;
Matches 133; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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OY 61 aagaagcgagtgacgaatttgctcgtgagcgtttttagagagatctggcgag 120
DB 258 aaaaaagcagcagtgagcttgctcgtgagcgtttttagagagatctggcgag 317
QY 121 acagtgctcccatgtacgaagcagagctcgt 153
DB 318 acggtgtcccgatgtatgaaagccgagctctg 350

RESULT 4
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AC A77843;
XX
DT 14-NOV-2000 (first entry)
XX
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:123.
XX
KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
XX Immunotherapy; diagnosis; progression; ss.
OS Homo sapiens.
XX
PN WO200037643-A2.

XX
PD 29-JUN-2000.
XX
XX
PF 23-DEC-1999; 99WO-US30909.
XX
XX 23-DEC-1998; 98US-0221298.
XX 02-JUL-1999; 99US-0347496.
PR 22-SEP-1999; 99US-0401064.
PR 19-NOV-1999; 99US-0444242.
PR 02-DEC-1999; 99US-0454150.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yugu J;
XX
DR WPI: 2000-442671/38.
XX
XX New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer -
XX
XX
PS Claim 1: Page 125-126; 229pp; English.
XX
XX Sequences A77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumours.
CC The invention also specifically discloses 8 human colon tumour proteins
CC (B11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be
CC cloned and then administered back to the patient to inhibit cancer
CC development. Nucleic acids encoding the polypeptides and antibodies
CC against the polypeptides may be used to determine the expression level
CC of a tumour protein of the invention, and therefore to determine whether
CC cancer cells are present. Such diagnostic methods may also be used to
CC monitor the progression of a cancer by repeating the processes at time
CC intervals, and comparing the current result to previous results. The
CC present sequence represents a cDNA encoding a human colon tumour
CC polypeptide.
CC
XX Sequence 1205 BP; 316 A; 248 C; 324 G; 317 T; 0 other;
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OY 61 aagaagcgagtgacgaatttgctcgtgagcgtttttagagagatctggcgag 120
DB 264 aaaaaagcagcagtgagcttgctcgtgagcgtttttagagagatctggcgag 323
QY 121 acagtgctcccatgtacgaagcagagctcgt 153
DB 324 acggtgtcccgatgtatgaaagccgagctctg 356

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XX
AC X09012;

DB 2926 ccgcttcgctcttcttgagaagaatcat 2956

RESULT 7

ID 012839 standard; DNA: 925 BP.

AC 012839;

DT 17-OCT-1991 (first entry)

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DE Pseudomonas aeruginosa.

XX Monoclonal antibody; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FH 366..729

XX FT /tag= a

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XX FT /note= "Claim 3"

XX PN JP03151876-A.

XX PD 28-JUN-1991.

XX PF 08-NOV-1989; 89JP-0291981.

XX PR 08-NOV-1989; 89JP-0291981.

XX PA (SUMO) SUMITOMO CHEM IND KK.

XX PA (SUMI -) SUMITOMO SEIYAKU KK.

XX DR WPI: 1991-234064/32.

XX DR P-PSDB; R13182.

XX PT Human antibody gene and corresp. recombinant plasmid or virus -

XX PT useful in mass -prodn. of human anti Pseudomonas aeruginosa LPS

XX PS outside core antibody.

XX PS Disclosure: Fig 2; 16pp; Japanese.

XX CC The region encoding the VH region is used to construct a recombinant

XX CC antibody with a lambda light chain. The antibody recognises an

XX CC antigenic determinant on the outside core in LPS of P. aeruginosa.

XX CC See also Q12840.

XX SQ Sequence 925 BP; 186 A; 231 C; 270 G; 237 T; 1 other;

XX

XX

XX

XX

XX

XX

AC 036133;

XX 25-MAY-1993 (first entry)

XX DT MH4H7 MAb heavy chain coding sequence.

XX DE Human; heavy chain; recombinant; monoclonal; antibody; MAb; MH4H7;

XX KW Namalwa; microbial infection; ss.

XX OS Synthetic.

XX XX

XX FH

XX FT

XX FT

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XX FT

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SQ Sequence 657 BP; 150 A; 150 C; 193 G; 164 T; 0 other;

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DB 81 tgccttcgagcagcgttttgaagagatctggagcagacagacagtgctcccatgtacga 140

DB 594 tgccttcgagcgtgggtcttctgatactcggccaaaggacaatggtcacgcgtctctc 653

DB 141 agg 143

DB 654 agg 656

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DB

DB

DB

RESULT 9

ID 036133 standard; DNA: 363 BP.

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AC C41830;
XX 17-OCT-2000 (first entry)
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
PN EPI033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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XX
AC C33133;
XX
DT 17-OCT-2000 (first entry)

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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 1908.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
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RESULT 12

C38945 C38945 standard; DNA; 627 BP.

XX AC C38945;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 22779.

KW Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.

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XX PD 06-SEP-2000.
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RESULT 15
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XX 17-JUL-1996 (first entry)
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XX KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX OS Homo sapiens.
XX PN W09514772-A1.
XX 01-JUN-1995.
XX PD 11-NOV-1994; 94WO-JP01916.
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 PA (OKUBO/) OKUBO K.
 XX
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PI Matsubara K, Okubo K;
 XX

DR WPI: 1995-206931/27.
 XX

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX

PS Claim 1; Page 528; 2245pp; Japanese.
 XX

XX A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in T19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using Poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
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SO Sequence 340 BP; 82 A; 87 C; 95 G; 75 T; 1 other;

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OY 66 ggcgagtgacgaatttgctgcggagcagt 95

DB 138 gccatgagctgacggtctccctgagcagt 167

Search completed: June 7, 2001, 00:32:01
 Job time: 8639 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 00:26:48 ; Search time 136.23 Seconds

(without alignments)
196.096 Million cell updates/sec

Title: US-09-587-574-10

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	27.2	17.8	559	4	US-09-040-984-45	Sequence 45, Appl1
4	26.6	17.4	4565	3	US-08-776-265-2	Sequence 2, Appl1
5	26.6	17.0	1902	2	US-09-258-257-1	Sequence 1, Appl1
6	26.6	17.0	1902	2	US-09-258-371-1	Sequence 1, Appl1
7	26.6	17.0	1902	4	US-08-569-721A-1	Sequence 1, Appl1
8	26.6	17.0	1902	4	US-08-751-230-1	Sequence 1, Appl1
9	26.6	17.0	1902	4	US-09-499-082-1	Sequence 1, Appl1
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21	25.4	16.6	10825	4	US-08-834-497A-3	Sequence 3, Appl1
22	25.4	16.6	10825	4	US-08-834-497A-5	Sequence 5, Appl1
23	25.4	16.6	10825	4	US-08-834-497A-7	Sequence 7, Appl1
24	25.4	16.6	10825	4	US-08-947-823-1	Sequence 1, Appl1
25	25.4	16.6	51952	4	US-08-724-394A-20	Sequence 20, Appl1
26	25.4	16.6	246240	2	US-08-724-394A-21	Sequence 21, Appl1
27	25.4	16.6	246240	2	US-08-724-394A-22	Sequence 22, Appl1

28	25.4	16.6	246240	2	US-08-724-394A-21	Sequence 21, Appl1
29	25.4	16.6	246240	4	US-08-724-394A-22	Sequence 22, Appl1
30	25.4	16.3	1289	4	US-08-358-627F-22	Sequence 22, Appl1
31	25.4	16.3	1620	6	5449756-10	Patent No. 5449756
32	25.4	16.3	2306	6	5198359-3	Patent No. 5198359
33	25.4	16.3	2306	6	5449756-3	Patent No. 5449756
34	25.4	16.3	5057	3	US-08-651-999A-6	Sequence 6, Appl1
35	25.4	16.3	11461	3	US-08-669-161A-29	Sequence 29, Appl1
36	24.8	16.2	2574	2	US-08-677-734A-8	Sequence 8, Appl1
37	24.6	16.1	3923	4	US-08-860-635A-20	Sequence 20, Appl1
38	24.6	16.1	34303	2	US-08-735-609-4	Sequence 4, Appl1
39	24.6	16.1	34303	2	US-08-735-609-4	Sequence 4, Appl1
40	24.6	16.1	34303	3	US-09-315-372-4	Sequence 4, Appl1
41	24.6	16.1	34303	3	US-09-245-497-4	Sequence 4, Appl1
42	24.6	16.1	34303	3	US-09-245-497-4	Sequence 4, Appl1
43	24.6	16.1	35935	2	US-08-735-609-1	Sequence 1, Appl1
44	24.6	16.1	35935	2	US-08-735-609-1	Sequence 1, Appl1
45	24.6	16.1	35935	3	US-08-379-452-43	Sequence 43, Appl1

ALIGNMENTS

RESULT 1
US-08-261-110A-3
Sequence 3, Application US/08261110A
Patent No. 5674992
GENERAL INFORMATION:
APPLICANT: JAGENDORF, ANDRE
APPLICANT: CERUTTI, HERIBERTO
TITLE OF INVENTION: CDNA ENCODING A RECA HOMOLOG IN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-JUN-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,332
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/10231(D-1292A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-261-110A-3

Query Match 18.0%; Score 27.6; DB 1; Length 1167;
Best Local Similarity 58.5%; Pred. No. 2.4;
Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,265
FILING DATE: 24-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Flinaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 03806.0394-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4444
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-776-265-2

Query Match 17.4%; Score 26.6; DB 3; Length 4565;
Best Local Similarity 63.1%; Pred. No. 9.1;
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 13 cacttaagagagcagctcagcaaaagggaattacaggtattattcaagaagcgagt 72
DB 4273 CACGTCGATGATGCTACACCTAAAGAAATTAGAAATATTCTCATTAAGTGCAC 4214
OY 73 gacga 77
DB 4213 CACGA 4209

RESULT 5
US-09-258-257-1/c
Sequence 1, Application US/09258257
Patent No. 5965398
GENERAL INFORMATION:
APPLICANT: GARKAVTSEV, Igor
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
NUMBER OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mool, Leslie A.

REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 109..738
US-09-258-257-1

Query Match 17.0%; Score 26; DB 2; Length 1902;
Best Local Similarity 57.3%; Pred. No. 10;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 6 cctgggcccacttaagagcagctcagcaaaagggaattacaggtattattcaaga 65
DB 1132 CATGCCCAATTAAATAAATTGTTCAATAATAATTACTGTATTAATAATAA 1073
OY 66 ggcgagtgacgaattgcctgc 87
DB 1072 AGCTAATGAATAATTTCCTTC 1051

RESULT 6
US-09-258-371-1/c
Sequence 1, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
NUMBER OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mool, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear


```

? APPLICANT: Helbing, Caren C.
? APPLICANT: Riabowol, Karl
? APPLICANT: Johnston, Randall N.
? APPLICANT: Garkavtsev, Igor
? TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
? NUMBER OF SEQUENCES: 23
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Burns, Doane, Swecker & Mathis
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/499,082
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/828,158
? FILING DATE: 27-MAR-1997
? APPLICATION NUMBER: US 08/751230
? FILING DATE: 15-NOV-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/569721
? FILING DATE: 08-DEC-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Mool, Leslie A.
? REGISTRATION NUMBER: 37,047
? REFERENCE/DOCKET NUMBER: 028722-148
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-854-7400
? TELEFAX: 650-854-8275
? INFORMATION FOR SEQ. ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1902 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 109..741
?
? US-09-499-082-1
?
Query Match 17.0%; Score 26; DB 4; Length 1902;
Best Local Similarity 57.3%; Pred. No. 10;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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OY 6 cctggcgccacttcaggagcgtcagcaaaagggaattacaggtatttcaggaa 65
DB 1132 CATGGCCAAATTAATAAAATTTTCATTAAGTATATATTACTTGATTAATAATAAAA 1073
OY 66 ggcgagtgacgaattgctgc 87
DB 1072 ACCTAATGAATATTTTCCTTC 1051
?
RESULT 10
? Sequence 9, Application US/09258371
? Patent No. 5986078
? GENERAL INFORMATION:
? APPLICANT: Garkavtsev, Igor
? APPLICANT: Riabowol, Karl
? TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
? NUMBER OF SEQUENCES: 23
? SUPPRESSOR GENE: INGI
```

```

? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Burns, Doane, Swecker & Mathis
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/258,371
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/751,230
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Mool, Leslie A.
? REGISTRATION NUMBER: 37,047
? REFERENCE/DOCKET NUMBER: 028722-144
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-854-7400
? TELEFAX: 415-854-8275
? INFORMATION FOR SEQ. ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2061 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 16..900
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? US-09-258-371-9
?
Query Match 17.0%; Score 26; DB 2; Length 2061;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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OY 6 cctggcgccacttcaggagcgtcagcaaaagggaattacaggtatttcaggaa 65
DB 1291 CATGGCCAAATTAATAAAATTTTCATTAAGTATATATTACTTGATTAATAATAAAA 1232
OY 66 ggcgagtgacgaattgctgc 87
DB 1231 ACCTAATGAATATTTTCCTTC 1210
?
RESULT 11
? Sequence 9, Application US/08751230
? Patent No. 6117633
? GENERAL INFORMATION:
? APPLICANT: Garkavtsev, Igor
? APPLICANT: Riabowol, Karl
? TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
? NUMBER OF SEQUENCES: 23
? SUPPRESSOR GENE: INGI
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Burns, Doane, Swecker & Mathis
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-08-751-230-9

Query Match 17.0%; Score 26; DB 4; Length 2061;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 6 cctgggccactcaaggagcagctcagcaaaagggaattcaggtattttcaaga 65
DB 1291 CATGGCCATTAAAAAATTTGTCATTAAGTAATTAATTTACTGTATTAATAAATAA 1232
OY 66 ggcgagtgacgaattgcctgc 87
DB 1231 ACCTAATGAATATTTTCCTTC 1210

RESULT 12
US-09-499-082-9/C
Sequence 9, Application US/09499082
Patent No. 6143522
GENERAL INFORMATION:
APPLICANT: Heibing, Caren C.
APPLICANT: Rabbowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-09-499-082-9

Query Match 17.0%; Score 26; DB 4; Length 2061;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 6 cctgggccactcaaggagcagctcagcaaaagggaattcaggtattttcaaga 65
DB 1291 CATGGCCATTAAAAAATTTGTCATTAAGTAATTAATTTACTGTATTAATAAATAA 1232
OY 66 ggcgagtgacgaattgcctgc 87
DB 1231 ACCTAATGAATATTTTCCTTC 1210

RESULT 13
US-08-846-762-1/C
Sequence 1, Application US/08846762A
Patent No. 5994072
GENERAL INFORMATION:
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: OF O-Antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 24417
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-08-846-762-1

Query Match 17.0%; Score 26; DB 2; Length 24417;
Best Local Similarity 50.8%; Pred. No. 28;
Matches 62; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 20093 TGCGCCATGGCCAGACGACGCGATCAGACGATGCTCAACCCAGTAGTTGAAC 20034
OY 61 aagaagcgagtgacgaatttgcctcgagagcagttttgagagagatctggagcagcag 120
DB 20033 ACCAGGGAACGCGACACCGCCGCGGAGCGGTACCATATAGCAGCAGCAGCAGG 19974
OY 121 ac 122
11

DB 19973 AC 19972

RESULT 14

US-08-469-412A-3/C

Sequence 3, Application US/08469412A

Patent No. 5856125

GENERAL INFORMATION:

APPLICANT: Mavrothalassitis, George J.

APPLICANT: Blair, Donald G.

APPLICANT: Fisher, Robert J.

APPLICANT: Beal Jr., Gregory J.

APPLICANT: Athanaslou, Merope A.

TITLE OF INVENTION: The ERF Genetic Locus and Its Products

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,412A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Mackowski, Eugenia

REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 015280-229000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2432 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 123..698

OTHER INFORMATION:

US-08-469-412A-3

/note- "human alternatively spliced ERF

US-08-469-412A-3

US-08-469-412A-3

US-08-469-412A-3

US-08-469-412A-3

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US-08-469-412A-3

US-08-469-412A-3

US-08-469-412A-3

US-08-469-412A-3

US-08-469-412A-3

Sgouras, Dionysios N.

TITLE OF INVENTION: The ERF Genetic Locus and Its Products

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,715

FILING DATE: 10-Feb-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Mackowski, Eugenia

REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 015280-229000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2432 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 123..698

OTHER INFORMATION:

/note- "human alternatively spliced ERF

(AERF) cDNA"

US-09-021-715-3

US-09-021-715-3

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Job time: 19755 sec

Query Match 16.6%; Score 25.4; DB 4; Length 2432;

Best Local Similarity 68.6%; Pred. No. 18; Mismatches 16; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 tgaccctgggacactcaagagcagctcagcaaaagggaattacagt 52

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DB 2240 TGCCCATGGCGCAGCTCTAGAGACAGCTGGGATGAAGGGTTGACCGGT 2190

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 23:00:49 ; Search time 3054.04 Seconds
(without alignments)
437.657 Million cell updates/sec

Title: US-09-587-574-10
Perfect score: 153
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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189: gb_est120:*

Result				Query				Description			
No.	Score	Match	Length	DB	ID						
1	121	79.1	548	7	AA446378	AA446378	258807	r			
2	116.8	76.3	495	139	BE755017	BE755017	208720	MA			
3	116.8	76.3	546	138	BE668565	BE668565	158407	MA			
4	88.6	57.9	1070	165	BE315156	BE315156	601140956				
5	88.2	57.6	427	149	BE521997	BE521997	UI-R-YO-a				
6	87.6	53.3	319	156	R75687	R75687	Y121006	rl			
7	85	55.6	601	165	BE314898	BE314898	601140035				
8	83.8	54.8	460	140	BE808273	BE808273	213437	MA			
9	83.8	54.8	487	111	AM140896	AM140896	EST290830				
10	83.8	54.8	503	143	BF076794	BF076794	226536	MA			
11	83.8	54.8	562	143	BF076028	BF076028	225414	MA			
12	82.2	53.7	435	3	AA170717	AA170717	ms70a09	r			
13	82.2	53.7	476	165	BE333754	BE333754	us27f06	y			
14	82.2	53.7	516	1	AA028403	AA028403	m121f04	r			
15	82.2	53.7	526	4	AA258709	AA258709	va36f09	r			
16	82.2	53.7	553	3	AA153185	AA153185	ms62d10	r			
17	80	52.3	471	143	BF039925	BF039925	BP250015A				
18	79.8	52.2	443	170	BF889872	BF889872	289473	MA			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	78.2	51.1	672	149	BF526991
20	75.8	49.5	442	31	AV671166
21	67.8	44.3	830	144	BF118962
22	67.2	43.9	238	156	TO71178
23	67.2	43.9	1049	144	BF137964
24	66.6	43.5	369	169	BF7575245
25	57.8	37.8	861	106	BF526080
26	57	37.3	176	115	AM445343
27	54.8	35.3	1053	231	CNS046VM
28	54.4	35.6	1031	231	CNS04RMU
29	52	34.0	654	219	AS315171
30	51.4	33.6	1018	230	CNS03D61
31	51.2	33.5	908	169	BF7889612
32	49.6	32.4	556	165	BE290973
33	49.2	32.2	732	140	BE882875
34	47.4	31.0	241	156	T32063
35	47.4	31.0	284	6	AA355700
36	46.6	30.5	135	115	AM407444
37	46.4	30.3	358	115	AM445734
38	44.8	29.3	913	144	BF178439
39	44.4	29.0	315	137	BE647747
40	43.2	28.2	766	129	AV400665
41	43	28.1	935	230	CNS021YW
42	39.4	25.8	762	230	CNS034Z1
43	38.6	25.2	736	156	T30966
44	38	24.8	549	10	AA69261
45	37.8	24.7	622	116	AW510244
					BF526991 602070270
					AV671166 AV671166
					BF118962 601755316
					TO71178 EST05067 Fee
					BF137964 601784640
					BF7575245 285352 NM
					BF526080 AM526080
					AM445343 81418 MAR
					AL274302 Tetradom
					AL304373 Tetradom
					AZ315171 IM0032J16
					AL238707 Tetradom
					BF7889612 602105217
					BE290973 601084133
					BE882875 601509279
					T32063 EST63287 HU
					AA355700 EST64142
					AM407444 UI-HF-BLUC
					AM445734 82895 MAR
					BF178439 601807890
					BE647747 UI-M-BH1-
					AV400665 AV400665
					AL177521 Tetradom
					AL122807 Tetradom
					T30966 EST75348 HU
					AA69261 HL08054.5
					AW510244 FK1B03.X

ALIGNMENTS

TGTACCAATCTGAAGTGGGGGCGGCCCTTAATTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match	Best Local Similarity	79.1%	Score 121;	DB 7;	Length 548;
Matches 133;	Conservative	0;	Mismatches 20;	Indels	0;
Gaps		0;			
QY 1	ltgacctgtggccacttcaagagcagctcagcaaaaggaaltacaggtattcttc 60				
Db 277	TTGACCCCTGTGGCCACTTTAAAGACGACGCTACACAAAAGGGAATATATGCTATTACTTC 336				
QY 61	aagaagggagatgaagaatttgcctgcggagagcaagttttgaagagatctgggaagcagcg 120				
Db 337	AAAAAAGCAAGCGAAGCATTTTCCCTGTGGAGCGGTGTTTGAGCAAAATCTGGAGGAGATGAG 396				
QY 121	acagtcctcccatgttacgaagcagagatccctg 153				
Db 397	ACGTGCTCTCCGATCTATGAAGCGCGGANTTCG 429				

LOCUS	BE755017	495 bp	mRNA	EST	15-SEP-2000
-------	----------	--------	------	-----	-------------

RESULT 1
AA446378

LOCUS	AAA445378	548 bp	mRNA	EST	03-JUN-1997
DEFINITION	zw58b07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone				
IMAGE:	774229 5', mRNA sequence.				

VERSION AA446378.1 GI:2159043

SOURCE human.

ORGANISM	Homo sapiens
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
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97	97
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99	99
100	100

REFERENCE
AUTHORS
1 (bases 1 to 548)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,

TITLE
,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997

JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LINTL ; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 490.
Location/Qualifiers

```
source      1. .548
/organism="Homo sapiens"
```

```
/db_xref="taxon:9606"  
/clone="IMAGE:774229"
```

```
/clone_lib="Soares_total"
/dev_stage="8-9 weeks"
```

```
/lab_host="DH10B"
/note="Vector: PT7T3D-F
```

polylinker; site_1: Not
was prepared from mRNA

(total) fetus material

BASE COUNT	ORIGIN	141 a	121 c	170 g	116 t
Query Match	Best Local Similarity	86.9%	Score 121;	DB 7;	Length 548;
Matches 133;	Conservative	0;	Mismatches 20;	Indels	0;
0;	Gaps	0;			
OY	1	ttgacctgggaccattcaagagcagctcagcaaaaggaattacagcgtatattc	60		
Db	277	ttgacctgggaccattcaagagcagctcagcaaaaggaattacagcgtatattc	336		
OY	61	aagaagcgagctgaagcaatttcctgcgagcagcttttgaagagatctggaagcagcg	120		
Db	337	aaaaagcagcagctgaagcaatttcctgcgagcagcttttgaagagatctggaagcagcg	396		
OY	121	acagtgctcccatgtacgaagcagcagctcgt	153		
Db	397	acggtgctcccatgtacgaagcagcagctcgt	429		
RESULT 2					
BE755017	495 bp	mRNA	EST	15-SEP-2000	
LOCUS	208720	MARC	2BOV	Bos	taurus
DEFINITION	BE755017				
ACCESSION	BE755017				
VERSION	BE755017.1				
KEYWORDS	EST.				
SOURCE	COV.				
ORGANISM	Bos taurus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
	1 (bases 1 to 495)				
	Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,				
	Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid				
	,W.W. and Keele,J.W.				
	Design and use of four pooled tissue normalized cDNA libraries for				
	EST discovery in cattle				
	Unpublished (2000)				
JOURNAL	Contact: Smith TPL				
COMMENT	USDA, ARS, US Meat Animal Research Center				
	PO Box 166, Clay Center, NE 68933-0166, USA				
	Tel: 402 762 4366				
	Fax: 402 762 4390				
	Email: smith@email.marc.usda.gov				
	Single pass sequencing. Bases called and alt_trimmed with phred				
	v0.980904.e. Vector identified by cross_match with the -minscore 10				
	and -minmatch 12 options.				
	PCR primers				
	FORWARD: AGGAACAGCATGATGACAT				
	BACKWARD: GTTTCACAGTCAAGAG				
	Plate: 56 row: K column: 12				
	Seq primer: ATTGAGTGACACTATAG.				
FEATURES	Location/Qualifiers				
source	1..495				
	/organism="Bos taurus"				
	/db_xref="taxon:9913"				
	/clone_lib="MARC 2BOV"				
	/tissue_type="pooled"				
	/lab_host="DH10B"				
	/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;				
	library made from pooled tissue from testis, thymus,				
	semitendinosus muscle, longissimus muscle, pancreas,				
	adrenal, and endometrium."				
BASE COUNT	103 a	148 c	164 g	80 t	
ORIGIN					

RESULT	5
LOCUS	BF521997
DEFINITION	BF521997 427 bp mRNA EST 11-DEC-2000
ACCESSION	U1-R-Y0-acc-b-09-0-U1.r1 U1-R-Y0 Rattus norvegicus cdna clone
VERSION	U1-R-Y0-acc-b-09-0-U1 5', mRNA sequence.
KEYWORDS	BF521997
SOURCE	BF521997.1 GI:11629964
ORGANISM	EST. Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 427) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996) 97044477 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msouares@iuiowa.uiowa.edu CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LNL (info@elme.lnl.gov). IMAGE ID= 1791410 Seq primer: M13 forward.

FEATURES	Location/Qualifiers
SOURCE	1. .427

```

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-Y0-acc-b-09-0-UI"
/clone_1lb="UI-R-Y0"
/seq_str="ad11t"

```

(/lab_host-DH10B (Life Technologies)" *note-Vector: pTR73D-Pac (Pharmacia)* with a modified polylinker. Site.1: Not I. Site.2: Eco RI. The UI-R-YO library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens), library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-YO) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-YO library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996)".

BASE COUNT	118 a	126 c	113 g	70 t
ORIGIN				

Query Match	57.68;	Score 88.2;	DB 149;	Length 427;
Best Local Similarity	96.88;	Pred. No. 1.4e-17;		
Matches 90; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```
Oy      1 ttgacctgggcactctcaaggagcagctcagcaaaaaagggaatracagtattatttc 600
```

Db 335 TTGACTCTGGGCCACTTCAAGGAGCAGCTCAGCAAAAGGAATTACAGGTATTACTTC 394

[illegible]

RESULT **6**

R75687

LOCUS	R75687	319 bp	mRNA	EST	06-JUN
DEFINITION	y121d06.r1 Soares breast 2NbHst Homo sapiens cDNA clone#				
IMAGE:	158891 5', mRNA sequence.				

VERSION R75687.1 GI:850369

SOURCE	human.
1	1
2	2
3	3
4	4
5	5
6	6
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9	9
10	10
11	11
12	12
13	13
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92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

Eukaryota; Metazoa;

REFERENCE 1 (bases 1 to 319)

, M., Hultman, M., Ku

R., Williamson, A.,

JOURNAL Unpublished (1995)

Washington University

Tel: 314 286 1800

Email: est@watson.wisc.edu

High quality sequencer

This clone is avail

Insert Length: 971

High quality sequen

source	1. .319
--------	---------

/db_xref="

```
/clone="IM
```

/sex="Female"

```
lab_host=
```

modified F

TGT TACCAAT

(Pharmacia

Library we
330 14522

Bonafido."

ORIGIN

Overall Match 57 39

Best Local Similarity	73.5%
Matches	111
Concave+divo	

017 7 455000455000300455000

36

70

80

90

100

110

120

130

140

150

160

170

180

190

200

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63 aaaaaaaatnaaaat

Query Match 57.38; Score 87.6; DB 156; Length 319;

QY 2 tgacctgggccaacttcgaagagcagctcagcaaaaaggaaattacagtatatctca 61
|||||
|||||

62 agaaagcgagtgacggaatttcctcgcgagcagtttttggagagatctggaacgacgaga 121

Db 96 AGAAGTACGACGAGCTTGCAGTGGGCTGTGAGAGAGGTTCCAGAGAGCAGG 155
OY 122 cagtgctcccaagtgacgaagcagagctcct 152
Db 156 CCGTCTGCGCCGCTTTNAGGAGAGATCAT 186

RESULT 7
LOCUS BE314898 601 bp mRNA EST 26-OCT-2000
DEFINITION 601140055F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049328 5',
mRNA sequence.
ACCESSION BE314898
VERSION BE314898.1 GI:9144981
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 601)
NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at: image.llnl.gov
Plate: L1CM93 row: e column: 09
High quality sequence stop: 600.

FEATURES
source
1. 601
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3049328"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 127 a 189 c 194 g 91 t

ORIGIN

Query Match 55.6%; Score 85; DB 165; Length 601;
Best Local Similarity 75.2%; Pred. No. 1.5e-16;
Matches 106; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 2 tgaccctgggcacttcaagagcagctcagcaaaaggaattacaggtattattca 61
Db 367 TCACCTGGGCGCAGTTCAAGAGAGCTGCTGACCAAAAAGCGACGATCACTTCA 426
OY 62 agaagcgagtgagcaatttccttcgagcagtttttgagagatctggagcagaga 121
Db 427 AGAAGTACGACGAGCTTGTACTGTGGGTGAGAGAGGTTGAGAGAGCAGG 486
OY 122 cagtgctcccaagtgacgaagcagagctcct 142
Db 487 CCGTCTGCGCCGCTTTTGAAG 507

RESULT 8

BE808273
LOCUS BE808273 460 bp mRNA EST 20-SEP-2000
DEFINITION 213437 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE808273
VERSION BE808273.1 GI:10239385
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 460)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.M. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 68 row: O column: 3
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source
1. 460
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitepidonous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT 86 a 133 c 166 g 74 t 1 others

ORIGIN

Query Match 54.8%; Score 83.8; DB 140; Length 460;
Best Local Similarity 72.2%; Pred. No. 3.5e-16;
Matches 109; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 2 tgaccctgggcacttcaagagcagctcagcaaaaggaattacaggtattattca 61
Db 147 TCACCTGGGCGCAGTTCAAGAGAGCTGCTGACCAAGAGGCACTACAGTTTACTTCA 206
OY 62 agaagcgagtgagcaatttccttcgagcagtttttgagagatctggagcagaga 121
Db 207 AGAAGTACGACGAGCTTGTACTGTGGGTGAGAGAGGTTGAGAGAGCAGG 266
OY 122 cagtgctcccaagtgacgaagcagagctcct 152
Db 267 CCGTCTGCGCCGCTTTTGAAGATCAT 297

RESULT 9
LOCUS AM140896 487 bp mRNA EST 30-OCT-1999
DEFINITION EST290830 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
RG1A543 5' end similar to GSK-3beta interacting protein Rax1n, mRNA
sequence.
ACCESSION AM140896
VERSION AM140896.1 GI:6160589
KEYWORDS EST.

[illegible]

Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR primers

FORWARD: AGCAACAGCTATGACCAT
BACKWARD: GTTTCACGCACGACG
Plate: 87 row: N column: 19
Seq primer: ATTACGTGACACTATG.

FEATURES

SOURCE

location/Qualifiers

1. 503

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_1id="MARC 2BOV"

/rname_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORF6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT

98 a 146 c 185 g 74 t

ORIGIN

Query Match 54.8%; Score 83.8; DB 143; Length 503;
Best Local Similarity 72.2%; Pred. No. 3,5e-16;
Matches 109; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 2 tgacctgggcactctcaagagcagctccacgaaagggaattaccgcatatcca 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 267 TCACCCTGGGCCAGTGTCAGAGCGTCTGACCAAGGCGAACTACAGGTTCTACTTCA 326
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 62 agaaagcgagtcgacgaatttcctcgcgagcagtcttgagaagatctggagcagcgsa 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 AGAAGTGAAGCAGCAGTTCACGTCGCCGCTGCTGTTCGAAGAGGTGCGTGAAGCACGG 386
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 122 cagtcgtcccacatgltacgaagcgagatcct 152
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 387 CTGTGCTCCCGTCTCTGCAGAGAAGATCAT 417
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11

BFO76028 562 bp mRNA EST 18-OCT-2000

LOCUS 225414 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.

DEFINITION BFO76028

VERSION BFO76028.1 GI:10869476

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

1 (bases 1 to 562)

Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrnkung,S.C., Freking,B.A., Rohrer,G.A., Laegreid ,W.W. and Keale,J.W.

Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers

FORWARD: AGCAACAGCTATGACCAT


```

/issue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCCGACATGATTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Felima
Bonaldo."

```

Query Match	Score	DB	Length
53.7%	82.2	165	476

best locally similarity 1.15%; Pseud. no. 1.1e-12;
Matches 108; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

2 **tgacctggccactcaagagcagctcagcaaaaggaattacagtatatttca** 61

DB 31 TCACCTCGGGCCAGTTCAGGAGCTGCTAACCAAGAGGGGAGCTACAGATATCTACTTTA 90

db 91 AGAAGTCAGTCATGAGTTGACTGTGCTGTGCTATTTCAGAGAGTACGGGAGGATGAGG 150

```

Qy      122  cagtgcctcccatgtacgaagcagatcc  152
          | | | | | | | | | |
Db      151  CCGTCTTGCCCTGCTTTGAAGAAAGATCAT  181

```

RESULT 14
AA028403

LOCUS	516 bp	mRNA	EST	16- AUG-1996
DEFINITION	AA028403	mouse embryo	NbME13.5	14.5 Mus musculus cDNA
	clone IMAGE:464191 5', mRNA sequence.			

ACCESSION	AA028403
VERSION	AA028403.1
KEYWORDS	GI:1494524 EST.

SOURCE ORGANISM

REFERENCE
1 (pages 1 to 516)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus

AUTHORS
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gessel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

TITLE Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HHMI Mouse EST Project

JOURNAL COMMENT
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TEL: 314 286 1800

For more information, contact the
 Fax: 314 286 1810
 Email: mouse@watson.wustl.edu
 This clone is available royalty-free

IMAGE Consortium (infoimage.llnl.gov) for further information.
MGI:278007
See ref. 28M13 and 28M14 from American

FEATURES

- High quality sequence stop: 493.
- Location/Qualifiers

```

1. 510
source
/organism="Mus musculus"
/strain="C57BL/6J"

```

```
/db_xref="taxon:10090"  
/clone="IMAGE:464191"  
/clone_lib="Soares mouse embryo NbME13.5 14.5"
```

```

/issue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes: pr773D-Pac (Pharmacia) with a modified
polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA
was primed with a Not I - 0190(41) primer [5',
TGTACCAATCTGAGAGCGCGCGGAATATTTTTTTTTTTTTTTT
3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2 1; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pr773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fátima Bonaldo. "

```

Query Match	53.78; Score 82.2; DB 1; Length 516;
-------------	--------------------------------------

Best Local Similarity 71.5%; Pred. NO. 1.1e-15;
Matches 108; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 2 tgaacctggccacttcaagagcagctcagcaaaaaggaaattacagtattatcca 61
| | | | | | | | | | | | | | | | | | | | | | | | | | |

Db . 333 TCACCCGTGGGCCAGTTCACAGAGCTGCTAACCAAGAGGGGAGCTACAGATACTACTTTA 392

Db 393 AGAAGTGAGTGTGAGTTGACTGTGCTGTGCTATTGTGAGGAGTACGGGAGGATGAGG 452

Db 453 CCGTCTTGCCCTGTCTTTGAAGAAAGATCAT 483

RESULT 15
AA259709

LOCUS	AA253709	526 bp	mRNA	EST	18-MAR-1997
DEFINITION	va36f09.t1 Soares mouse 3MEL2.5 Mus musculus cDNA clone				
IMAGE:	733481 5', mRNA sequence.				

ACCESSION	AA259709
VERSION	AA259709.1
	GI:1896194

KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
1 (bases 1 to 526)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathia; Muridae; Murinae; Mus

AUTHORS Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubois, J., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.

TITLE Theisling, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HIMI Mouse EST Project

JOURNAL COMMENT
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMT Mouse EST Project

Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This place is available royalty-free through RIN : contact the

IMAGE Consortium (info@image.llnl.gov) f
MGI:450529

seq primer: -20mms rev2 E110M Antisense
High quality sequence stop: 485.
Location/Qualifiers
505

```
source      1. .526
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /sex="Female"
            /age="10000"
```

/db_xref=taxon:10090

```

/clone="IMAGE:73481"
/clone_lib="Soares mouse 3NME12 5"
/sex="unknown"
/tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
/note="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15', TGTACCAATCTGAAGTGGAGCGCGCCCTTATTTTATTTTATTTT
3', on total mouse RNA [provided by Minoru KO, Wayne
State Univ.]; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      111 a      116 c      172 g      127 t
ORIGIN

```

```

Query Match      53.7%; Score 82.2; DB 4; Length 526;
Best Local Similarity 71.5%; Pred. No. 1,1e-15;
Matches 108; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 2 tgacctgggcaactcaagaagcagcagcaaaaaagggaaattacaggtattttca 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 112 TCACCTGGGCGCAGTCAAGAGAGCTCTAACCAAGAGGAGGAGACTACACTTCTTA 171

QY 62 aagaagcgagtgacgaatttgctgcgagcagttttgaagagatctggagcagcaga 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 172 ACAGAGTGAGTGTGACTGTGGTGTGATTGTGAGGAGTACGGGAGGATGAGG 231

QY 122 cagtgcctcccaatgtacgaagcagatcct 152
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 232 CCGTCTTGCGCTGCTTTGAGAGAAAGATCAT 262

```

Search completed: June 6, 2001, 23:00:52
Job time: 15536 sec